

XX AC ADD12949;
 XX DT 01-JAN-2004 (first entry)
 XX DE HCV NS3 probe.
 XX KW double-stranded RNA; dsRNA; infection; NS3 helicase; virucide;
 XX KW antiinflammatory; hepatotropic; hepatitis C virus infection; ss; probe.
 XX OS Hepatitis C virus.
 XX FH Key Location/Qualifiers
 XX FT modified_base 1
 XX FT /*tag= a
 XX FT /mod_base= OTHER
 XX FT /note= "FAM labelled"
 XX FT modified_base 30
 XX FT /*tag= b
 XX FT /mod_base= OTHER
 XX FT /note= "TAMRA labelled"
 XX PN WO2003035876-A1.
 XX PD 01-MAY-2003.
 XX KW 25-OCT-2002; 2002WO-EP011973.
 XX PR 26-OCT-2001; 2001DE-01055280.
 XX PR 29-NOV-2001; 2001DE-01058411.
 XX PR 07-DEC-2001; 2001DE-01060151.
 XX PR 09-JAN-2002; 2002WO-EP000151.
 XX PR 09-JAN-2002; 2002WO-EP000152.
 XX PR 02-AUG-2002; 2002DE-01035621.
 XX PA (RIBO-) RIBOPHARMA AG.
 XX PI Krebs A, John M, Schuppan D, Limmer S, Kreutzer R;
 XX WPI; 2003-430419/40.
 XX DT New double-stranded RNA for treating viral infections, useful especially
 XX PT for hepatitis C infection, is complementary to a region of a positive-
 XX PT strand RNA viral genome.
 XX PS Disclosure; SEQ ID NO 5; 35pp; German.
 XX CC This invention describes a novel use of a double-stranded RNA for
 XX CC treating infections by a (+)-strand RNA virus, where one strand (S1) of
 XX CC dsRNA includes a segment that is at least partly complementary to the
 XX CC translatable region of the viral genome. dsRNA is directed against
 XX CC hepatitis C virus (HCV) and inhibits expression of a polyprotein encoded
 XX CC by the viral genome, preferably a protease or helicase and most
 XX CC particularly the NS3 helicase, with the complementary region, in the
 XX CC reading direction of viral RNA, being upstream of, or within, the
 XX CC helicase coding region. dsRNA has, at least one end, an overhang of 1-4,
 XX CC preferably 2-3 nucleotides particularly at the 3'-end of S1. The second
 XX CC strand (S2) of dsRNA contains a 2-nucleotide overhang at the 3'-end of S1
 XX CC but no overhang at the other end (blunt). A single overhang increases
 XX CC inhibitory activity without causing significant loss of in vivo
 XX CC stability. dsRNA is formulated with a conventional solvent (especially
 XX CC phosphate-buffered saline) or it is incorporated into a micellar
 XX CC structure, particularly a liposome, viral capsid, capsoid or a polymeric
 XX CC nano- or micro-capsule (or it is bound to such capsules). The products of
 XX CC the invention have virucide, antiinflammatory and hepatotropic activity.
 XX CC dsRNA is administered by inhalation, infusion or injection, or orally,
 XX CC especially by intravenous or intraperitoneal injection or infusion. dsRNA
 XX CC is specifically used for treatment of hepatitis C virus infections. dsRNA
 XX CC permanently destroys the integrity of the viral genome. HuH-7 cells were
 XX CC transfected with double-stranded RNA (dsRNA), directed against the NS3
 XX CC coding region of the hepatitis C virus (HCV) genome and a fragment of the
 XX CC HCV genome that replicated stably without formation of infectious
 XX CC particles. Transfection with dsRNA resulted in a 60-fold inhibition of

CC viral RNA production, relative to transfection with an irrelevant control
 CC dsRNA. This sequence represents a probe used to detect the HCV NS3 gene.
 XX
 SQ Sequence 30 BP; 8 A; 8 C; 7 G; 7 T; 0 U; 0 Other;
 Query Match 61.0%; Score 12.8; DB 10; Length 30;
 Best Local Similarity 87.5%; Pred. No. 3.2e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 CGTACGGTCTAATGAC 19
 |||||
 DB 15 CGGACGCTCTAATGAC 30
 RESULT 12
 ABI95516
 ID ABI95516 standard; DNA; 20 BP.
 XX
 AC ABI95516;
 XX
 DT 16-FEB-2002 (first entry)
 XX
 DE Capture oligonucleotide Zip ID#2603 oligo #9.
 XX
 KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.
 XX
 OS Synthetic.
 XX
 PN WO200179548-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010958.
 XX
 PR 14-APR-2000; 2000US-0197271P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;
 XX
 DR WPI; 2002-034366/04.
 XX
 PT Designing capture oligonucleotide probes for use on a support to which
 XX PT complementary oligonucleotides hybridize with little mismatch.
 XX
 PS Example 5; Fig 29; 300pp; English.
 XX
 CC The present invention describes a method (M1) for designing capture
 XX CC oligonucleotide probes (I) for use on a support to which complementary
 XX CC oligonucleotide probes (II) will hybridize with little mismatch, where
 XX CC (I) have melting temperatures within a narrow range. The method is useful
 XX CC for detecting infectious diseases caused by bacterial infectious agents
 XX CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 XX CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 XX CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 XX CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 XX CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 XX CC medinis. The method is also useful for detecting genetic diseases such
 XX CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 XX CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 XX CC involved in DNA amplification, replication, recombination or repair, the
 XX CC cancer is specifically associated with a gene selected from BRCA1 gene,
 XX CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 XX CC method is also used for environmental monitoring, forensics and the food
 XX CC and feed industry, detecting comprises scanning (using e.g. a scanning
 XX CC electron microscope and infrared microscope) the support at the
 XX CC particular sites and identifying if ligation of the oligonucleotide probe
 XX CC sets occurred and correlating (using a computer) identified ligation to a
 XX CC presence or absence of the target nucleotide sequences. ABI92074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention

SQ Sequence 20 BP; 2 A; 4 C; 8 G; 6 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 20;
 Best Local Similarity 78.9%; Pred. NO. 4e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTAATGACCG 21
 ||||| ||||| ||||| |||||
 Db 2 GCGTCTGGTCTAGTGACCG 20

RESULT 13

ABI87602
 ID ABI87602 standard; DNA; 24 BP.

XX AC ABI87602;

XX DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#2603 oligo #1.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX PT Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification
 CC of the present invention

SQ Sequence 24 BP; 2 A; 5 C; 10 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 24;
 Best Local Similarity 78.9%; Pred. NO. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTAATGACCG 21
 ||||| ||||| ||||| |||||
 Db 2 GCGTCTGGTCTAGTGACCG 20

RESULT 14

ABI87603/c
 ID ABI87603 standard; DNA; 24 BP.

XX AC ABI87603;

XX DT 15-FEB-2002 (first entry)

XX DE Capture oligonucleotide Zip ID#2603 oligo #2.

XX KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
 KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
 KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity; cancer;
 KW oncogene; tumour suppressor; human papillomavirus; forensic;
 KW environmental monitoring; food industry; feed industry; ss.

XX OS Synthetic.

XX PN WO200179548-A2.

XX PD 25-OCT-2001.

XX PF 04-APR-2001; 2001WO-US010958.

XX PR 14-APR-2000; 2000US-0197271P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Barany F, Zirvi M, Gerry NP, Favis R, Kliman R;

XX DR WPI; 2002-034366/04.

XX PT Designing capture oligonucleotide probes for use on a support to which
 XX complementary oligonucleotides hybridize with little mismatch.

XX PS Example 5; Fig 25; 300pp; English.

XX The present invention describes a method (M1) for designing capture
 CC oligonucleotide probes (I) for use on a support to which complementary
 CC oligonucleotide probes (II) will hybridise with little mismatch, where
 CC (I) have melting temperatures within a narrow range. The method is useful
 CC for detecting infectious diseases caused by bacterial infectious agents
 CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
 CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
 CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
 CC Epstein-Barr virus and polio virus, and parasitic infectious agents
 CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
 CC medinensis. The method is also useful for detecting genetic diseases such
 CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
 CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
 CC involved in DNA amplification, replication, recombination or repair, the
 CC cancer is specifically associated with a gene selected from BRCA1 gene,
 CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
 CC method is also used for environmental monitoring, forensics and the food
 CC and feed industry, detecting comprises scanning (using e.g. a scanning
 CC electron microscope and infrared microscope) the support at the
 CC particular sites and identifying if ligation of the oligonucleotide probe
 CC sets occurred and correlating (using a computer) identified ligation to a
 CC presence or absence of the target nucleotide sequences. ABI82074 to

CC ABI97546 represent oligonucleotide sequences used in the exemplification
CC of the present invention

XX SQ Sequence 24 BP; 7 A; 10 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 24;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
||||| ||||| |||||
Db 23 GCGTCTGCTCTAGTGACG 5

RESULT 15
ACI25753/c
ID ACI25753 standard; DNA; 25 BP.

XX AC ACI25753;
XX 13-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 25744.

DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.
XX US2003104410-A1.
XX 05-JUN-2003.
XX 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 25744; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 5 A; 9 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 60.0%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
||||| ||||| |||||
Db 25 GCGTTCGCTCTAGGACG 7

RESULT 16
ACK18838
ID ACK18838 standard; DNA; 25 BP.

XX AC ACK18838;
XX 14-OCT-2003 (first entry)
XX Human microarray DNA oligonucleotide SEQ ID NO 118819.

DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.
XX US2003104410-A1.
XX 05-JUN-2003.
XX 15-MAR-2002; 2002US-00098263.
XX 16-MAR-2001; 2001US-0276759P.
XX (AFFY-) AFFYMETRIX INC.
XX Mittmann MP;
XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
XX Southern, Northern or dot-blot hybridization to identify or detect the
XX sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 118819; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
XX acid probes including one of 2,018,500 fully defined sequences, or its
XX perfect match, perfect mismatch, antisense match or antisense mismatch.
XX Also disclosed is a method of gene expression analysis. The array is used
XX in monitoring gene expression levels by hybridisation to a DNA library,
XX in analysis of genetic variation or in hybridisation of tag-labelled
XX compounds. The nucleic acid probes are specifically designed for analysis
XX of at least one target sequence. The method of analysis comprises
XX hybridising at least one or more nucleic acids to at least two or more
XX nucleic acid probes and detecting the hybridisation. The nucleic acid
XX probes are attached to a solid support. The analysis comprises monitoring
XX gene expression levels, identifying biallelic markers or polymorphisms,
XX or family members of a gene and a cross-species comparison. Each of the
XX nucleic acids further comprises a tag sequence. The array of nucleic acid
XX probes is useful in in situ hybridisation, in Southern, Northern or dot-
XX blot hybridisation to identify or detect the sequence or specific
XX mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX primer extensions or in screening cDNA or genomic libraries or subclones
XX for additional subclones containing segments of DNA that have been
XX isolated and previously sequenced. The sequence presented is one of the
XX nucleic acid probes incorporated in the microarray. Note: The sequence
XX data for this patent can also be obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html

Query Match 60.0%; Score 12.6; DB 9; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GCGTACGGTCTTAATGACG 21
| | | | | | | | | |
Db 3 GTGTGCGTCCGAATGACG 21

RESULT 17
ACI56057/c
ID ACI56057 standard; DNA; 25 BP.

XX AC ACI56057;

XX DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 56048:

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW Genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 56048; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 7 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTTAATGAC 19
| | | | | | | | | |
Db 24 TCGAACACGGTGTATGAC 6

RESULT 18
ACK18839
ID ACK18839 standard; DNA; 25 BP.

XX AC ACK18839;

XX DT 14-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 118820.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW Genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 118820; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 6 A; 5 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 9; Length 25;

Best Local Similarity 78.9%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 ||| ||||| ||||| ||
 Db 3 GTGTGCGGTCCAATGACAG 21

RESULT 19
 AAC97127
 ID AAC97127 standard; DNA; 26 BP.
 XX
 AC AAC97127;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE
 XX
 XX Cytochrome b PCR primer: SEQ ID 102.
 XX
 KW Mutation detection; fungi; cytochrome b; strobilurin analogue resistance;
 KW single nucleotide polymorphism; PCR primer; fungal resistance; crop;
 KW fruit; vegetable; ss.
 XX
 OS Venturia inaequalis.
 XX
 PN WO200066773-A2.
 XX
 PD 09-NOV-2000.
 XX
 XX 26-APR-2000; 2000WO-GB001620.
 PF
 PR 30-APR-1999; 95GB-00010100.
 PR 13-MAR-2000; 2000GB-00006004.
 PR 31-MAR-2000; 2000GB-00007901.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Windass JD, Heaney SP, Renwick A, Whitcombe DM, Little S;
 PI Gibson NJ, Theaker J, Stanger CP;
 XX
 DR WPI; 2001-007234/01.
 XX
 XX Detecting a cytochrome b mutation which leads to resistance to
 PT strobilurin analogs or compounds in the same resistance group in fungal
 PT nucleic acid using a single nucleotide polymorphism detection technique.
 XX
 PS Disclosure; Page 35; 173pp; English.
 XX
 CC The present invention relates to a method for detecting mutations in
 CC fungal cytochrome b coding sequences which give rise to resistance to
 CC strobilurin analogues. The method uses a single nucleotide polymorphism
 CC (SNP) detection technique. The present sequence is a PCR primer used in
 CC the method of the present invention. The method is suitable for
 CC monitoring fungal resistance to a strobilurin analogue or a compound in
 CC the same cross resistance group in crops such as cereals, fruit and
 CC vegetables such as canola, sunflower, tobacco, sugarbeet, cotton, soya,
 CC maize, wheat, barley, rice, sorghum, tomatoes, mangoes, peaches, apples,
 CC pears, strawberries, bananas, melons, potatoes and carrot
 XX
 SQ Sequence 26 BP; 7 A; 4 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 26;
 Best Local Similarity 78.9%; Pred. No. 4.1e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GCGTACGGTCTAATGACC 20
 ||| ||||| ||||| ||
 Db 2 CGTGTATGTCATGACC 20

RESULT 20
 AAZ50914
 ID AAZ50914 standard; DNA; 31 BP.
 XX
 AC AAZ50914;
 XX

DT 31-MAY-2000 (first entry)
 XX
 DE PCR primer RO204 to amplify Ptac promoter.
 XX
 KW Plasmid PRAB-84-69; recombinant; beta-casein; PCR primer; Ptac promoter;
 KW casein kinase II alpha subunit; casein kinase II beta subunit;
 KW kanamycin resistance marker; iminopeptidase; genetic stability;
 KW pharmaceutical; nutritional composition; vaccine formulation; ss.
 XX
 OS Unidentified.
 XX
 PN WO200008174-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 06-AUG-1999; 99WO-US017873.
 XX
 PR 07-AUG-1998; 98US-00131028.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Mukerji P, Lemmel SA, Leonard AE, Chaudhary S;
 XX
 DR WPI; 2000-205721/18.
 XX
 XX Recombinant construct useful for producing human milk protein, edible
 PT plant protein, antibody, antigen or hormone, comprises nucleotide
 PT sequences expressing beta-casein protein.
 XX
 PS Example 1; Page 11; 73pp; English.
 XX
 CC The patent discloses a method of producing human milk protein, edible
 CC plant protein, antibody or an antigen in a host cell. It involves
 CC transforming host cells with a vector comprising the gene of interest
 CC linked to a promoter and nucleotide sequences encoding subunits of a
 CC kinase, resistance marker and a peptidase. This method is useful for
 CC improving the genetic stability of a plasmid-containing cell during
 CC fermentation. Proteins produced may be used in pharmaceutical or
 CC nutritional compositions and in vaccine formulations. The present
 CC sequence is that of PCR primer RO204, used to amplify Ptac promoter with
 CC multiple cloning site and rrnBT102 terminator from plasmid PKK223-3. The
 CC PCR product is used for construction of plasmid PRAB-84-69. PRAB-84-69
 CC construct comprises genes encoding human beta-casein, casein kinase II
 CC alpha and beta subunits, bacterial kanamycin resistance marker and
 CC iminopeptidase
 XX
 SQ Sequence 31 BP; 7 A; 6 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 60.0%; Score 12.6; DB 3; Length 31;
 Best Local Similarity 78.9%; Pred. No. 4.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 ||| ||||| ||||| ||
 Db 12 GAGTACTGTCTCATGACCG 30

RESULT 21
 AAT04264
 ID AAT04264 standard; DNA; 33 BP.
 XX
 AC AAT04264;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE Primer #259 for IA beta chain gene.
 XX
 KW Polymerase chain reaction; PCR; primer; amplify;
 KW major histocompatibility complex; MHC; T-cell receptor; TCR;
 KW autoimmune disease; immunodeficiency disease; immune response;
 KW immunoproliferation disease; graft-host rejection; therapy; ss.
 XX
 OS Synthetic.

KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; anti-HCV;
KW viral replication; degenerative; disease state; HBV infection;
KW HCV infection; cirrhosis; liver failure; hepatocellular carcinoma;
KW hepatotropic; cytostatic; virucide; antiinflammatory; ss.
XX Hepatitis C virus.
OS
XX
XX WO200281494-A1.
XX
XX PD 17-OCT-2002.
XX
XX PF 26-MAR-2002; 2002WO-US009187.
XX
XX PR 26-MAR-2001; 2001US-00817879.
XX PR 08-JUN-2001; 2001US-00877478.
XX PR 08-JUN-2001; 2001US-0296876P.
XX PR 24-OCT-2001; 2001US-0335059P.
XX PR 05-DEC-2001; 2001US-0337055P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MACE/) MACEJAK D.
XX PA (MCSW/) MCSWIGGEN J.
XX PA (MORR/) MORRISSEY D.
XX PA (PAVC/) PAVCO P.
XX PA (LEEP/) LEE P.
XX PA (DRAP/) DRAPER K.
XX PA (ROBE/) ROBERTS E.
XX
XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX PI Draper K, Roberts E;
XX
XX DR WPI; 2003-229207/22.
XX
XX PT Novel compound useful for treating cirrhosis, liver failure,
XX PT hepatocellular carcinoma, or condition associated with hepatitis C virus
XX PT infection.
XX
XX PS Claim 1; Page 322; 387pp; English.
XX
XX CC The present invention relates to nucleic acid molecules which modulate
XX CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX CC inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
XX CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX CC as oligonucleotides that specifically bind the Enhancer I region of HBV
XX CC DNA. The nucleic acids may be used to modulate the expression of HBV
XX CC genes and HBV viral replication. Also disclosed is a method for screening
XX CC compounds and/or potential therapies directed against HBV, and compounds
XX CC that modulate the expression and/or replication of HCV. The compounds and
XX CC methods of the invention are useful for the treatment of degenerative and
XX CC disease states related to HBV and HCV infection, replication and gene
XX CC expression such as cirrhosis, liver failure, and hepatocellular
XX CC carcinoma. The present sequence represents one of the anti-HCV nucleic
XX CC acid molecules disclosed in the present invention
XX
XX SQ Sequence 36 BP; 10 A; 6 C; 14 G; 0 T; 5 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 8; Length 36;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
DB 34 TCGCNTCGGCCTAAGGCC 15

RESULT 24
ACN19551

ID ACN19551 standard; RNA; 37 BP.
XX ACN19551;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE WNV Zinzyme SEQ ID NO 19567.
XX
XX KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX KW encephalitis; myocarditis; meningitis; infection; hepatitis;
XX KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX KW Amberyne; Zinzyme; ss.
XX OS
XX West Nile Virus.
XX PN WO200268637-A2.
XX
XX PD 06-SEP-2002.
XX
XX PF 19-OCT-2001; 2001WO-US048350.
XX
XX PR 20-OCT-2000; 2000US-0242411P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX
XX PI Blatt L, Mcswiggen JA;
XX
XX DR WPI; 2002-706994/76.
XX
XX PT New nucleic acid molecule that modulates replication of West Nile Virus
XX PT (WNV). useful for treating a condition related to WNV infection e.g.
XX PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX PS Claim 24; SEQ ID NO 19567; 495pp; English.
XX
XX CC The invention relates to nucleic acid molecules that modulate replication
XX CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX CC treating a condition related to WNV infection e.g. pancreatitis,
XX CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX CC molecule is selected from the group of ribozymes consisting of
XX CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberyne and Zinzyme. The
XX CC nucleic acid molecules further comprise at least five ribose residues, at
XX CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX CC least three of the 5' terminal nucleotides and a 3' end modification of a
XX CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX CC in the specification. The present sequence is that of a nucleic acid
XX CC molecule of the invention
XX
XX SQ Sequence 37 BP; 11 A; 8 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 37;
Best Local Similarity 57.9%; Pred. No. 4.3e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
DB 18 CGAGUGAGGUCUAGUGACC 36

RESULT 25
ACN31602
ID ACN31602 standard; RNA; 37 BP.
XX ACN31602;
XX
XX DT 22-APR-2004 (first entry)
XX
XX DE WNV minus strand Zinzyme SEQ ID NO 31618.

```
XX  WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW  virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW  encephalitis; myocarditis; meningitis; infection; hepatitis;
KW  liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX  Amberzyme; Zinzyme; ss.
XX
OS  West Nile Virus.
XX
PN  WO200268637-A2.
XX
PD  06-SEP-2002.
XX
PF  19-OCT-2001; 2001WO-US048350.
XX
PR  20-OCT-2000; 2000US-0242411P.
XX
PA  (RIBO-) RIBOZYME PHARM INC.
PA  (BLAT/) BLATT L.
PA  (MCSW/) MCSWIGGEN J A.
XX
PI  Blatt L, Mcswiggen JA;
XX  WPI; 2002-706994/76.
XX
DR  New nucleic acid molecule that modulates replication of West Nile Virus
XX  (WNV), useful for treating a condition related to WNV infection e.g.
XX  pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS  Claim 24; SEQ ID NO 31618; 495pp; English.
XX
CC  The invention relates to nucleic acid molecules that modulate replication
XX  of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX  treating a condition related to WNV infection e.g. pancreatitis,
XX  encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX  liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX  molecule is selected from the group of ribozymes consisting of
XX  Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX  nucleic acid molecules further comprise at least five ribose residues, at
XX  least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX  least three of the 5' terminal nucleotides and a 3' end modification of a
XX  3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX  are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX  in the specification. The present sequence is that of a nucleic acid
XX  molecule of the invention
XX
SQ  Sequence 37 BP; 9 A; 9 C; 13 G; 0 T; 6 U; 0 Other;
    Query Match      60.0%; Score 12.6; DB 6; Length 37;
    Best Local Similarity 57.9%; Pred. No. 4.3e+03;
    Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy  2 CGCGTACGGTCTAATGACC 20
Db  18 CGAGUGAGGUCUAGUGACC 36
    |||: |||: |||: |||:
    |||: |||: |||: |||:

RESULT 26
ACN19001
ID  ACN19001 standard; RNA; 37 BP.
XX
AC  ACN19001;
XX
DT  22-APR-2004 (first entry)
XX
DE  WNV Zinzyme SEQ ID NO 19017.
XX
XX  WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW  virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW  encephalitis; myocarditis; meningitis; infection; hepatitis;
KW  liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX  Amberzyme; Zinzyme; ss.
XX
```

```
OS  West Nile Virus.
XX
PN  WO200268637-A2.
XX
PD  06-SEP-2002.
XX
PF  19-OCT-2001; 2001WO-US048350.
XX
PR  20-OCT-2000; 2000US-0242411P.
XX
PA  (RIBO-) RIBOZYME PHARM INC.
PA  (BLAT/) BLATT L.
PA  (MCSW/) MCSWIGGEN J A.
XX
PI  Blatt L, Mcswiggen JA;
XX  WPI; 2002-706994/76.
XX
DR  New nucleic acid molecule that modulates replication of West Nile Virus
XX  (WNV), useful for treating a condition related to WNV infection e.g.
XX  pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
PS  Claim 24; SEQ ID NO 19017; 495pp; English.
XX
CC  The invention relates to nucleic acid molecules that modulate replication
XX  of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX  treating a condition related to WNV infection e.g. pancreatitis,
XX  encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX  liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX  molecule is selected from the group of ribozymes consisting of
XX  Hammerhead, inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
XX  nucleic acid molecules further comprise at least five ribose residues, at
XX  least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX  least three of the 5' terminal nucleotides and a 3' end modification of a
XX  3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX  are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX  in the specification. The present sequence is that of a nucleic acid
XX  molecule of the invention
XX
SQ  Sequence 37 BP; 10 A; 6 C; 15 G; 0 T; 6 U; 0 Other;
    Query Match      60.0%; Score 12.6; DB 6; Length 37;
    Best Local Similarity 57.9%; Pred. No. 4.3e+03;
    Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy  2 CGCGTACGGTCTAATGACC 20
Db  18 CGAGUGAGGUCUAGUGACC 36
    |||: |||: |||: |||:
    |||: |||: |||: |||:

RESULT 27
ACAO7993
ID  ACAO7993 standard; RNA; 37 BP.
XX
AC  ACAO7993;
XX
DT  03-JUN-2003 (first entry)
XX
DE  Necrosis factor kappa B (NFkB) sub-unit modulating zinzyme #97.
XX
XX  Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW  G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;
KW  prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW  stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW  head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW  multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
KW  paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
KW  doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
KW  radiation therapy; inflammatory disease; asthma; diabetes;
KW  rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW  gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW  transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW  allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
```

XX OS Synthetic.

XX FN US2002177568-A1.

XX PD 28-NOV-2002.

XX XX 23-MAY-2001; 2001US-00864785.

XX PR 07-DEC-1992; 92US-00987132.

XX PR 18-MAY-1994; 94US-00245466.

XX PR 15-AUG-1994; 94US-00291932.

XX PR 23-DEC-1996; 96US-00777916.

XX XX (STIN/) STINCHOMB D T.

XX PA (MCSW/) MCSWIGGEN J.

XX PA (DRAP/) DRAPER K G.

XX XX Stinchcomb DT, Mcswiggen J, Draper KG;

XX DR WPI; 2003-340953/32.

XX XX Novel enzymatic nucleic acid molecules which down regulates expression of

XX PT a sequence encoding a subunit of nuclear factor kappa B useful for

XX PT treating cancer, inflammatory disorders and autoimmune diseases.

XX PS Claim 2; Page 39; 72pp; English.

XX XX The invention describes an enzymatic nucleic acid molecule (I) which down

XX CC regulates expression of a sequence encoding a subunit of nuclear factor

XX CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme

XX CC configuration. The enzymatic nucleic acid molecule is adapted to treat

XX CC cancer and is useful for down-regulating REL-A activity in a cell, for

XX CC treating a patient having a condition associated with the level of REL-A.

XX CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in

XX CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and

XX CC antisense nucleic acid molecules are useful for treating breast, lung,

XX CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,

XX CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or

XX CC multidrug resistant cancer. The method involves use of other drug

XX CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or

XX CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

XX CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,

XX CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic

XX CC acid molecules are also useful for treating inflammatory disease such as

XX CC rheumatoid arthritis, testenosis, asthma, Crohn's disease, diabetes,

XX CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft

XX CC rejection, gene therapy applications, ischaemia/reperfusion injury

XX CC (central nervous system (CNS) and myocardial), glomerulonephritis,

XX CC sepsis, allergic airway inflammation, inflammatory bowel disease or

XX CC infection. This sequence represents an enzymatic nucleic acid used to

XX CC modulate the function of a necrosis factor kappa B sub-unit

XX SQ Sequence 37 BP; 11 A; 9 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 8; Length 37;

Best Local Similarity 57.9%; Pred. No. 4.3e+03;

Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTATGACC 20

Db 18 CGAGUGAGGUCUAAUGGCC 36

RESULT 28

ABK04673/c

ID ABK04673 standard; RNA; 38 BP.

XX AC ABK04673;

XX DT 12-MAR-2002 (first entry)

XX DE Human NOGO Inozyme substrate sequence #150.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;

KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;

KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;

KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;

KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;

KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;

KW inflammatory arthropathy; central nervous system injury;

KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;

KW chemotherapeutic-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;

KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200159103-A2.

XX PD 16-AUG-2001.

XX PF 09-FEB-2001; 2001WO-US004273.

XX PR 11-FEB-2000; 2000US-0181797P.

XX PR 28-FEB-2000; 2000US-0185516P.

XX PR 06-MAR-2000; 2000US-0187128P.

XX XX (RIBO-) RIBOZYME PHARM INC.

XX PA (BLAT/) BLATT L.

XX PA (MCSW/) MCSWIGGEN J.

XX XX (CHOW/) CHOWKIRA B M.

XX PI Blatt L, Mcswiggen J, Chowkira BM;

XX DR WPI; 2001-607195/69.

XX XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX PT constructs, which down regulate expression of a CD20 gene or neurite

XX PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX PT central nervous system injury.

XX PS Claim 89; Page 80; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates

XX expression of a CD20 gene and a nucleic acid molecule which down

XX regulates expression of a neurite growth inhibitor gene (NOGO). The

XX nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a

XX DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule

XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or

XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

XX with a VGY motif). The CD20-targeting nucleic acid is used to cleave RNA

XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.

XX Furthermore, it may be contacted with a cell to reduce CD20 activity of

XX the cell and treat a patient having a condition associated with the level

XX of CD20. The treatment may further comprise the use of one or more

XX therapies. In particular, the CD20 targeting nucleic acid may be used to

XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-

XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell

XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,

XX immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-

XX targeting nucleic acid is used to cleave RNA of the NOGO gene in the

XX presence of a divalent cation that is preferably Mg²⁺. Furthermore, the

XX nucleic acid may be contacted with a cell to reduce NOGO activity of the

XX cell and treat a patient having a condition associated with the level of

XX NOGO. The treatment may further comprise the use of one or more

XX therapies. In particular, the NOGO-targeting nucleic acid may be used to

XX treat central nervous system (CNS) injury and cerebrovascular accident

XX (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),

XX chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),

XX Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

XX disease, muscular dystrophy, and/or other neurodegenerative disease

XX states which respond to the modulation of NOGO expression. The present

CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 38 BP; 9 A; 8 C; 14 G; 0 T; 6 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| ||||| |||||
 DB 35 TCGCNTTCGGCTTAACGGCC 16
 RESULT 29
 ABK04649/c
 ID ABK04649 standard; RNA; 38 BP.
 XX
 AC ABK04649;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme substrate sequence #126.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 XX WPI; 2001-607195/69.
 XX
 DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 89; Page 80; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA

CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targetting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence
 XX
 SQ Sequence 38 BP; 6 A; 12 C; 14 G; 0 T; 5 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 4; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| ||||| |||||
 DB 35 TCGCNTTCGGCTTAACGGCC 16
 RESULT 30
 ABQ72447
 ID ABQ72447 standard; DNA; 38 BP.
 XX
 AC ABQ72447;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE PCR primer MKV24 for ScFv and Fab library generation.
 XX
 KW PCR; primer; replicable genetic package; phage display; scFv; Fab;
 KW heavy chain variable region; light chain variable region; HP6002; HP6025;
 KW HP6054; ss.
 XX
 OS Synthetic.
 XX
 PN WO200194950-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 05-JUN-2001; 2001WO-US018421.
 XX
 PR 05-JUN-2000; 2000US-0209503P.
 PR 04-JUN-2001; 2001US-00874547.
 XX
 XX (ZYOM-) ZYOMYX INC.
 PA
 XX Nock S, Kassner PD;
 PI
 XX WPI; 2002-519063/55.
 DR
 XX Screening phase displayed peptides, for obtaining a replicable genetic
 PT package (RGP) that displays a fusion protein that binds to a target
 PT molecule, comprises contacting the molecule with an uncleared cell
 PT culture comprising the RGPs.
 PT
 XX

PS Example 1; Page 20; 39pp; English.

XX The present invention relates to a method for screening replicable
 CC genetic packages (RGP) to obtain RGP that display on their surface a
 CC fusion protein that specifically binds to a target molecule. The method
 CC comprises contacting a target molecule with an uncleared cell culture
 CC having: (i) RGP, each displaying a fusion protein having a surface-
 CC displayed RGP polypeptide and a potential binding polypeptide; and (ii)
 CC cells in which RGP were amplified. Phage displaying antibody fragments
 CC scfvs or Fabs were generated by PCR amplification of cDNA corresponding
 CC to the heavy and light chain variable regions from the HP6002, HP6025,
 CC and HP6054 hybridomas. The regions were amplified using the PCR primers
 CC ABQ72365-ABQ72448

XX SQ Sequence 38 BP; 8 A; 13 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 78.9%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGACC 20
 ||||| ||| |||||
 Db 12 CGCGGACATTGTAATGACC 30

RESULT 31
 ABK20307/c
 ID ABK20307 standard; RNA; 38 BP.

XX AC ABK20307;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG inozyme, Seq ID No 2954.

XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

XX OS Homo sapiens.

XX PN WO200188124-A2.

XX XX 22-NOV-2001.

XX PF 16-MAY-2001; 2001WO-US015866.

XX PR 16-MAY-2000; 2000US-00572021.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX DR WPI; 2002-082995/11.

XX Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX PS Claim 5; Page 74; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention

XX SQ Sequence 38 BP; 7 A; 10 C; 14 G; 0 T; 6 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 75.0%; Pred. No. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||| |||||
 Db 35 TCGCNTTCGGCCTAACGCC 16

RESULT 32
 ABK20420/c

XX ID ABK20420 standard; RNA; 38 BP.

XX AC ABK20420;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG inozyme, Seq ID No 3067.

XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

XX OS Homo sapiens.

XX PN WO200188124-A2.

XX XX 22-NOV-2001.

XX PF 16-MAY-2001; 2001WO-US015866.

XX PR 16-MAY-2000; 2000US-00572021.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX DR WPI; 2002-082995/11.

XX Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX XX

PS Claim 5; Page 76; 149pp; English.

XX The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX Sequence 38 BP; 8 A; 6 C; 15 G; 0 T; 8 U; 1 Other;

SQ

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||

Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 33

ABK58655/c

ID ABK58655 standard; RNA; 38 BP.

XX

AC ABK58655;

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3026.

XX

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

KW acetylcysteine.

XX

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PN 14-FEB-2002.

XX

PD 09-AUG-2001; 2001WO-US024970.

XX

PF 09-AUG-2000; 2000US-0224383P.

XX

PR (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX

DR WPI; 2002-217145/27.

XX Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.

XX

PS Claim 5; Page 71; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down

CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes

CC by cleaving RNA derived from the genes. The nucleic acid sequences are

CC useful as pharmaceutical agents for treating conditions such as chronic

CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic

CC fibrosis, obstructive bowel syndrome and any other diseases or conditions

CC that are related to or will respond to the levels of CLCA1 in a cell or

CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,

CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises

CC the use of one or more therapies under conditions suitable for the

CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,

CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The

CC nucleic acids of the invention are also used as diagnostic tools to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of CLCA1 RNA in a cell. This sequence represents an

XX enzymatic nucleic acid molecule of the invention

SQ Sequence 38 BP; 8 A; 7 C; 12 G; 0 T; 10 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;

Best Local Similarity 75.0%; Pred. No. 4.3e+03;

Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||

Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 34

ABK58826/c

ID ABK58826 standard; RNA; 38 BP.

XX

AC ABK58826;

XX

DT 02-JUL-2002 (first entry)

XX

DE Human CLCA1 gene enzymatic nucleic acid #3197.

XX

XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;

KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;

KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;

KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

KW acetylcysteine.

XX

OS Homo sapiens.

XX

PN WO200211674-A2.

XX

PN 14-FEB-2002.

XX

PD 09-AUG-2001; 2001WO-US024970.

XX

PF 09-AUG-2000; 2000US-0224383P.

XX

PR (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

XX

XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

XX

DR WPI; 2002-217145/27.

XX

PT Enzymatic polynucleotide that down regulates expression of chloride

PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.
 PS Claim 5; Page 76; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
 CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 SQ Sequence 38 BP; 9 A; 9 C; 12 G; 0 T; 7 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 75.0%; Pred. NO. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| |||||
 Db 35 TCGCNTTCGGCCTAACGGCC 16
 RESULT 35
 ACN17900/c
 ID ACN17900 standard; RNA; 38 BP.
 AC ACN17900;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Inozyme SEQ ID NO 17916.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 FN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 DR WPI; 2002-706994/76.
 XX
 CC New nucleic acid molecule that modulates replication of West Nile Virus
 CC (WNV), useful for treating a condition related to WNV infection e.g.
 CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 24; SEQ ID NO 17916; 495pp; English.
 XX

CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention
 XX
 SQ Sequence 38 BP; 7 A; 9 C; 12 G; 0 T; 9 U; 1 Other;
 Query Match 60.0%; Score 12.6; DB 6; Length 38;
 Best Local Similarity 75.0%; Pred. NO. 4.3e+03;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 TCGCGTACGGTCTAATGACC 20
 ||||| ||||| ||||| |||||
 Db 35 TCGCNTTCGGCCTAACGGCC 16
 RESULT 36
 ACN17240/c
 ID ACN17240 standard; RNA; 38 BP.
 XX
 AC ACN17240;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE WNV Inozyme SEQ ID NO 17243.
 XX
 KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 FN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;
 XX
 DR WPI; 2002-706994/76.
 XX
 CC New nucleic acid molecule that modulates replication of West Nile Virus
 CC (WNV), useful for treating a condition related to WNV infection e.g.
 CC pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 PS Claim 24; SEQ ID NO 17243; 495pp; English.
 XX
 CC The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 38 BP; 6 A; 6 C; 15 G; 0 T; 10 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 37
ACN16711/c
ID ACN16711 standard; RNA; 38 BP.

XX ACN16711;

XX 22-APR-2004 (first entry)

XX WNV Inozyme SEQ ID NO 16714.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 16714; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 38 BP; 9 A; 11 C; 11 G; 0 T; 6 U; 1 Other;
Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 38

ACN30373/c

ID ACN30373 standard; RNA; 38 BP.

XX ACN30373;

XX 22-APR-2004 (first entry)

XX WNV minus strand Inozyme SEQ ID NO 30389.

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 30389; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 7 U; 1 Other;

Query Match 60.0%; Score 12.6; DB 6; Length 38;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||| | ||| ||| |||
Db 35 TCGCNTTCGGCCCTAACGGCC 16

RESULT 39

ACN29690/c
ID ACN29690 standard; RNA; 38 BP.

XX
AC ACN29690;

XX
DT 22-APR-2004 (first entry)

XX
DE WNV minus strand Inozyme SEQ ID NO 29706.

XX
KW WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KW viricide; neuroprotective; antibacterial; replication; pancreatitis;
KW encephalitis; myocarditis; meningitis; infection; hepatitis;
KW liver failure; cancer; cirrhosis; Hammerhead; DNzyme;
KW Amberzyme; Zinzyme; ss.

XX West Nile Virus.

XX
PN WO200268637-A2.

XX PD 06-SEP-2002.

XX
PF 19-OCT-2001; 2001WO-US048350.

XX
PR 20-OCT-2000; 2000US-0242411P.

XX
PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.

XX
PI Blatt L, Mcswiggen JAXX WPI; 2002-706994/76.
DR

XX
PT New nucleic acid mol

PT (WNV), useful for treating a condition related to WNV infection e.g. pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX
PS Claim 24; SEQ ID NO 29706; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

Sequence 38 BP; 7 A; 11 C; 13 G; 0 T; 6 U; 1 Other;
XX SQ

Query Match	60.0%	Score 12.6;	DB 6;	Length 38;
Best Local Similarity	75.0%;	Pred. No. 4.3e+03;		
Matches 15;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||| | | | | | | |
Db 35 TCGCNTTCGGCCTAACGGCC 16

RECIT T AD

RESUL 40
ACN27931/c

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 24.3034 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631b-2

Perfect score: 21

Sequence: 1 tcgcgtacggctaatgacgc 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents_NA.*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCUTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.2	62.9	35	US-09-056-052-12	Sequence 12, Appl
C 2	13.2	62.9	39	US-09-056-052-13	Sequence 13, Appl
C 3	12.6	60.0	31	US-09-131-028A-17	Sequence 17, Appl
C 4	12.6	60.0	33	US-08-207-481-29	Sequence 29, Appl
C 5	12.6	60.0	33	PCT-US95-02689-31	Sequence 31, Appl
C 6	12.6	60.0	38	US-09-371-722B-11935	Sequence 11935, A
C 7	12.6	60.0	38	US-09-371-722B-13181	Sequence 13181, A
C 8	12.6	60.0	38	US-09-371-722B-13811	Sequence 13811, A
C 9	12.6	60.0	38	US-08-874-547-83	Sequence 83, Appl
C 10	12.4	59.0	38	US-08-373-124A-1680	Sequence 1680, Ap
C 11	12.4	59.0	38	US-08-435-628-1680	Sequence 1680, Ap
C 12	12.2	58.1	20	US-09-198-452A-1954	Sequence 4954, Ap
C 13	12.2	58.1	21	5451502-8	Patent No. 5451502
C 14	12.2	58.1	41	US-09-313-221A-19	Sequence 19, Appl
C 15	12.2	57.1	25	US-08-860-882A-75	Sequence 75, Appl
C 16	12.2	57.1	25	US-09-011-769A-61	Sequence 61, Appl
C 17	12.2	57.1	29	US-09-814-351-25	Sequence 25, Appl
C 18	12.2	57.1	32	US-09-709-103-34	Sequence 34, Appl
C 19	12.2	57.1	32	US-09-439-410A-34	Sequence 34, Appl
C 20	12.2	57.1	38	US-09-371-722B-7357	Sequence 7357, Ap
C 21	12.2	57.1	38	US-09-371-722B-7797	Sequence 7797, Ap
C 22	12.2	57.1	38	US-09-371-722B-8104	Sequence 8104, Ap
C 23	12.2	57.1	38	US-09-371-722B-8341	Sequence 8341, Ap
C 24	12.2	57.1	38	US-09-371-722B-9392	Sequence 9392, Ap
C 25	12.2	57.1	38	US-09-371-722B-9781	Sequence 9781, Ap
C 26	12.2	57.1	38	US-09-371-722B-9974	Sequence 9974, Ap
C 27	12.2	57.1	38	US-09-371-722B-10321	Sequence 10321, A

C 28	12	57.1	38	4	US-09-371-772B-10352	Sequence 10352, A
C 29	12	57.1	38	4	US-09-371-772B-10512	Sequence 10512, A
C 30	11.6	55.2	20	3	US-09-172-045-20	Sequence 20, Appl
C 31	11.6	55.2	20	4	US-09-342-325C-20	Sequence 20, Appl
C 32	11.6	55.2	35	3	US-09-056-052-10	Sequence 10, Appl
C 33	11.6	55.2	37	4	US-10-009-332-10	Sequence 10, Appl
C 34	11.6	55.2	38	4	US-09-371-772B-11413	Sequence 11413, A
C 35	11.6	55.2	38	4	US-09-371-772B-12074	Sequence 12074, A
C 36	11.6	55.2	38	4	US-09-371-772B-12155	Sequence 12155, A
C 37	11.6	55.2	38	4	US-09-371-772B-12380	Sequence 12380, A
C 38	11.6	55.2	38	4	US-09-371-772B-12396	Sequence 12396, A
C 39	11.6	55.2	38	4	US-09-371-772B-13189	Sequence 13189, A
C 40	11.6	55.2	38	4	US-09-371-772B-13450	Sequence 13450, A
C 41	11.6	55.2	39	3	US-09-056-052-11	Sequence 11, Appl
C 42	11.6	55.2	39	3	US-09-198-955A-26	Sequence 26, Appl
C 43	11.6	55.2	39	3	US-09-694-531-26	Sequence 26, Appl
C 44	11.6	55.2	39	4	US-10-072-152-26	Sequence 26, Appl
C 45	11.4	54.3	27	4	US-09-877-243A-11	Sequence 11, Appl
C 46	11.4	54.3	27	4	US-09-877-243A-12	Sequence 12, Appl
C 47	11.4	54.3	28	3	US-09-518-386B-31	Sequence 31, Appl
C 48	11.4	54.3	37	2	US-08-527-060-30	Sequence 30, Appl
C 49	11.4	54.3	43	1	US-08-616-133-5	Sequence 5, Appl
C 50	11.4	54.3	43	1	US-08-802-985-5	Sequence 5, Appl
C 51	11.4	54.3	44	1	US-08-452-083-17	Sequence 17, Appl
C 52	11.4	54.3	44	1	US-08-452-083-18	Sequence 18, Appl
C 53	11.2	53.3	28	3	US-08-781-620B-14	Sequence 14, Appl
C 54	11.2	53.3	31	3	US-08-860-904-23	Sequence 23, Appl
C 55	11.2	53.3	31	3	US-08-679-645-388	Sequence 388, Ap
C 56	11.2	53.3	34	3	US-09-205-114-3	Sequence 3, Appl
C 57	11.2	53.3	34	4	US-10-038-520-3	Sequence 3, Appl
C 58	11.2	53.3	38	4	US-09-874-547-65	Sequence 65, Appl
C 59	11.2	53.3	42	2	US-08-343-443B-55	Sequence 55, Appl
C 60	11.2	53.3	48	6	5240845-9	Patent No. 5240845
C 61	11.2	53.3	48	6	5240845-10	Patent No. 5240845
C 62	11	52.4	17	3	US-08-584-040-8046	Sequence 8046, Ap
C 63	11	52.4	17	3	US-08-584-040-8047	Sequence 8047, Ap
C 64	11	52.4	17	4	US-09-371-772B-3829	Sequence 3829, Ap
C 65	11	52.4	17	4	US-09-371-772B-3830	Sequence 3830, Ap
C 66	11	52.4	20	4	US-09-422-978-6875	Sequence 6875, Ap
C 67	11	52.4	20	4	US-09-198-452A-5503	Sequence 5503, Ap
C 68	11	52.4	22	4	US-10-270-313-4	Sequence 4, Appl
C 69	11	52.4	24	2	US-08-324-003A-6	Sequence 6, Appl
C 70	11	52.4	24	2	US-08-324-003A-7	Sequence 7, Appl
C 71	11	52.4	24	3	US-08-937-993-44	Sequence 44, Appl
C 72	11	52.4	24	4	US-09-755-836-6	Sequence 6, Appl
C 73	11	52.4	24	4	US-09-755-836-7	Sequence 7, Appl
C 74	11	52.4	32	4	US-09-527-073-15	Sequence 15, Appl
C 75	11	52.4	36	2	US-08-709-874A-29	Sequence 29, Appl
C 76	11	52.4	36	2	US-08-897-340-8	Sequence 8, Appl
C 77	11	52.4	36	3	US-09-252-329-8	Sequence 29, Appl
C 78	11	52.4	36	3	US-09-104-382-29	Sequence 29, Appl
C 79	11	52.4	36	4	US-09-833-555-29	Sequence 29, Appl
C 80	11	52.4	37	4	US-09-629-732-12	Sequence 12, Appl
C 81	11	52.4	38	4	US-09-371-772B-7156	Sequence 7156, Ap
C 82	11	52.4	38	4	US-09-371-772B-7161	Sequence 7161, Ap
C 83	11	52.4	38	4	US-09-371-772B-7794	Sequence 7794, Ap
C 84	11	52.4	38	4	US-09-371-772B-9089	Sequence 9089, Ap
C 85	11	52.4	38	4	US-09-371-772B-9378	Sequence 9378, Ap
C 86	11	52.4	38	4	US-09-371-772B-9462	Sequence 9462, Ap
C 87	11	52.4	38	4	US-09-371-772B-9690	Sequence 9690, Ap
C 88	11	52.4	38	4	US-09-371-772B-9720	Sequence 9720, Ap
C 89	11	52.4	38	4	US-09-371-772B-9731	Sequence 9731, Ap
C 90	11	52.4	38	4	US-09-371-772B-9766	Sequence 9766, Ap
C 91	11	52.4	38	4	US-09-371-772B-9773	Sequence 9773, Ap
C 92	11	52.4	38	4	US-09-371-772B-10480	Sequence 10480, A
C 93	11	52.4	38	4	US-09-371-772B-10654	Sequence 10654, A
C 94	11	52.4	38	4	US-09-371-772B-10718	Sequence 10718, A
C 95	11	52.4	38	4	US-09-371-772B-10776	Sequence 10776, A
C 96	11	52.4	38	4	US-09-371-772B-10822	Sequence 10822, A
C 97	11	52.4	38	4	US-09-371-772B-10962	Sequence 10962, A
C 98	11	52.4	38	4	US-09-371-772B-11224	Sequence 11224, A
C 99	11	52.4	38	4	US-09-371-772B-11244	Sequence 11244, A
C 100	11	52.4	38	4	US-09-371-772B-11261	Sequence 11261, A

C 101	11	52.4	38	4	US-09-371-772B-11301	Sequence 11301, A	174	11	52.4	38	4	US-09-874-547-79	Sequence 79, Appl
C 102	11	52.4	38	4	US-09-371-772B-11309	Sequence 11309, A	175	11	52.4	38	4	US-09-874-547-84	Sequence 84, Appl
C 103	11	52.4	38	4	US-09-371-772B-11358	Sequence 11358, A	176	11	52.4	40	3	US-09-133-914-5	Sequence 5, Appl
C 104	11	52.4	38	4	US-09-371-772B-11365	Sequence 11365, A	C 177	11	52.4	40	3	US-09-469-197-5	Sequence 5, Appl
C 105	11	52.4	38	4	US-09-371-772B-11401	Sequence 11401, A	C 178	11	52.4	40	4	US-09-949-109-5	Sequence 238, App
C 106	11	52.4	38	4	US-09-371-772B-11624	Sequence 11624, A	C 179	11	52.4	42	1	US-08-433-126A-238	Sequence 238, App
C 107	11	52.4	38	4	US-09-371-772B-11674	Sequence 11674, A	C 180	11	52.4	42	2	US-08-433-124A-238	Sequence 238, App
C 108	11	52.4	38	4	US-09-371-772B-11776	Sequence 11776, A	181	11	52.4	42	2	US-08-846-338-17	Sequence 17, Appl
C 109	11	52.4	38	4	US-09-371-772B-11790	Sequence 11790, A	C 182	11	52.4	42	3	US-08-976-413A-238	Sequence 238, App
C 110	11	52.4	38	4	US-09-371-772B-11810	Sequence 11810, A	C 183	11	52.4	42	5	PCT-US96-06059-238	Sequence 11, Appl
C 111	11	52.4	38	4	US-09-371-772B-11831	Sequence 11831, A	184	10.8	51.4	19	3	US-08-072-064-11	Sequence 37, Appl
C 112	11	52.4	38	4	US-09-371-772B-11859	Sequence 11859, A	185	10.8	51.4	20	2	US-08-557-128-37	Sequence 5, Appl
C 113	11	52.4	38	4	US-09-371-772B-11880	Sequence 11880, A	186	10.8	51.4	20	4	US-09-930-589-5	Sequence 1315, Ap
C 114	11	52.4	38	4	US-09-371-772B-11897	Sequence 11897, A	187	10.8	51.4	27	3	US-08-584-040-1315	Sequence 6604, Ap
C 115	11	52.4	38	4	US-09-371-772B-11904	Sequence 11904, A	188	10.8	51.4	27	3	US-08-584-040-6604	Sequence 6805, Ap
C 116	11	52.4	38	4	US-09-371-772B-11924	Sequence 11924, A	189	10.8	51.4	27	3	US-08-584-040-6805	Sequence 26, Appl
C 117	11	52.4	38	4	US-09-371-772B-11927	Sequence 11927, A	190	10.8	51.4	31	3	US-09-195-666A-26	Sequence 26, Appl
C 118	11	52.4	38	4	US-09-371-772B-12021	Sequence 12021, A	C 191	10.8	51.4	31	3	US-09-635-705-26	Sequence 26, Appl
C 119	11	52.4	38	4	US-09-371-772B-12024	Sequence 12024, A	C 192	10.8	51.4	31	4	US-09-634-858A-26	Sequence 26, Appl
C 120	11	52.4	38	4	US-09-371-772B-12030	Sequence 12030, A	C 193	10.8	51.4	31	4	US-08-869-927C-26	Sequence 23, Appl
C 121	11	52.4	38	4	US-09-371-772B-12063	Sequence 12063, A	C 194	10.8	51.4	34	2	US-08-319-866-23	Sequence 23, Appl
C 122	11	52.4	38	4	US-09-371-772B-12108	Sequence 12108, A	C 195	10.8	51.4	34	4	US-08-809-917-23	Sequence 407, App
C 123	11	52.4	38	4	US-09-371-772B-12168	Sequence 12168, A	C 196	10.8	51.4	36	1	US-08-363-240A-407	Sequence 812, App
C 124	11	52.4	38	4	US-09-371-772B-12194	Sequence 12194, A	197	10.8	51.4	36	2	US-08-232-820A-812	Sequence 812, App
C 125	11	52.4	38	4	US-09-371-772B-12218	Sequence 12218, A	C 198	10.8	51.4	36	3	US-08-071-845-812	Sequence 635, App
C 126	11	52.4	38	4	US-09-371-772B-12281	Sequence 12281, A	C 199	10.8	51.4	38	1	US-08-435-628-635	Sequence 8412, Ap
C 127	11	52.4	38	4	US-09-371-772B-12284	Sequence 12284, A	200	10.8	51.4	38	1	US-09-371-772B-8412	Sequence 10476, A
C 128	11	52.4	38	4	US-09-371-772B-12288	Sequence 12288, A	201	10.8	51.4	38	4	US-09-371-772B-10476	Sequence 10663, A
C 129	11	52.4	38	4	US-09-371-772B-12310	Sequence 12310, A	202	10.8	51.4	38	4	US-09-371-772B-10663	Sequence 18, Appl
C 130	11	52.4	38	4	US-09-371-772B-12330	Sequence 12330, A	203	10.8	51.4	39	2	US-08-467-963C-18	Sequence 18, Appl
C 131	11	52.4	38	4	US-09-371-772B-12360	Sequence 12360, A	204	10.8	51.4	39	2	US-08-838-189D-18	Sequence 18, Appl
C 132	11	52.4	38	4	US-09-371-772B-12375	Sequence 12375, A	205	10.8	51.4	39	3	US-08-852-344D-18	Sequence 18, Appl
C 133	11	52.4	38	4	US-09-371-772B-12455	Sequence 12455, A	206	10.8	51.4	39	3	US-08-344-639E-18	Sequence 18, Appl
C 134	11	52.4	38	4	US-09-371-772B-12461	Sequence 12461, A	207	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 135	11	52.4	38	4	US-09-371-772B-12503	Sequence 12503, A	208	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 136	11	52.4	38	4	US-09-371-772B-12557	Sequence 12557, A	209	10.8	51.4	39	3	US-08-467-969A-18	Sequence 18, Appl
C 137	11	52.4	38	4	US-09-371-772B-12588	Sequence 12588, A	210	10.8	51.4	39	3	US-08-001-554A-18	Sequence 22, Appl
C 138	11	52.4	38	4	US-09-371-772B-12598	Sequence 12598, A	C 211	10.8	51.4	45	1	US-08-483-415-22	Sequence 18, Appl
C 139	11	52.4	38	4	US-09-371-772B-12636	Sequence 12636, A	C 212	10.8	51.4	45	6	5487983-19	Patent No. 5487983
C 140	11	52.4	38	4	US-09-371-772B-12669	Sequence 12669, A	C 213	10.6	50.5	18	3	US-09-156-807-25	Sequence 25, Appl
C 141	11	52.4	38	4	US-09-371-772B-12681	Sequence 12681, A	C 214	10.6	50.5	18	4	US-09-387-341-127	Sequence 127, App
C 142	11	52.4	38	4	US-09-371-772B-12685	Sequence 12685, A	C 215	10.6	50.5	18	4	US-09-422-978-5416	Sequence 5416, Ap
C 143	11	52.4	38	4	US-09-371-772B-12700	Sequence 12700, A	C 216	10.6	50.5	21	3	US-09-344-520-3	Sequence 3, Appl
C 144	11	52.4	38	4	US-09-371-772B-12700	Sequence 12700, A	C 217	10.6	50.5	23	3	US-09-275-680-13	Sequence 13, Appl
C 145	11	52.4	38	4	US-09-371-772B-13192	Sequence 13192, A	C 218	10.6	50.5	24	3	US-08-624-655A-3	Sequence 3, Appl
C 146	11	52.4	38	4	US-09-371-772B-13218	Sequence 13218, A	C 219	10.6	50.5	30	4	US-09-293-427-8	Sequence 8, Appl
C 147	11	52.4	38	4	US-09-371-772B-13226	Sequence 13226, A	220	10.6	50.5	30	4	US-09-859-724-2	Sequence 2, Appl
C 148	11	52.4	38	4	US-09-371-772B-13246	Sequence 13246, A	C 221	10.6	50.5	34	4	US-09-387-375-6	Sequence 6, Appl
C 149	11	52.4	38	4	US-09-371-772B-13253	Sequence 13253, A	C 222	10.6	50.5	34	4	US-10-041-400A-6	Sequence 11, Appl
C 150	11	52.4	38	4	US-09-371-772B-13421	Sequence 13421, A	C 223	10.6	50.5	36	1	US-08-074-121-11	Sequence 11, Appl
C 151	11	52.4	38	4	US-09-371-772B-13441	Sequence 13441, A	C 224	10.6	50.5	36	5	PCT-US94-06447-11	Sequence 517, App
C 152	11	52.4	38	4	US-09-371-772B-13487	Sequence 13487, A	C 225	10.6	50.5	37	3	US-08-471-039-517	Sequence 517, App
C 153	11	52.4	38	4	US-09-371-772B-13518	Sequence 13518, A	C 226	10.6	50.5	37	3	US-08-559-390-517	Sequence 517, App
C 154	11	52.4	38	4	US-09-371-772B-13529	Sequence 13529, A	C 227	10.6	50.5	37	5	PCT-US93-11198-517	Sequence 517, App
C 155	11	52.4	38	4	US-09-371-772B-13591	Sequence 13591, A	C 228	10.6	50.5	38	4	US-09-371-772B-11237	Sequence 11237, A
C 156	11	52.4	38	4	US-09-371-772B-13633	Sequence 13633, A	C 229	10.6	50.5	38	4	US-09-371-772B-11239	Sequence 11239, A
C 157	11	52.4	38	4	US-09-371-772B-13652	Sequence 13652, A	C 230	10.6	50.5	38	4	US-09-371-772B-11295	Sequence 11295, A
C 158	11	52.4	38	4	US-09-371-772B-13669	Sequence 13669, A	C 231	10.6	50.5	38	4	US-09-371-772B-11305	Sequence 11305, A
C 159	11	52.4	38	4	US-09-371-772B-13681	Sequence 13681, A	C 232	10.6	50.5	38	4	US-09-371-772B-11315	Sequence 11315, A
C 160	11	52.4	38	4	US-09-371-772B-13710	Sequence 13710, A	C 233	10.6	50.5	38	4	US-09-371-772B-11418	Sequence 11418, A
C 161	11	52.4	38	4	US-09-371-772B-13740	Sequence 13740, A	C 234	10.6	50.5	38	4	US-09-371-772B-11448	Sequence 11448, A
C 162	11	52.4	38	4	US-09-371-772B-13758	Sequence 13758, A	C 235	10.6	50.5	38	4	US-09-371-772B-11514	Sequence 11514, A
C 163	11	52.4	38	4	US-09-371-772B-13760	Sequence 13760, A	C 236	10.6	50.5	38	4	US-09-371-772B-11514	Sequence 11514, A
C 164	11	52.4	38	4	US-09-371-772B-13805	Sequence 13805, A	C 237	10.6	50.5	38	4	US-09-371-772B-11607	Sequence 11607, A
C 165	11	52.4	38	4	US-09-371-772B-13816	Sequence 13816, A	C 238	10.6	50.5	38	4	US-09-371-772B-11647	Sequence 11647, A
C 166	11	52.4	38	4	US-09-371-772B-13833	Sequence 13833, A	C 239	10.6	50.5	38	4	US-09-371-772B-11650	Sequence 11650, A
C 167	11	52.4	38	4	US-09-371-772B-13887	Sequence 13887, A	C 240	10.6	50.5	38	4	US-09-371-772B-11689	Sequence 11689, A
C 168	11	52.4	38	4	US-09-371-772B-13922	Sequence 13922, A	C 241	10.6	50.5	38	4	US-09-371-772B-11700	Sequence 11700, A
C 169	11	52.4	38	4	US-09-371-772B-13931	Sequence 13931, A	C 242	10.6	50.5	38	4	US-09-371-772B-11713	Sequence 11713, A
C 170	11	52.4	38	4	US-09-371-772B-13974	Sequence 13974, A	C 243	10.6	50.5	38	4	US-09-371-772B-11733	Sequence 11733, A
C 171	11	52.4	38	4	US-09-371-772B-13985	Sequence 13985, A	C 244	10.6	50.5	38	4	US-09-371-772B-11796	Sequence 11796, A
C 172	11	52.4	38	4	US-09-371-772B-14014	Sequence 14014, A	C 245	10.6	50.5	38	4	US-09-371-772B-11798	Sequence 11798, A
C 173	11	52.4	38	4	US-09-874-547-75	Sequence 75, Appl	C 246	10.6	50.5	38	4	US-09-371-772B-11818	Sequence 11818, A

C 247	10.6	50.5	38	4	US-09-371-772B-11824	Sequence 11824, A	C 320	10.6	50.5	45	3	US-08-939-323-13	Sequence 13, Appl
C 248	10.6	50.5	38	4	US-09-371-772B-11847	Sequence 11847, A	C 321	10.6	50.5	47	4	US-09-422-978-495	Sequence 495, App
C 249	10.6	50.5	38	4	US-09-371-772B-11849	Sequence 11849, A	C 322	10.6	50.5	47	4	US-09-422-978-2156	Sequence 2156, App
C 250	10.6	50.5	38	4	US-09-371-772B-11851	Sequence 11851, A	C 323	10.4	49.5	18	3	US-08-642-807A-11	Sequence 11, Appl
C 251	10.6	50.5	38	4	US-09-371-772B-11871	Sequence 11871, A	C 324	10.4	49.5	20	4	US-09-527-030G-150	Sequence 150, App
C 252	10.6	50.5	38	4	US-09-371-772B-11957	Sequence 11957, A	C 325	10.4	49.5	21	4	US-09-501-612A-27	Sequence 27, Appl
C 253	10.6	50.5	38	4	US-09-371-772B-11973	Sequence 11973, A	C 326	10.4	49.5	22	4	US-09-527-030G-151	Sequence 151, App
C 254	10.6	50.5	38	4	US-09-371-772B-11983	Sequence 11983, A	C 327	10.4	49.5	22	4	US-08-470-179-197	Sequence 197, App
C 255	10.6	50.5	38	4	US-09-371-772B-12000	Sequence 12000, A	C 328	10.4	49.5	24	3	US-07-876-288-12	Sequence 12, Appl
C 256	10.6	50.5	38	4	US-09-371-772B-12007	Sequence 12007, A	C 329	10.4	49.5	25	4	US-09-538-709-348	Sequence 348, App
C 257	10.6	50.5	38	4	US-09-371-772B-12038	Sequence 12038, A	C 330	10.4	49.5	27	1	US-08-513-764-6	Sequence 6, Appl
C 258	10.6	50.5	38	4	US-09-371-772B-12049	Sequence 12049, A	C 331	10.4	49.5	29	3	US-09-118-841B-20	Sequence 20, Appl
C 259	10.6	50.5	38	4	US-09-371-772B-12053	Sequence 12053, A	C 332	10.4	49.5	29	3	US-09-414-439-20	Sequence 20, Appl
C 260	10.6	50.5	38	4	US-09-371-772B-12096	Sequence 12096, A	C 333	10.4	49.5	32	4	US-09-373-720-3	Sequence 3, Appl
C 261	10.6	50.5	38	4	US-09-371-772B-12117	Sequence 12117, A	C 334	10.4	49.5	33	3	US-09-303-064-42	Sequence 42, Appl
C 262	10.6	50.5	38	4	US-09-371-772B-12178	Sequence 12178, A	C 335	10.4	49.5	33	3	US-09-086-503-42	Sequence 42, Appl
C 263	10.6	50.5	38	4	US-09-371-772B-12180	Sequence 12180, A	C 336	10.4	49.5	33	3	US-09-301-593-76	Sequence 76, Appl
C 264	10.6	50.5	38	4	US-09-371-772B-12184	Sequence 12184, A	C 337	10.4	49.5	34	1	US-08-044-621D-16	Sequence 16, Appl
C 265	10.6	50.5	38	4	US-09-371-772B-12192	Sequence 12192, A	C 338	10.4	49.5	34	1	US-08-044-621D-22	Sequence 22, Appl
C 266	10.6	50.5	38	4	US-09-371-772B-12210	Sequence 12210, A	C 339	10.4	49.5	34	1	US-08-803-973-8	Sequence 8, Appl
C 267	10.6	50.5	38	4	US-09-371-772B-12224	Sequence 12224, A	C 340	10.4	49.5	34	1	US-08-803-972-8	Sequence 8, Appl
C 268	10.6	50.5	38	4	US-09-371-772B-12238	Sequence 12238, A	C 341	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
C 269	10.6	50.5	38	4	US-09-371-772B-12241	Sequence 12241, A	C 342	10.4	49.5	35	4	US-09-165-868-9	Sequence 9, Appl
C 270	10.6	50.5	38	4	US-09-371-772B-12270	Sequence 12270, A	C 343	10.4	49.5	36	2	US-08-292-620A-805	Sequence 805, App
C 271	10.6	50.5	38	4	US-09-371-772B-12286	Sequence 12286, A	C 344	10.4	49.5	36	2	US-08-292-620A-815	Sequence 815, App
C 272	10.6	50.5	38	4	US-09-371-772B-12364	Sequence 12364, A	C 345	10.4	49.5	36	2	US-08-292-620A-1147	Sequence 1147, App
C 273	10.6	50.5	38	4	US-09-371-772B-12368	Sequence 12368, A	C 346	10.4	49.5	36	2	US-08-292-620A-1186	Sequence 1186, App
C 274	10.6	50.5	38	4	US-09-371-772B-12387	Sequence 12387, A	C 347	10.4	49.5	36	2	US-08-292-620A-1195	Sequence 1195, App
C 275	10.6	50.5	38	4	US-09-371-772B-12404	Sequence 12404, A	C 348	10.4	49.5	36	2	US-08-292-620A-1225	Sequence 1225, App
C 276	10.6	50.5	38	4	US-09-371-772B-12424	Sequence 12424, A	C 349	10.4	49.5	36	2	US-08-292-620A-1289	Sequence 1289, App
C 277	10.6	50.5	38	4	US-09-371-772B-12428	Sequence 12428, A	C 350	10.4	49.5	36	2	US-08-292-620A-1346	Sequence 1346, App
C 278	10.6	50.5	38	4	US-09-371-772B-12444	Sequence 12444, A	C 351	10.4	49.5	36	3	US-09-071-845-806	Sequence 806, App
C 279	10.6	50.5	38	4	US-09-371-772B-12471	Sequence 12471, A	C 352	10.4	49.5	36	3	US-09-071-845-815	Sequence 815, App
C 280	10.6	50.5	38	4	US-09-371-772B-12584	Sequence 12584, A	C 353	10.4	49.5	36	3	US-09-071-845-1147	Sequence 1147, App
C 281	10.6	50.5	38	4	US-09-371-772B-12590	Sequence 12590, A	C 354	10.4	49.5	36	3	US-09-071-845-1186	Sequence 1186, App
C 282	10.6	50.5	38	4	US-09-371-772B-12690	Sequence 12690, A	C 355	10.4	49.5	36	3	US-09-071-845-1195	Sequence 1195, App
C 283	10.6	50.5	38	4	US-09-371-772B-13197	Sequence 13197, A	C 356	10.4	49.5	36	3	US-09-071-845-1225	Sequence 1225, App
C 284	10.6	50.5	38	4	US-09-371-772B-13238	Sequence 13238, A	C 357	10.4	49.5	36	3	US-09-071-845-1289	Sequence 1289, App
C 285	10.6	50.5	38	4	US-09-371-772B-13364	Sequence 13364, A	C 358	10.4	49.5	36	3	US-09-071-845-1346	Sequence 1346, App
C 286	10.6	50.5	38	4	US-09-371-772B-13405	Sequence 13405, A	C 359	10.4	49.5	36	3	US-08-948-381-19	Sequence 19, Appl
C 287	10.6	50.5	38	4	US-09-371-772B-13435	Sequence 13435, A	C 360	10.4	49.5	38	4	US-09-371-772B-7201	Sequence 7201, App
C 288	10.6	50.5	38	4	US-09-371-772B-13452	Sequence 13452, A	C 361	10.4	49.5	38	4	US-09-371-772B-7293	Sequence 7293, App
C 289	10.6	50.5	38	4	US-09-371-772B-13455	Sequence 13455, A	C 362	10.4	49.5	38	4	US-09-371-772B-7344	Sequence 7344, App
C 290	10.6	50.5	38	4	US-09-371-772B-13501	Sequence 13501, A	C 363	10.4	49.5	38	4	US-09-371-772B-7348	Sequence 7348, App
C 291	10.6	50.5	38	4	US-09-371-772B-13521	Sequence 13521, A	C 364	10.4	49.5	38	4	US-09-371-772B-7361	Sequence 7361, App
C 292	10.6	50.5	38	4	US-09-371-772B-13525	Sequence 13525, A	C 365	10.4	49.5	38	4	US-09-371-772B-7364	Sequence 7364, App
C 293	10.6	50.5	38	4	US-09-371-772B-13539	Sequence 13539, A	C 366	10.4	49.5	38	4	US-09-371-772B-7390	Sequence 7390, App
C 294	10.6	50.5	38	4	US-09-371-772B-13558	Sequence 13558, A	C 367	10.4	49.5	38	4	US-09-371-772B-7394	Sequence 7394, App
C 295	10.6	50.5	38	4	US-09-371-772B-13611	Sequence 13611, A	C 368	10.4	49.5	38	4	US-09-371-772B-7401	Sequence 7401, App
C 296	10.6	50.5	38	4	US-09-371-772B-13617	Sequence 13617, A	C 369	10.4	49.5	38	4	US-09-371-772B-7424	Sequence 7424, App
C 297	10.6	50.5	38	4	US-09-371-772B-13626	Sequence 13626, A	C 370	10.4	49.5	38	4	US-09-371-772B-7428	Sequence 7428, App
C 298	10.6	50.5	38	4	US-09-371-772B-13645	Sequence 13645, A	C 371	10.4	49.5	38	4	US-09-371-772B-7441	Sequence 7441, App
C 299	10.6	50.5	38	4	US-09-371-772B-13662	Sequence 13662, A	C 372	10.4	49.5	38	4	US-09-371-772B-7482	Sequence 7482, App
C 300	10.6	50.5	38	4	US-09-371-772B-13664	Sequence 13664, A	C 373	10.4	49.5	38	4	US-09-371-772B-7485	Sequence 7485, App
C 301	10.6	50.5	38	4	US-09-371-772B-13675	Sequence 13675, A	C 374	10.4	49.5	38	4	US-09-371-772B-7521	Sequence 7521, App
C 302	10.6	50.5	38	4	US-09-371-772B-13679	Sequence 13679, A	C 375	10.4	49.5	38	4	US-09-371-772B-7552	Sequence 7552, App
C 303	10.6	50.5	38	4	US-09-371-772B-13684	Sequence 13684, A	C 376	10.4	49.5	38	4	US-09-371-772B-7556	Sequence 7556, App
C 304	10.6	50.5	38	4	US-09-371-772B-13718	Sequence 13718, A	C 377	10.4	49.5	38	4	US-09-371-772B-7558	Sequence 7558, App
C 305	10.6	50.5	38	4	US-09-371-772B-13722	Sequence 13722, A	C 378	10.4	49.5	38	4	US-09-371-772B-7583	Sequence 7583, App
C 306	10.6	50.5	38	4	US-09-371-772B-13724	Sequence 13724, A	C 379	10.4	49.5	38	4	US-09-371-772B-7590	Sequence 7590, App
C 307	10.6	50.5	38	4	US-09-371-772B-13764	Sequence 13764, A	C 380	10.4	49.5	38	4	US-09-371-772B-7619	Sequence 7619, App
C 308	10.6	50.5	38	4	US-09-371-772B-13838	Sequence 13838, A	C 381	10.4	49.5	38	4	US-09-371-772B-7652	Sequence 7652, App
C 309	10.6	50.5	38	4	US-09-371-772B-13853	Sequence 13853, A	C 382	10.4	49.5	38	4	US-09-371-772B-7696	Sequence 7696, App
C 310	10.6	50.5	38	4	US-09-371-772B-13882	Sequence 13882, A	C 383	10.4	49.5	38	4	US-09-371-772B-7738	Sequence 7738, App
C 311	10.6	50.5	38	4	US-09-371-772B-13907	Sequence 13907, A	C 384	10.4	49.5	38	4	US-09-371-772B-7838	Sequence 7838, App
C 312	10.6	50.5	38	4	US-09-371-772B-13934	Sequence 13934, A	C 385	10.4	49.5	38	4	US-09-371-772B-7922	Sequence 7922, App
C 313	10.6	50.5	38	4	US-09-371-772B-13970	Sequence 13970, A	C 386	10.4	49.5	38	4	US-09-371-772B-7973	Sequence 7973, App
C 314	10.6	50.5	38	4	US-09-371-772B-13976	Sequence 13976, A	C 387	10.4	49.5	38	4	US-09-371-772B-8031	Sequence 8031, App
C 315	10.6	50.5	38	4	US-09-371-772B-14021	Sequence 14021, A	C 388	10.4	49.5	38	4	US-09-371-772B-8084	Sequence 8084, App
C 316	10.6	50.5	38	4	US-09-874-547-67	Sequence 67, Appl	C 389	10.4	49.5	38	4	US-09-371-772B-8105	Sequence 8105, App
C 317	10.6	50.5	39	4	US-09-060-299-189	Sequence 189, App	C 390	10.4	49.5	38	4	US-09-371-772B-8166	Sequence 8166, App
C 318	10.6	50.5	39	4	US-09-402-923A-189	Sequence 189, App	C 391	10.4	49.5	38	4	US-09-371-772B-8168	Sequence 8168, App
C 319	10.6	50.5	45	1	US-08-681-935-13	Sequence 13, Appl	C 392	10.4	49.5	38	4	US-09-371-772B-8173	Sequence 8173, App

539	10.2	48.6	20	3	US-09-048-810-6	Sequence 6, Appli	612	10.2	48.6	45	4	US-09-096-700-305	Sequence 305, App
540	10.2	48.6	20	3	US-09-167-151-4	Sequence 4, Appli	613	10.2	48.6	45	4	US-09-903-603A-305	Sequence 305, App
541	10.2	48.6	20	4	US-09-980-052-64	Sequence 64, Appli	614	10.2	48.6	47	4	US-09-422-978B-3195	Sequence 3195, Ap
542	10.2	48.6	20	4	US-09-842-347A-4	Sequence 4, Appli	615	10.2	48.6	48	1	US-08-604-913B-9	Sequence 9, Appli
543	10.2	48.6	21	4	US-09-622-166A-30	Sequence 30, Appli	616	10.2	48.6	49	4	US-09-538-709-122	Sequence 122, App
544	10.2	48.6	21	4	US-09-657-472-350	Sequence 350, App	617	10.2	48.6	49	4	US-09-538-709-1285	Sequence 1285, Ap
545	10.2	48.6	22	3	US-09-037-327-11	Sequence 11, Appli	618	10.2	48.6	50	4	US-09-470-661A-36	Sequence 36, Appli
546	10.2	48.6	24	4	US-09-360-545-9	Sequence 9, Appli	619	10	47.6	17	3	US-08-584-040-3963	Sequence 3963, Ap
547	10.2	48.6	24	4	US-10-142-231-78	Sequence 78, Appli	620	10	47.6	17	3	US-08-584-040-3964	Sequence 3964, Ap
548	10.2	48.6	25	2	US-08-631-751A-7	Sequence 7, Appli	621	10	47.6	17	4	US-09-371-772B-1730	Sequence 1730, Ap
549	10.2	48.6	26	3	US-08-986-837-5	Sequence 5, Appli	622	10	47.6	17	4	US-09-371-772B-1731	Sequence 1731, Ap
550	10.2	48.6	26	4	US-09-809-592-5	Sequence 5, Appli	623	10	47.6	17	4	US-09-371-772B-6370	Sequence 6370, Ap
551	10.2	48.6	27	3	US-08-584-040-666	Sequence 666, App	624	10	47.6	18	3	US-08-584-040-4467	Sequence 4467, Ap
552	10.2	48.6	27	3	US-08-584-040-1419	Sequence 1419, Ap	625	10	47.6	18	4	US-09-371-772B-2180	Sequence 2180, Ap
553	10.2	48.6	27	3	US-08-584-040-3300	Sequence 3300, Ap	626	10	47.6	20	1	US-07-767-135-15	Sequence 15, Appli
554	10.2	48.6	27	3	US-08-584-040-6284	Sequence 6284, Ap	627	10	47.6	20	1	US-07-841-652-22	Sequence 22, Appli
555	10.2	48.6	27	3	US-08-584-040-6348	Sequence 6348, Ap	628	10	47.6	20	1	US-09-422-978B-9310	Sequence 9310, Ap
556	10.2	48.6	29	3	US-08-612-973-94	Sequence 94, Appli	629	10	47.6	20	4	US-03-198-452A-3752	Sequence 3752, Ap
557	10.2	48.6	29	3	US-08-927-597-94	Sequence 94, Appli	630	10	47.6	21	3	US-09-203-231B-87	Sequence 87, Appli
558	10.2	48.6	31	4	US-09-530-157B-5	Sequence 5, Appli	631	10	47.6	22	1	US-08-482-577B-29	Sequence 29, Appli
559	10.2	48.6	33	1	US-08-624-545-11	Sequence 11, Appli	632	10	47.6	22	2	US-08-288-508C-20	Sequence 20, Appli
560	10.2	48.6	33	3	US-09-168-406A-12	Sequence 12, Appli	633	10	47.6	22	3	US-08-289-222E-33	Sequence 33, Appli
561	10.2	48.6	35	3	US-08-507-426C-12	Sequence 12, Appli	634	10	47.6	22	3	US-09-218-176-12	Sequence 12, Appli
562	10.2	48.6	35	4	US-09-705-014-12	Sequence 12, Appli	635	10	47.6	22	3	US-03-054-526B-33	Sequence 33, Appli
563	10.2	48.6	35	4	US-09-894-799-30	Sequence 30, Appli	636	10	47.6	22	3	US-08-943-731-238	Sequence 238, App
564	10.2	48.6	36	1	US-08-604-913B-8	Sequence 8, Appli	637	10	47.6	22	4	US-09-386-450D-20	Sequence 20, Appli
565	10.2	48.6	36	1	US-08-604-913B-8	Sequence 8, Appli	638	10	47.6	24	1	US-08-117-329-1	Sequence 1, Appli
566	10.2	48.6	36	3	US-08-358-627F-27	Sequence 27, Appli	639	10	47.6	24	3	US-09-016-542-6	Sequence 6, Appli
567	10.2	48.6	36	4	US-08-465-712C-27	Sequence 27, Appli	640	10	47.6	24	3	US-09-540-699-2	Sequence 2, Appli
568	10.2	48.6	36	4	US-09-552-733-27	Sequence 27, Appli	641	10	47.6	24	3	US-09-540-699-3	Sequence 3, Appli
569	10.2	48.6	36	4	US-09-293-427-33	Sequence 33, Appli	642	10	47.6	24	4	US-09-404-448-4	Sequence 4, Appli
570	10.2	48.6	36	4	US-09-925-27	Sequence 27, Appli	643	10	47.6	27	1	US-08-400-256-10	Sequence 10, Appli
571	10.2	48.6	37	1	US-08-276-852-133	Sequence 133, App	644	10	47.6	27	1	US-08-578-649-9	Sequence 9, Appli
572	10.2	48.6	37	1	US-08-276-852-134	Sequence 134, App	645	10	47.6	27	2	US-08-997-080-131	Sequence 131, App
573	10.2	48.6	37	1	US-08-899-575-133	Sequence 133, App	646	10	47.6	27	2	US-08-997-362-131	Sequence 131, App
574	10.2	48.6	37	1	US-08-899-575-133	Sequence 133, App	647	10	47.6	27	3	US-08-975-365-10	Sequence 10, Appli
575	10.2	48.6	37	1	US-08-899-575-133	Sequence 133, App	648	10	47.6	27	3	US-09-095-855-131	Sequence 131, App
576	10.2	48.6	37	1	US-08-899-575-134	Sequence 134, App	649	10	47.6	27	3	US-09-324-542-131	Sequence 131, App
577	10.2	48.6	37	3	US-08-961-083-310	Sequence 310, App	650	10	47.6	27	4	US-09-205-426-131	Sequence 131, App
578	10.2	48.6	37	4	US-09-470-661A-31	Sequence 31, Appli	651	10	47.6	30	2	US-08-545-562A-54	Sequence 54, Appli
579	10.2	48.6	37	4	US-09-536-784-310	Sequence 310, App	652	10	47.6	31	1	US-08-145-061-15	Sequence 15, Appli
580	10.2	48.6	37	5	PCT-US95-08743-133	Sequence 133, App	653	10	47.6	33	1	US-08-184-607-3	Sequence 3, Appli
581	10.2	48.6	37	5	PCT-US95-08743-134	Sequence 134, App	654	10	47.6	33	1	US-08-184-607-4	Sequence 4, Appli
582	10.2	48.6	38	1	US-08-373-124A-957	Sequence 957, App	655	10	47.6	33	4	US-09-813-781-127	Sequence 127, App
583	10.2	48.6	38	1	US-08-435-628-957	Sequence 957, App	656	10	47.6	35	2	US-08-965-780-2	Sequence 2, Appli
584	10.2	48.6	38	4	US-09-474-432B-1045	Sequence 1045, App	657	10	47.6	35	3	US-08-458-237-1	Sequence 1, Appli
585	10.2	48.6	38	4	US-09-371-772B-7784	Sequence 7784, App	658	10	47.6	35	3	US-08-458-237-3	Sequence 3, Appli
586	10.2	48.6	38	4	US-09-371-772B-8516	Sequence 8516, App	659	10	47.6	35	3	US-08-458-237-5	Sequence 5, Appli
587	10.2	48.6	38	4	US-09-371-772B-8869	Sequence 8869, App	660	10	47.6	35	3	US-08-458-237-6	Sequence 6, Appli
588	10.2	48.6	38	4	US-09-371-772B-10175	Sequence 10175, A	661	10	47.6	35	3	US-08-458-237-7	Sequence 7, Appli
589	10.2	48.6	38	4	US-09-371-772B-10234	Sequence 10234, A	662	10	47.6	35	3	US-08-458-237-8	Sequence 8, Appli
590	10.2	48.6	38	4	US-09-371-772B-11439	Sequence 11439, A	663	10	47.6	35	3	US-08-458-237-9	Sequence 9, Appli
591	10.2	48.6	38	4	US-09-371-772B-13916	Sequence 13916, A	664	10	47.6	35	3	US-08-458-237-10	Sequence 10, Appli
592	10.2	48.6	38	4	US-09-476-387-1044	Sequence 1044, App	665	10	47.6	35	3	US-08-458-237-11	Sequence 11, Appli
593	10.2	48.6	38	4	US-09-874-547-77	Sequence 66, Appli	666	10	47.6	35	3	US-08-458-237-12	Sequence 12, Appli
594	10.2	48.6	38	4	US-09-874-547-77	Sequence 77, Appli	667	10	47.6	35	3	US-08-458-237-13	Sequence 13, Appli
595	10.2	48.6	39	5	PCT-US95-03866-26	Sequence 26, Appli	668	10	47.6	35	3	US-09-149-727-28	Sequence 28, Appli
596	10.2	48.6	40	1	US-07-931-473B-153	Sequence 153, App	669	10	47.6	35	4	US-09-270-957-67	Sequence 67, Appli
597	10.2	48.6	40	1	US-07-714-131C-153	Sequence 153, App	670	10	47.6	35	4	US-08-459-340-2	Sequence 2, Appli
598	10.2	48.6	40	1	US-08-412-110-153	Sequence 153, App	671	10	47.6	35	4	US-08-459-340-3	Sequence 3, Appli
599	10.2	48.6	40	1	US-08-409-442A-153	Sequence 153, App	672	10	47.6	35	4	US-08-459-340-4	Sequence 4, Appli
600	10.2	48.6	40	2	US-08-469-609A-153	Sequence 153, App	673	10	47.6	35	4	US-08-459-340-5	Sequence 5, Appli
601	10.2	48.6	40	2	US-08-324-362-1	Sequence 1, Appli	674	10	47.6	35	4	US-08-459-340-6	Sequence 6, Appli
602	10.2	48.6	40	2	US-08-324-362-2	Sequence 2, Appli	675	10	47.6	35	4	US-08-459-340-7	Sequence 7, Appli
603	10.2	48.6	40	3	US-09-143-190-153	Sequence 153, App	676	10	47.6	35	4	US-08-459-340-8	Sequence 8, Appli
604	10.2	48.6	40	3	US-09-448-478-12	Sequence 12, Appli	677	10	47.6	35	4	US-08-459-340-9	Sequence 9, Appli
605	10.2	48.6	40	3	US-09-502-344-153	Sequence 153, App	678	10	47.6	35	4	US-08-459-340-10	Sequence 10, Appli
606	10.2	48.6	44	3	US-09-448-478-11	Sequence 11, Appli	679	10	47.6	35	4	US-08-459-340-11	Sequence 11, Appli
607	10.2	48.6	45	3	US-09-177-268-2	Sequence 2, Appli	680	10	47.6	35	4	US-08-459-340-12	Sequence 12, Appli
608	10.2	48.6	45	4	US-09-656-010-2	Sequence 305, App	681	10	47.6	35	4	US-08-459-340-13	Sequence 13, Appli
609	10.2	48.6	45	4	US-09-907-794A-305	Sequence 305, App	682	10	47.6	35	4	PCT-US93-07603-12	Sequence 12, Appli
610	10.2	48.6	45	4	US-09-905-125A-305	Sequence 305, App	683	10	47.6	35	5	PCT-US93-07603-13	Sequence 13, Appli
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c 685	10	47.6	36	1	US-08-074-121-8	Sequence 8, Appli	c 758	10	47.6	38	4	US-09-371-772B-9051	Sequence 9051, Ap
c 686	10	47.6	36	5	PCR-US94-06447-8	Sequence 8, Appli	c 759	10	47.6	38	4	US-09-371-772B-9092	Sequence 9092, Ap
c 687	10	47.6	36	6	RE34606-16	Patent No. R334,60	c 760	10	47.6	38	4	US-09-371-772B-9093	Sequence 9093, Ap
c 688	10	47.6	38	3	US-09-232-479-18	Sequence 18, Appl	c 761	10	47.6	38	4	US-09-371-772B-9099	Sequence 9099, Ap
c 689	10	47.6	38	4	US-09-784-990-18	Sequence 18, Appl	c 762	10	47.6	38	4	US-09-371-772B-9111	Sequence 9111, Ap
c 690	10	47.6	38	4	US-09-371-772B-7146	Sequence 7146, Ap	c 763	10	47.6	38	4	US-09-371-772B-9141	Sequence 9141, Ap
c 691	10	47.6	38	4	US-09-371-772B-7148	Sequence 7148, Ap	c 764	10	47.6	38	4	US-09-371-772B-9166	Sequence 9166, Ap
c 692	10	47.6	38	4	US-09-371-772B-7149	Sequence 7149, Ap	c 765	10	47.6	38	4	US-09-371-772B-9195	Sequence 9195, Ap
c 693	10	47.6	38	4	US-09-371-772B-7150	Sequence 7150, Ap	c 766	10	47.6	38	4	US-09-371-772B-9196	Sequence 9196, Ap
c 694	10	47.6	38	4	US-09-371-772B-7163	Sequence 7163, Ap	c 767	10	47.6	38	4	US-09-371-772B-9255	Sequence 9255, Ap
c 695	10	47.6	38	4	US-09-371-772B-7165	Sequence 7165, Ap	c 768	10	47.6	38	4	US-09-371-772B-9273	Sequence 9273, Ap
c 696	10	47.6	38	4	US-09-371-772B-7167	Sequence 7167, Ap	c 769	10	47.6	38	4	US-09-371-772B-9283	Sequence 9283, Ap
c 697	10	47.6	38	4	US-09-371-772B-7200	Sequence 7200, Ap	c 770	10	47.6	38	4	US-09-371-772B-9304	Sequence 9304, Ap
c 698	10	47.6	38	4	US-09-371-772B-7232	Sequence 7232, Ap	c 771	10	47.6	38	4	US-09-371-772B-9369	Sequence 9369, Ap
c 699	10	47.6	38	4	US-09-371-772B-7256	Sequence 7256, Ap	c 772	10	47.6	38	4	US-09-371-772B-9381	Sequence 9381, Ap
c 700	10	47.6	38	4	US-09-371-772B-7263	Sequence 7263, Ap	c 773	10	47.6	38	4	US-09-371-772B-9389	Sequence 9389, Ap
c 701	10	47.6	38	4	US-09-371-772B-7291	Sequence 7291, Ap	c 774	10	47.6	38	4	US-09-371-772B-9390	Sequence 9390, Ap
c 702	10	47.6	38	4	US-09-371-772B-7299	Sequence 7299, Ap	c 775	10	47.6	38	4	US-09-371-772B-9404	Sequence 9404, Ap
c 703	10	47.6	38	4	US-09-371-772B-7337	Sequence 7337, Ap	c 776	10	47.6	38	4	US-09-371-772B-9415	Sequence 9415, Ap
c 704	10	47.6	38	4	US-09-371-772B-7340	Sequence 7340, Ap	c 777	10	47.6	38	4	US-09-371-772B-9429	Sequence 9429, Ap
c 705	10	47.6	38	4	US-09-371-772B-7342	Sequence 7342, Ap	c 778	10	47.6	38	4	US-09-371-772B-9470	Sequence 9470, Ap
c 706	10	47.6	38	4	US-09-371-772B-7356	Sequence 7356, Ap	c 779	10	47.6	38	4	US-09-371-772B-9477	Sequence 9477, Ap
c 707	10	47.6	38	4	US-09-371-772B-7392	Sequence 7392, Ap	c 780	10	47.6	38	4	US-09-371-772B-9496	Sequence 9496, Ap
c 708	10	47.6	38	4	US-09-371-772B-7446	Sequence 7446, Ap	c 781	10	47.6	38	4	US-09-371-772B-9503	Sequence 9503, Ap
c 709	10	47.6	38	4	US-09-371-772B-7517	Sequence 7517, Ap	c 782	10	47.6	38	4	US-09-371-772B-9504	Sequence 9504, Ap
c 710	10	47.6	38	4	US-09-371-772B-7540	Sequence 7540, Ap	c 783	10	47.6	38	4	US-09-371-772B-9545	Sequence 9545, Ap
c 711	10	47.6	38	4	US-09-371-772B-7582	Sequence 7582, Ap	c 784	10	47.6	38	4	US-09-371-772B-9629	Sequence 9629, Ap
c 712	10	47.6	38	4	US-09-371-772B-7591	Sequence 7591, Ap	c 785	10	47.6	38	4	US-09-371-772B-9663	Sequence 9663, Ap
c 713	10	47.6	38	4	US-09-371-772B-7604	Sequence 7604, Ap	c 786	10	47.6	38	4	US-09-371-772B-9693	Sequence 9693, Ap
c 714	10	47.6	38	4	US-09-371-772B-7605	Sequence 7605, Ap	c 787	10	47.6	38	4	US-09-371-772B-9597	Sequence 9597, Ap
c 715	10	47.6	38	4	US-09-371-772B-7636	Sequence 7636, Ap	c 788	10	47.6	38	4	US-09-371-772B-9630	Sequence 9630, Ap
c 716	10	47.6	38	4	US-09-371-772B-7638	Sequence 7638, Ap	c 789	10	47.6	38	4	US-09-371-772B-9639	Sequence 9639, Ap
c 717	10	47.6	38	4	US-09-371-772B-7639	Sequence 7639, Ap	c 790	10	47.6	38	4	US-09-371-772B-9659	Sequence 9659, Ap
c 718	10	47.6	38	4	US-09-371-772B-7723	Sequence 7723, Ap	c 791	10	47.6	38	4	US-09-371-772B-9712	Sequence 9712, Ap
c 719	10	47.6	38	4	US-09-371-772B-7764	Sequence 7764, Ap	c 792	10	47.6	38	4	US-09-371-772B-9770	Sequence 9770, Ap
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c 721	10	47.6	38	4	US-09-371-772B-7774	Sequence 7774, Ap	c 794	10	47.6	38	4	US-09-371-772B-9776	Sequence 9776, Ap
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c 724	10	47.6	38	4	US-09-371-772B-7869	Sequence 7869, Ap	c 797	10	47.6	38	4	US-09-371-772B-9798	Sequence 9798, Ap
c 725	10	47.6	38	4	US-09-371-772B-7885	Sequence 7885, Ap	c 798	10	47.6	38	4	US-09-371-772B-9833	Sequence 9833, Ap
c 726	10	47.6	38	4	US-09-371-772B-7899	Sequence 7899, Ap	c 799	10	47.6	38	4	US-09-371-772B-9876	Sequence 9876, Ap
c 727	10	47.6	38	4	US-09-371-772B-7918	Sequence 7918, Ap	c 800	10	47.6	38	4	US-09-371-772B-9891	Sequence 9891, Ap
c 728	10	47.6	38	4	US-09-371-772B-7924	Sequence 7924, Ap	c 801	10	47.6	38	4	US-09-371-772B-9901	Sequence 9901, Ap
c 729	10	47.6	38	4	US-09-371-772B-8063	Sequence 8063, Ap	c 802	10	47.6	38	4	US-09-371-772B-9923	Sequence 9923, Ap
c 730	10	47.6	38	4	US-09-371-772B-8089	Sequence 8089, Ap	c 803	10	47.6	38	4	US-09-371-772B-9960	Sequence 9960, Ap
c 731	10	47.6	38	4	US-09-371-772B-8108	Sequence 8108, Ap	c 804	10	47.6	38	4	US-09-371-772B-9968	Sequence 9968, Ap
c 732	10	47.6	38	4	US-09-371-772B-8129	Sequence 8129, Ap	c 805	10	47.6	38	4	US-09-371-772B-9970	Sequence 9970, Ap
c 733	10	47.6	38	4	US-09-371-772B-8133	Sequence 8133, Ap	c 806	10	47.6	38	4	US-09-371-772B-9978	Sequence 9978, Ap
c 734	10	47.6	38	4	US-09-371-772B-8145	Sequence 8145, Ap	c 807	10	47.6	38	4	US-09-371-772B-9987	Sequence 9987, Ap
c 735	10	47.6	38	4	US-09-371-772B-8159	Sequence 8159, Ap	c 808	10	47.6	38	4	US-09-371-772B-9987	Sequence 9987, Ap
c 736	10	47.6	38	4	US-09-371-772B-8169	Sequence 8169, Ap	c 809	10	47.6	38	4	US-09-371-772B-10010	Sequence 10010, A
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c 738	10	47.6	38	4	US-09-371-772B-8287	Sequence 8287, Ap	c 811	10	47.6	38	4	US-09-371-772B-10035	Sequence 10035, A
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c 740	10	47.6	38	4	US-09-371-772B-8375	Sequence 8375, Ap	c 813	10	47.6	38	4	US-09-371-772B-10231	Sequence 10231, A
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c 742	10	47.6	38	4	US-09-371-772B-8420	Sequence 8420, Ap	c 815	10	47.6	38	4	US-09-371-772B-10266	Sequence 10266, A
c 743	10	47.6	38	4	US-09-371-772B-8440	Sequence 8440, Ap	c 816	10	47.6	38	4	US-09-371-772B-10271	Sequence 10271, A
c 744	10	47.6	38	4	US-09-371-772B-8541	Sequence 8541, Ap	c 817	10	47.6	38	4	US-09-371-772B-10290	Sequence 10290, A
c 745	10	47.6	38	4	US-09-371-772B-8660	Sequence 8660, Ap	c 818	10	47.6	38	4	US-09-371-772B-10320	Sequence 10320, A
c 746	10	47.6	38	4	US-09-371-772B-8667	Sequence 8667, Ap	c 819	10	47.6	38	4	US-09-371-772B-10338	Sequence 10338, A
c 747	10	47.6	38	4	US-09-371-772B-8689	Sequence 8689, Ap	c 820	10	47.6	38	4	US-09-371-772B-10420	Sequence 10420, A
c 748	10	47.6	38	4	US-09-371-772B-8740	Sequence 8740, Ap	c 821	10	47.6	38	4	US-09-371-772B-10452	Sequence 10452, A
c 749	10	47.6	38	4	US-09-371-772B-8746	Sequence 8746, Ap	c 822	10	47.6	38	4	US-09-371-772B-10464	Sequence 10464, A
c 750	10	47.6	38	4	US-09-371-772B-8748	Sequence 8748, Ap	c 823	10	47.6	38	4	US-09-371-772B-10495	Sequence 10495, A
c 751	10	47.6	38	4	US-09-371-772B-8780	Sequence 8780, Ap	c 824	10	47.6	38	4	US-09-371-772B-10513	Sequence 10513, A
c 752	10	47.6	38	4	US-09-371-772B-8874	Sequence 8874, Ap	c 825	10	47.6	38	4	US-09-371-772B-10525	Sequence 10525, A
c 753	10	47.6	38	4	US-09-371-772B-8907	Sequence 8907, Ap	c 826	10	47.6	38	4	US-09-371-772B-10548	Sequence 10548, A
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c 757	10	47.6	38	4	US-09-371-772B-9023	Sequence 9023, Ap	c 830	10	47.6	38	4	US-09-371-772B-10554	Sequence 10554, A

c 977 10 47.6 38 4 US-09-371-772B-13998
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979 10 47.6 38 4 US-09-874-547-62
980 10 47.6 38 4 US-09-874-547-68
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c 985 10 47.6 40 1 US-08-422-101-25
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c 987 10 47.6 40 2 US-08-422-092-25
c 988 10 47.6 40 3 US-08-422-093-25
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c 990 10 47.6 40 3 US-09-416-050A-62
c 991 10 47.6 40 3 US-09-664-800-62
c 992 10 47.6 40 3 US-09-665-309-62
c 993 10 47.6 40 3 US-09-661-563-62
994 10 47.6 40 4 US-09-538-709-1188
995 10 47.6 49 1 US-07-615-448A-9
996 10 47.6 49 1 US-08-196-361-9
997 10 47.6 49 2 US-08-446-934-9
998 10 47.6 49 2 US-08-448-128-9
999 10 47.6 49 3 US-08-948-703-9
1000 10 47.6 50 4 US-08-956-171E-2881

ALIGNMENTS

RESULT 1
US-09-056-052-12/c
; Sequence 12, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; TYPE: DNA
; LENGTH: 35
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-056-052-12

Query Match 62.9%; Score 13.2; DB 3; Length 35;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACGGTCTAATGAC 19
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Db 27 CGGTGCGTCTAATGAC 10

RESULT 2
US-09-056-052-13
; Sequence 13, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; NAME/KEY: misc feature
; LOCATION: (1)-(4)
; OTHER INFORMATION: 'n' can be any base A, T, G, or C
US-09-056-052-13

Query Match 62.9%; Score 13.2; DB 3; Length 39;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGGTACGGTCTAATGAC 19
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Db 13 CGGTGCGTCTAATGAC 30

RESULT 3
US-09-131-028A-17
; Sequence 17, Application US/09131028A
; Patent No. 6287866
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Lemmel, Steven A.
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Chaudhary, Sunita
; TITLE OF INVENTION: BETA-CASIN EXPRESSING CONSTRUCTS
; FILE REFERENCE: 6004 US P1
; CURRENT APPLICATION NUMBER: US/09/131,028A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: US 08/064,440
; PRIOR FILING DATE: 1993-05-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer RO204
US-09-131-028A-17

Query Match 60.0%; Score 12.6; DB 3; Length 31;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CGGTACGGTCTAATGACCG 21
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Db 12 GAGTACTGTCTCATGACG 30

RESULT 4
US-08-207-481-29
; Sequence 29, Application US/08207481
; Patent No. 5820866
; GENERAL INFORMATION:
; APPLICANT: Kappler, John W.
; APPLICANT: Marrack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL
; TITLE OF INVENTION: REGULATION
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESS: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA

ZIP: 80202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,481
FILING DATE: 04-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-0223
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-207-481-29

Query Match 60.0%; Score 12.6; DB 1; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAATGACG 21
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Db 2 GCGTACGAACGAATGAACG 20

RESULT 5
PCT-US95-02689-31
; Sequence 31, Application PC/TUS9502689
; GENERAL INFORMATION:
; APPLICANT: National Jewish Center for Immunology and
; APPLICANT: Respiratory Medicine
; APPLICANT: Kappler, John W.
; APPLICANT: Martack, Philippa
; TITLE OF INVENTION: PRODUCT AND PROCESS FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHERIDAN ROSS & MCINTOSH
; STREET: 1700 LINCOLN STREET, SUITE 3500
; CITY: DENVER
; STATE: COLORADO
; COUNTRY: USA
; ZIP: 80202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02689
; FILING DATE: 03-MAR-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-8-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-0223
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-02689-31

Query Match 60.0%; Score 12.6; DB 5; Length 33;
Best Local Similarity 78.9%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTTAATGACG 21
||||| |
Db 2 GCGTACGAACGAATGAACG 20

RESULT 6
US-09-371-772B-11935/c
; Sequence 11935, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11935
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-11935

Query Match 60.0%; Score 12.6; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTTAATGACC 20
||||| |
Db 35 TCGCNTTCGGCCTAACGCC 16

RESULT 7
US-09-371-772B-13181/c
; Sequence 13181, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MEHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08

; INFORMATION FOR SEQ ID NO: 1680:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-373-124A-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 64.3%; Pred. No. 8.4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGA 18
|:|||||:|:|
Db 2 GUACGGUCUGAUGA 15

RESULT 11

US-08-435-628-1680
; Sequence 1680, Application US/08435628

; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: McSwiggen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/435,628

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/373,124

; FILING DATE: January 13, 1995

; APPLICATION NUMBER: 08/245,466

; FILING DATE: May 18, 1994

; APPLICATION NUMBER: 08/192,943

; FILING DATE: February 7, 1994

; APPLICATION NUMBER: 07/987,132

; FILING DATE: December 7, 1992

; APPLICATION NUMBER: 07/936,422

; FILING DATE: August 26, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/035

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 1680:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-435-628-1680

Query Match 59.0%; Score 12.4; DB 1; Length 38;
Best Local Similarity 64.3%; Pred. No. 8.4e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGA 18
|:|||||:|:|
Db 2 GUACGGUCUGAUGA 15

RESULT 12

US-09-198-452A-4954
; Sequence 4954, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffiths, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 4954

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-4954

Query Match 58.1%; Score 12.2; DB 4; Length 20;

Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGA 18
|||||:|:|

Db 2 CGCGACGCTATAATGA 18
|||||:|:|

RESULT 13

5451502-8

; Patent No. 5451502

; APPLICANT: GEORGE JR., ALBERT L.

; TITLE OF INVENTION: RESTRICTION AMPLIFICATION ASSAY

; NUMBER OF SEQUENCES: 18

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/114,997

; FILING DATE: 31-AUG-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 998,644

; FILING DATE: 16-DEC-1992

; APPLICATION NUMBER: 790,174

; FILING DATE: 12-NOV-1991

; APPLICATION NUMBER: 519,146

; FILING DATE: 04-MAY-1990

; SEQ ID NO:8

; LENGTH: 21

5451502-8

Query Match 58.1%; Score 12.2; DB 6; Length 21;

Best Local Similarity 82.4%; Pred. No. 1e+03; 3; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATG 17
|||||:|:|

Db 5 TCGCATAGGTCGAATG 21
|||||:|:|

RESULT 14

US-09-313-221A-19/c

; Sequence 19, Application US/09313221A

; Patent No. 6468743

; GENERAL INFORMATION:

; APPLICANT: Thomas L. Romick (Inventor)

APPLICANT: Mark S. Fraser (Inventor)
TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
FILE REFERENCE: HUNT-042784
CURRENT FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: US 09/313,221A
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 145
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 41
TYPE: DNA
ORGANISM: Escherichia coli
US-09-313-221A-19

Query Match 58.1%; Score 12.2; DB 4; Length 41;
Best Local Similarity 82.4%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATG 17
DB 24 TCGGCACGGTATATG 8

RESULT 15
US-08-860-882A-75/c
Sequence 75, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-75

Query Match 57.1%; Score 12; DB 2; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
DB 20 TCGCGACTGGGCTTATGACC 1

RESULT 16
US-09-011-769A-61/c
Sequence 61, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
APPLICANT: BLAXEY, David C.
APPLICANT: DAVIES, David H.
APPLICANT: HENNAM, John F.
APPLICANT: HENNEQUIN, Laurent F.A.
APPLICANT: MARSHAM, Peter R.
APPLICANT: DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-011-769A-61

Query Match 57.1%; Score 12; DB 4; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
DB 20 TCGCGACTGGGCTTATGACC 1

RESULT 17
US-09-814-351-25/c
Sequence 25, Application US/09814351
Patent No. 6692736
GENERAL INFORMATION:

```
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human UPII (PCR primer 127.2.1)
US-09-814-351-25

Query Match      57.1%; Score 12; DB 4; Length 29;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2  CGCGTACGGTCTAATGACG 21
Db  25 CGCGGCCCTAGTAGACG 6

RESULT 18
US-09-709-103-34/c
; Sequence 34, Application US/09709103
; Patent No. 6733991
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS Proteins and Nucleic Acid Molecules and Uses Therefor
; FILE REFERENCE: 60388-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/709,103
; CURRENT FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe/Primer
US-09-709-103-34

Query Match      57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  21 TCGGCCAGTTTCATGACC 2

RESULT 19
US-09-439-410A-34/c
; Sequence 34, Application US/09439410A
; Patent No. 6746852
; GENERAL INFORMATION:
; APPLICANT: Cismowski, Mary
; APPLICANT: Duzic, Emir
; TITLE OF INVENTION: AGS PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 1919/60388-B
; CURRENT APPLICATION NUMBER: US/09/439,410A
; CURRENT FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
```

```
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Probe/Primer
US-09-439-410A-34

Query Match      57.1%; Score 12; DB 4; Length 32;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  21 TCGGCCAGTTTCATGACC 2

RESULT 20
US-09-371-772B-7357/c
; Sequence 7357, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7357
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7357

Query Match      57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1  TCGGTACGGTCTAATGACC 20
Db  35 TCGCTTCGGCCTAACGCC 16

RESULT 21
US-09-371-772B-7797/c
; Sequence 7797, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
```

; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7797
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7797

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 22

US-09-371-772B-8104/c
; Sequence 8104, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8104
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8104

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 23

US-09-371-772B-8341/c
; Sequence 8341, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US/09/371,772B
; PRIOR APPLICATION NUMBER: US 60/005,974

; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8341
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8341

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 24

US-09-371-772B-9392/c
; Sequence 9392, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9392
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9392

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCCTAACGGCC 16

RESULT 25

US-09-371-772B-9781/c
; Sequence 9781, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US/09/371,772B
; PRIOR APPLICATION NUMBER: US 60/005,974

; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9781
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9781

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 26

US-09-371-772B-9974/c
; Sequence 9974, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9974

; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9974

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 27

US-09-371-772B-10321/c
; Sequence 10321, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10321
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10321

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 28

US-09-371-772B-10352/c
; Sequence 10352, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10352
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10352

Query Match 57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| ||||| |||||
Db 35 TCGCTTTCGGCCTAACGGCC 16

RESULT 29

US-09-371-772B-10512/c
; Sequence 10512, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam

```
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10512
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10512

Query Match          57.1%; Score 12; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCTTCGGCTACGGCC 16

RESULT 30
US-09-172-045-20
; Sequence 20, Application US/09172045
; Patent No. 6277594
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Nakata, Katsunori
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: Hiraki-03497
; CURRENT APPLICATION NUMBER: US/09/172,045
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: JP98/86979
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP98/121456
; EARLIER FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-172-045-20

Query Match          55.2%; Score 11.6; DB 3; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 3 CTCCTTCGGTGTAAATGAC 20

RESULT 31
US-09-342-325C-20
; Sequence 20, Application US/09342325C
; Patent No. 6500637
; GENERAL INFORMATION:
; APPLICANT: Mikoshiba, Katsuhiko
```

```
; APPLICANT: Aruga, Jun
; APPLICANT: Nagai, Takeharu
; APPLICANT: Katsunori, Nakata
; TITLE OF INVENTION: Neurogenesis Inducing Gene
; FILE REFERENCE: HIRAKI-03814
; CURRENT APPLICATION NUMBER: US/09/342,325C
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: JP98/86979
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: JP98/121456
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 09/172,045
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-342-325C-20

Query Match          55.2%; Score 11.6; DB 4; Length 20;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 3 CTCCTTCGGTGTAAATGAC 20

RESULT 32
US-09-056-052-10/c
; Sequence 10, Application US/09056052
; Patent No. 6090556
; GENERAL INFORMATION:
; APPLICANT: Kato, Kikuya
; TITLE OF INVENTION: Adaptor-Tagged Competitive PCR
; FILE REFERENCE: 07898/026001
; CURRENT APPLICATION NUMBER: US/09/056,052
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: JP88495/1997
; EARLIER FILING DATE: 1997-04-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-056-052-10

Query Match          55.2%; Score 11.6; DB 3; Length 35;
Best Local Similarity 77.8%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTTAATGAC 19
    ||||| ||||| ||||| |||||
Db 27 CGAGTGGCTTCTTAACGAC 10

RESULT 33
US-10-009-332-10
; Sequence 10, Application US/10009332
; Patent No. 6716613
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; APPLICANT: Kazusa DNA Research Institute
; TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
; FILE REFERENCE: Q67541
; CURRENT APPLICATION NUMBER: US/10/009,332
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; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEHB00, 876-J (237/198)
;

```

```

, TYPE: RNA
, ORGANISM: Artificial Sequence
, FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
, NAME/KEY: misc feature
, LOCATION: (31)_(31)
, OTHER INFORMATION: n stands for inosine
US-09-371-772B-12074

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; OTHER INFORMATION: n stands for inosine
;
; LOCATION: (31)..(31)
;
; NAME/KEY: misc feature
;
; OTHER INFORMATION: Location of interest sequence: 59474949-59475000
US-09-371-772B-12074

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```

Query Match      55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred: No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2  CGCGTACGGTCTAATGACC 20
      ||| ||| ||| ||| |||
DB   34  CGCNTTCGGCCTAACGGCC 16

RESULT 36
US-09-371-772B-12155/c
; Sequence 12155, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MEBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371.772B

```

```

:
:
: TYPE: RNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
: NAME/KEY: misc feature
: LOCATION: (31)..(31)
: OTHER INFORMATION: n stands for inosine
US-09-371-772B-12155

```

```

; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12155

```

```

Query Match          55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  CGCGTACGGTCTAATGACC 20
        ||| ||| ||| ||| |||
Db      34  CGCNTTCGGCCTAACGGCC 16

RESULT 37

```

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US-09-371-772B-12380/c
; Sequence 12380, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12380
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12380

Query Match          55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
   ||| ||| ||| ||| |||
DB 34 CGCNTTCGGCCTAACGGCC 16

RESULT 38
US-09-371-772B-12396/c
; Sequence 12396, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12396
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12396

Query Match          55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
   ||| ||| ||| ||| |||
DB 34 CGCNTTCGGCCTAACGGCC 16

RESULT 39
US-09-371-772B-13189/c
; Sequence 13189, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13189
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13189

Query Match          55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
   ||| ||| ||| ||| |||
DB 34 CGCNTTCGGCCTAACGGCC 16

RESULT 40
US-09-371-772B-13450/c
; Sequence 13450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13450
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-12396

Query Match          55.2%; Score 11.6; DB 4; Length 38;
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Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
   ||| ||| ||| ||| |||
DB 34 CGCNTTCGGCCTAACGGCC 16

RESULT 39
US-09-371-772B-13189/c
; Sequence 13189, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13189
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13189

Query Match          55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
   ||| ||| ||| ||| |||
DB 34 CGCNTTCGGCCTAACGGCC 16

RESULT 40
US-09-371-772B-13450/c
; Sequence 13450, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13450
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13189
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-371-772B-13450

Query Match 55.2%; Score 11.6; DB 4; Length 38;
Best Local Similarity 73.7%; Pred. NO. 2.4e+03;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGCGTACGGTCTAATGACC 20
||| | ||| ||| | ||
Db 34 CGCNTTCGGCCTAACGGCC 16

Search completed: November 23, 2004, 22:26:04
Job time : 30.3034 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 98.4719 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21

Sequence: 1 tcgcgtacgtctaatgacgg 21

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	21	100.0	21	14	Sequence 2, Appli
3	21	100.0	21	15	US-10-087-631B-17
4	21	100.0	21	15	Sequence 17, Appli
5	14.2	67.6	25	15	US-10-098-263B-56047
6	13.6	64.8	29	16	US-09-374-046A-218
7	13.6	64.8	29	16	US-10-616-263-218
8	13.6	64.8	37	16	US-10-138-674-20182
9	13.6	64.8	37	16	US-10-138-674-20479
10	13.6	64.8	37	17	US-10-287-949A-20182
11	13.6	64.8	37	17	US-10-287-949A-20479
12	13.4	63.8	25	15	US-10-098-263B-9436

C 13	13.2	62.9	25	15	US-10-098-263B-88235	Sequence 88235, A
C 14	13.2	62.9	25	15	US-10-098-263B-88853	Sequence 88853, A
C 15	13	61.9	25	15	US-10-098-263B-71593	Sequence 71593, A
C 16	12.8	61.0	25	15	US-10-098-263B-71008	Sequence 71008, A
C 17	12.6	60.0	25	15	US-10-098-263B-25744	Sequence 25744, A
C 18	12.6	60.0	25	15	US-10-098-263B-56048	Sequence 56048, A
C 19	12.6	60.0	25	15	US-10-098-263B-118819	Sequence 118819, A
C 20	12.6	60.0	25	15	US-10-098-263B-118820	Sequence 118820, A
C 21	12.6	60.0	36	9	US-09-864-785-3885	Sequence 3885, Ap
C 22	12.6	60.0	37	9	US-09-864-785-1812	Sequence 1812, Ap
C 23	12.6	60.0	37	10	US-09-740-332-9583	Sequence 9583, Ap
C 24	12.6	60.0	37	10	US-09-817-879-9583	Sequence 9583, Ap
C 25	12.6	60.0	37	16	US-10-138-674-18225	Sequence 18225, A
C 26	12.6	60.0	37	16	US-10-138-674-18462	Sequence 18462, A
C 27	12.6	60.0	37	16	US-10-138-674-20525	Sequence 20525, A
C 28	12.6	60.0	37	17	US-10-287-949A-18225	Sequence 18225, A
C 29	12.6	60.0	37	17	US-10-287-949A-18462	Sequence 18462, A
C 30	12.6	60.0	37	17	US-10-287-949A-20525	Sequence 20525, A
C 31	12.6	60.0	37	17	US-10-669-841-16128	Sequence 16128, A
C 32	12.6	60.0	38	9	US-09-874-547-83	Sequence 83, Appli
C 33	12.6	60.0	38	9	US-09-864-785-1169	Sequence 1169, Ap
C 34	12.6	60.0	38	10	US-09-780-533A-3557	Sequence 3557, Ap
C 35	12.6	60.0	38	10	US-09-780-533A-3581	Sequence 3581, Ap
C 36	12.6	60.0	38	10	US-09-927-046-3026	Sequence 3026, Ap
C 37	12.6	60.0	38	10	US-09-927-046-3197	Sequence 3197, Ap
C 38	12.6	60.0	38	10	US-09-877-478-3468	Sequence 3468, Ap
C 39	12.6	60.0	38	10	US-09-848-754A-5094	Sequence 5094, Ap
C 40	12.6	60.0	38	10	US-09-848-754A-5300	Sequence 5300, Ap
C 41	12.6	60.0	38	15	US-10-230-006-911	Sequence 911, App
C 42	12.6	60.0	38	15	US-10-230-006-1011	Sequence 1011, Ap
C 43	12.6	60.0	38	15	US-10-230-006-1101	Sequence 1101, Ap
C 44	12.6	60.0	38	16	US-10-342-902-3468	Sequence 3468, Ap
C 45	12.6	60.0	38	16	US-10-342-902-3764	Sequence 3764, Ap
C 46	12.6	60.0	38	16	US-10-138-674-14212	Sequence 14212, A
C 47	12.6	60.0	38	16	US-10-138-674-15458	Sequence 15458, A
C 48	12.6	60.0	38	16	US-10-138-674-16088	Sequence 16088, A
C 49	12.6	60.0	38	17	US-10-287-949A-14212	Sequence 14212, A
C 50	12.6	60.0	38	17	US-10-287-949A-15458	Sequence 15458, A
C 51	12.6	60.0	38	17	US-10-287-949A-16088	Sequence 16088, A
C 52	12.6	60.0	38	17	US-10-712-672-3553	Sequence 3553, Ap
C 53	12.6	60.0	38	17	US-10-712-672-3746	Sequence 3746, Ap
C 54	12.6	60.0	38	17	US-10-712-672-4178	Sequence 4178, Ap
C 55	12.6	60.0	38	17	US-10-712-672-4185	Sequence 4185, Ap
C 56	12.6	60.0	38	17	US-10-669-841-8359	Sequence 8359, Ap
C 57	12.6	60.0	38	17	US-10-669-841-8655	Sequence 8655, Ap
C 58	12.6	60.0	42	9	US-09-101-807-5	Sequence 5, Appli
C 59	12.6	60.0	42	9	US-10-022-832-39	Sequence 39, Appli
C 60	12.4	59.0	34	14	US-09-780-533A-4554	Sequence 4554, Ap
C 61	12.4	59.0	38	10	US-10-289-762-4954	Sequence 4954, Ap
C 62	12.2	58.1	25	15	US-10-098-263B-17473	Sequence 17473, A
C 63	12.2	58.1	25	15	US-10-098-263B-26429	Sequence 26429, A
C 64	12.2	58.1	25	15	US-10-098-263B-27175	Sequence 27175, A
C 65	12.2	58.1	25	15	US-10-098-263B-36699	Sequence 36699, A
C 66	12.2	58.1	34	18	US-10-679-032-16	Sequence 16, Appli
C 67	12.2	58.1	37	10	US-09-927-046-3626	Sequence 3626, Ap
C 68	12.2	58.1	37	10	US-09-927-046-3631	Sequence 3631, Ap
C 69	12.2	58.1	37	10	US-09-927-046-3664	Sequence 3664, Ap
C 70	12.2	58.1	37	10	US-09-848-754A-5959	Sequence 5959, Ap
C 71	12.2	58.1	37	10	US-09-848-754A-6388	Sequence 6388, Ap
C 72	12.2	58.1	37	10	US-09-969-373-3705	Sequence 3705, Ap
C 73	12	57.1	19	9	US-10-308-343-2	Sequence 2, Appli
C 74	12	57.1	25	15	US-10-098-263B-3823	Sequence 3823, Ap
C 75	12	57.1	25	15	US-10-098-263B-3824	Sequence 3824, Ap
C 76	12	57.1	25	15	US-10-098-263B-16652	Sequence 16652, A
C 77	12	57.1	25	15	US-10-098-263B-68752	Sequence 68752, A
C 78	12	57.1	25	15	US-10-098-263B-116682	Sequence 116682, A
C 79	12	57.1	25	15	US-10-098-263B-122296	Sequence 122296, A
C 80	12	57.1	25	15	US-10-098-263B-128394	Sequence 128394, A
C 81	12	57.1	25	9	US-09-814-292-23	Sequence 23, Appli
C 82	12	57.1	29	9	US-09-814-357-25	Sequence 25, Appli
C 83	12	57.1	29	10	US-09-814-351-25	Sequence 25, Appli
C 84	12	57.1	32	10	US-10-804-491-34	Sequence 34, Appli
C 85	12	57.1	32	17		

C 86	12	57.1	36	9	US-09-504-231A-1730	Sequence 1730, Ap	C 159	11.6	55.2	25	15	US-10-098-263B-7785	Sequence 7785, Ap
C 87	12	57.1	36	9	US-09-504-231A-1937	Sequence 1937, Ap	C 160	11.6	55.2	25	15	US-10-098-263B-33569	Sequence 33569, A
C 88	12	57.1	36	9	US-09-504-231A-1964	Sequence 1964, Ap	C 161	11.6	55.2	25	15	US-10-098-263B-46344	Sequence 46344, A
C 89	12	57.1	36	9	US-09-504-231A-2066	Sequence 2066, Ap	C 162	11.6	55.2	25	15	US-10-098-263B-53837	Sequence 53837, A
C 90	12	57.1	36	9	US-09-274-553D-1730	Sequence 1730, Ap	C 163	11.6	55.2	25	15	US-10-098-263B-72451	Sequence 72451, A
C 91	12	57.1	36	9	US-09-274-553D-1937	Sequence 1937, Ap	C 164	11.6	55.2	25	15	US-10-098-263B-77366	Sequence 77366, A
C 92	12	57.1	36	9	US-09-274-553D-1964	Sequence 1964, Ap	C 165	11.6	55.2	25	15	US-10-098-263B-77668	Sequence 77668, A
C 93	12	57.1	36	9	US-09-274-553D-2066	Sequence 2066, Ap	C 166	11.6	55.2	25	15	US-10-098-263B-88236	Sequence 88236, A
C 94	12	57.1	37	9	US-09-864-785-1970	Sequence 1970, Ap	C 167	11.6	55.2	25	15	US-10-098-263B-88854	Sequence 88854, A
C 95	12	57.1	37	10	US-09-927-046-3651	Sequence 3651, Ap	C 168	11.6	55.2	25	15	US-10-098-263B-100370	Sequence 100370, A
C 96	12	57.1	37	10	US-09-848-754A-9434	Sequence 9434, Ap	C 169	11.6	55.2	25	15	US-10-098-263B-107021	Sequence 107021, A
C 97	12	57.1	37	10	US-09-827-395A-1775	Sequence 1775, Ap	C 170	11.6	55.2	25	15	US-10-098-263B-109470	Sequence 109470, A
C 98	12	57.1	37	15	US-10-156-306-2859	Sequence 2859, Ap	C 171	11.6	55.2	25	15	US-10-098-263B-127486	Sequence 127486, A
C 99	12	57.1	37	15	US-10-156-306-2682	Sequence 2682, Ap	C 172	11.6	55.2	30	10	US-09-854-867-555	Sequence 555, App
C 100	12	57.1	37	15	US-10-156-306-6238	Sequence 6238, Ap	C 173	11.6	55.2	34	9	US-09-864-785-3884	Sequence 3884, Ap
C 101	12	57.1	37	15	US-10-430-882-1775	Sequence 1775, Ap	C 174	11.6	55.2	36	16	US-10-420-194-621	Sequence 621, App
C 102	12	57.1	37	16	US-10-138-674-20375	Sequence 20375, A	C 175	11.6	55.2	37	10	US-09-927-046-3621	Sequence 3621, Ap
C 103	12	57.1	37	16	US-10-138-674-20459	Sequence 20459, A	C 176	11.6	55.2	37	10	US-09-927-046-3682	Sequence 3682, Ap
C 104	12	57.1	37	17	US-10-287-949A-20375	Sequence 20375, A	C 177	11.6	55.2	37	10	US-09-848-754A-6416	Sequence 6416, Ap
C 105	12	57.1	37	17	US-10-287-949A-20459	Sequence 20459, A	C 178	11.6	55.2	37	15	US-10-156-306-6108	Sequence 6108, Ap
C 106	12	57.1	38	10	US-09-730-289B-2014	Sequence 2014, Ap	C 179	11.6	55.2	37	16	US-10-138-674-18325	Sequence 18325, A
C 107	12	57.1	38	10	US-09-927-046-2466	Sequence 2466, Ap	C 180	11.6	55.2	37	16	US-10-138-674-18329	Sequence 18329, A
C 108	12	57.1	38	10	US-09-877-478-2875	Sequence 2875, Ap	C 181	11.6	55.2	37	16	US-10-138-674-20309	Sequence 20309, A
C 109	12	57.1	38	10	US-09-848-754A-4055	Sequence 4055, Ap	C 182	11.6	55.2	37	16	US-10-138-674-20416	Sequence 20416, A
C 110	12	57.1	38	10	US-09-848-754A-4084	Sequence 4084, Ap	C 183	11.6	55.2	37	16	US-10-138-674-20440	Sequence 20440, A
C 111	12	57.1	38	10	US-09-848-754A-4297	Sequence 4297, Ap	C 184	11.6	55.2	37	17	US-10-287-949A-18325	Sequence 18325, A
C 112	12	57.1	38	10	US-09-930-423-1813	Sequence 1813, Ap	C 185	11.6	55.2	37	17	US-10-287-949A-18329	Sequence 18329, A
C 113	12	57.1	38	15	US-09-745-237A-1813	Sequence 1813, Ap	C 186	11.6	55.2	37	17	US-10-287-949A-20309	Sequence 20309, A
C 114	12	57.1	38	15	US-10-156-306-856	Sequence 856, App	C 187	11.6	55.2	37	17	US-10-287-949A-20416	Sequence 20416, A
C 115	12	57.1	38	15	US-10-156-306-1164	Sequence 1164, Ap	C 188	11.6	55.2	37	17	US-10-287-949A-20440	Sequence 20440, A
C 116	12	57.1	38	15	US-10-156-306-4610	Sequence 4610, Ap	C 189	11.6	55.2	37	17	US-10-763-210-10	Sequence 10, Appl
C 117	12	57.1	38	16	US-10-342-902-2875	Sequence 2875, Ap	C 190	11.6	55.2	38	9	US-09-864-785-856	Sequence 856, App
C 118	12	57.1	38	16	US-10-138-674-9634	Sequence 9634, Ap	C 191	11.6	55.2	38	9	US-09-864-785-859	Sequence 859, App
C 119	12	57.1	38	16	US-10-138-674-10074	Sequence 10074, A	C 192	11.6	55.2	38	9	US-09-864-785-1222	Sequence 1222, Ap
C 120	12	57.1	38	16	US-10-138-674-10381	Sequence 10381, A	C 193	11.6	55.2	38	9	US-09-864-785-1327	Sequence 1327, Ap
C 121	12	57.1	38	16	US-10-138-674-10618	Sequence 10618, A	C 194	11.6	55.2	38	10	US-09-780-533A-3460	Sequence 3460, Ap
C 122	12	57.1	38	16	US-10-138-674-11669	Sequence 11669, A	C 195	11.6	55.2	38	10	US-09-780-533A-3528	Sequence 3528, Ap
C 123	12	57.1	38	16	US-10-138-674-12058	Sequence 12058, A	C 196	11.6	55.2	38	10	US-09-780-533A-3534	Sequence 3534, Ap
C 124	12	57.1	38	16	US-10-138-674-12251	Sequence 12251, A	C 197	11.6	55.2	38	10	US-09-780-533A-3542	Sequence 3542, Ap
C 125	12	57.1	38	16	US-10-138-674-12598	Sequence 12598, A	C 198	11.6	55.2	38	10	US-09-780-533A-3570	Sequence 3570, Ap
C 126	12	57.1	38	16	US-10-138-674-12629	Sequence 12629, A	C 199	11.6	55.2	38	10	US-09-780-533A-3621	Sequence 3621, Ap
C 127	12	57.1	38	16	US-10-138-674-12789	Sequence 12789, A	C 200	11.6	55.2	38	10	US-09-780-533A-3630	Sequence 3630, Ap
C 128	12	57.1	38	17	US-10-287-949A-9634	Sequence 9634, Ap	C 201	11.6	55.2	38	10	US-09-780-533A-3642	Sequence 3642, Ap
C 129	12	57.1	38	17	US-10-287-949A-10074	Sequence 10074, A	C 202	11.6	55.2	38	10	US-09-780-533A-3781	Sequence 3781, Ap
C 130	12	57.1	38	17	US-10-287-949A-10381	Sequence 10381, A	C 203	11.6	55.2	38	10	US-09-780-533A-4158	Sequence 4158, Ap
C 131	12	57.1	38	17	US-10-287-949A-10618	Sequence 10618, A	C 204	11.6	55.2	38	10	US-09-780-533A-4200	Sequence 4200, Ap
C 132	12	57.1	38	17	US-10-287-949A-11669	Sequence 11669, A	C 205	11.6	55.2	38	10	US-09-927-046-2935	Sequence 2935, Ap
C 133	12	57.1	38	17	US-10-287-949A-12058	Sequence 12058, A	C 206	11.6	55.2	38	10	US-09-927-046-3993	Sequence 3993, Ap
C 134	12	57.1	38	17	US-10-287-949A-12251	Sequence 12251, A	C 207	11.6	55.2	38	10	US-09-927-046-3354	Sequence 3354, Ap
C 135	12	57.1	38	17	US-10-287-949A-12598	Sequence 12598, A	C 208	11.6	55.2	38	10	US-09-877-478-3450	Sequence 3450, Ap
C 136	12	57.1	38	17	US-10-287-949A-12629	Sequence 12629, A	C 209	11.6	55.2	38	10	US-09-877-478-3564	Sequence 3564, Ap
C 137	12	57.1	38	17	US-10-287-949A-12789	Sequence 12789, A	C 210	11.6	55.2	38	10	US-09-877-478-3569	Sequence 3569, Ap
C 138	12	57.1	38	17	US-10-669-841-7766	Sequence 7766, Ap	C 211	11.6	55.2	38	10	US-09-877-478-3604	Sequence 3604, Ap
C 139	12	57.1	50	15	US-10-173-730-7	Sequence 7, Appli	C 212	11.6	55.2	38	10	US-09-877-478-3684	Sequence 3684, Ap
C 140	12	57.1	50	16	US-10-662-188-193	Sequence 193, App	C 213	11.6	55.2	38	10	US-09-877-478-3836	Sequence 3836, Ap
C 141	11.8	56.2	15	9	US-09-504-231A-905	Sequence 905, App	C 214	11.6	55.2	38	10	US-09-877-478-3891	Sequence 3891, Ap
C 142	11.8	56.2	15	9	US-09-274-553D-905	Sequence 905, App	C 215	11.6	55.2	38	10	US-09-848-754A-4612	Sequence 4612, Ap
C 143	11.8	56.2	17	10	US-09-740-332-1151	Sequence 1151, Ap	C 216	11.6	55.2	38	10	US-09-848-754A-4622	Sequence 4622, Ap
C 144	11.8	56.2	17	10	US-09-817-879-1151	Sequence 1151, Ap	C 217	11.6	55.2	38	10	US-09-848-754A-4627	Sequence 4627, Ap
C 145	11.8	56.2	17	10	US-10-669-841-3744	Sequence 3744, Ap	C 218	11.6	55.2	38	10	US-09-848-754A-4630	Sequence 4630, Ap
C 146	11.8	56.2	25	15	US-10-098-263B-9435	Sequence 9435, Ap	C 219	11.6	55.2	38	10	US-09-848-754A-4632	Sequence 4632, Ap
C 147	11.8	56.2	25	15	US-10-098-263B-20460	Sequence 20460, A	C 220	11.6	55.2	38	10	US-09-848-754A-5112	Sequence 5112, Ap
C 148	11.8	56.2	25	15	US-10-098-263B-28862	Sequence 28862, A	C 221	11.6	55.2	38	10	US-09-848-754A-5174	Sequence 5174, Ap
C 149	11.8	56.2	25	15	US-10-098-263B-32872	Sequence 32872, A	C 222	11.6	55.2	38	10	US-09-848-754A-5281	Sequence 5281, Ap
C 150	11.8	56.2	25	15	US-10-098-263B-36930	Sequence 36930, A	C 223	11.6	55.2	38	10	US-09-848-754A-5395	Sequence 5395, Ap
C 151	11.8	56.2	25	15	US-10-098-263B-86994	Sequence 86994, A	C 224	11.6	55.2	38	10	US-09-848-754A-5435	Sequence 5435, Ap
C 152	11.8	56.2	25	15	US-10-098-263B-98332	Sequence 98332, A	C 225	11.6	55.2	38	10	US-09-848-754A-5519	Sequence 5519, Ap
C 153	11.8	56.2	38	10	US-09-877-478-2972	Sequence 2972, Ap	C 226	11.6	55.2	38	10	US-09-930-423-2065	Sequence 2065, Ap
C 154	11.8	56.2	38	16	US-10-342-902-2972	Sequence 2972, Ap	C 227	11.6	55.2	38	10	US-09-930-423-2091	Sequence 2091, Ap
C 155	11.8	56.2	38	17	US-10-669-841-7863	Sequence 7863, Ap	C 228	11.6	55.2	38	10	US-09-930-423-2097	Sequence 2097, Ap
C 156	11.6	55.2	20	15	US-10-244-367-20	Sequence 20, Appl	C 229	11.6	55.2	38	10	US-09-930-423-2102	Sequence 2102, Ap
C 157	11.6	55.2	25	15	US-10-098-263B-787	Sequence 787, App	C 230	11.6	55.2	38	10	US-09-930-423-2106	Sequence 2106, Ap
C 158	11.6	55.2	25	15	US-10-098-263B-788	Sequence 788, App	C 231	11.6	55.2	38	10		

C 232	11.6	55.2	38	10	US-09-930-423-2119	Sequence 2119, Ap	C 305	11.6	55.2	38	17	US-10-712-672-3305	Sequence 3305, Ap
C 233	11.6	55.2	38	10	US-09-930-423-2199	Sequence 2199, Ap	C 306	11.6	55.2	38	17	US-10-712-672-3326	Sequence 3326, Ap
C 234	11.6	55.2	38	10	US-09-930-423-2248	Sequence 2248, Ap	C 307	11.6	55.2	38	17	US-10-712-672-3370	Sequence 3370, Ap
C 235	11.6	55.2	38	10	US-09-930-423-2254	Sequence 2574, Ap	C 308	11.6	55.2	38	17	US-10-712-672-3401	Sequence 3401, Ap
C 236	11.6	55.2	38	10	US-09-930-423-2575	Sequence 2595, Ap	C 309	11.6	55.2	38	17	US-10-712-672-3412	Sequence 3412, Ap
C 237	11.6	55.2	38	10	US-09-827-395A-1245	Sequence 1245, Ap	C 310	11.6	55.2	38	17	US-10-712-672-3434	Sequence 3434, Ap
C 238	11.6	55.2	38	10	US-09-827-395A-1307	Sequence 1307, Ap	C 311	11.6	55.2	38	17	US-10-712-672-3494	Sequence 3494, Ap
C 239	11.6	55.2	38	10	US-09-827-395A-1337	Sequence 1337, Ap	C 312	11.6	55.2	38	17	US-10-712-672-3559	Sequence 3559, Ap
C 240	11.6	55.2	38	10	US-09-827-395A-1379	Sequence 1379, Ap	C 313	11.6	55.2	38	17	US-10-712-672-3666	Sequence 3666, Ap
C 241	11.6	55.2	38	10	US-09-827-395A-1404	Sequence 1404, Ap	C 314	11.6	55.2	38	17	US-10-712-672-3701	Sequence 3701, Ap
C 242	11.6	55.2	38	10	US-09-827-395A-1411	Sequence 1411, Ap	C 315	11.6	55.2	38	17	US-10-712-672-3708	Sequence 3708, Ap
C 243	11.6	55.2	38	10	US-09-827-395A-1465	Sequence 1465, Ap	C 316	11.6	55.2	38	17	US-10-712-672-3729	Sequence 3729, Ap
C 244	11.6	55.2	38	10	US-09-792-818-1284	Sequence 1284, Ap	C 317	11.6	55.2	38	17	US-10-712-672-3761	Sequence 3761, Ap
C 245	11.6	55.2	38	10	US-09-792-818-1359	Sequence 1359, Ap	C 318	11.6	55.2	38	17	US-10-712-672-4076	Sequence 4076, Ap
C 246	11.6	55.2	38	10	US-09-745-237A-2065	Sequence 2065, Ap	C 319	11.6	55.2	38	17	US-10-669-841-8341	Sequence 8341, Ap
C 247	11.6	55.2	38	10	US-09-745-237A-2091	Sequence 2091, Ap	C 320	11.6	55.2	38	17	US-10-669-841-8455	Sequence 8455, Ap
C 248	11.6	55.2	38	10	US-09-745-237A-2097	Sequence 2097, Ap	C 321	11.6	55.2	38	17	US-10-669-841-8460	Sequence 8460, Ap
C 249	11.6	55.2	38	10	US-09-745-237A-2102	Sequence 2102, Ap	C 322	11.6	55.2	38	17	US-10-669-841-8495	Sequence 8495, Ap
C 250	11.6	55.2	38	10	US-09-745-237A-2106	Sequence 2106, Ap	C 323	11.6	55.2	38	17	US-10-669-841-8575	Sequence 8575, Ap
C 251	11.6	55.2	38	10	US-09-745-237A-2119	Sequence 2119, Ap	C 324	11.6	55.2	38	17	US-10-669-841-8727	Sequence 8727, Ap
C 252	11.6	55.2	38	10	US-09-745-237A-2199	Sequence 2199, Ap	C 325	11.6	55.2	38	17	US-10-669-841-8782	Sequence 8782, Ap
C 253	11.6	55.2	38	10	US-09-745-237A-2248	Sequence 2248, Ap	C 326	11.6	55.2	39	13	US-10-072-152-26	Sequence 26, Appl
C 254	11.6	55.2	38	10	US-09-745-237A-2574	Sequence 2574, Ap	C 327	11.6	55.2	39	15	US-10-277-471A-11	Sequence 11, Appl
C 255	11.6	55.2	38	10	US-09-745-237A-2595	Sequence 2595, Ap	C 328	11.6	55.2	39	15	US-10-339-674-633	Sequence 633, Appl
C 256	11.6	55.2	38	15	US-10-156-306-2222	Sequence 2222, Ap	C 329	11.6	55.2	39	15	US-10-339-674-6335	Sequence 2615, Ap
C 257	11.6	55.2	38	15	US-10-156-306-5439	Sequence 5439, Ap	C 330	11.6	55.2	39	16	US-10-655-433-26	Sequence 26, Appl
C 258	11.6	55.2	38	15	US-10-156-306-5442	Sequence 5442, Ap	C 331	11.6	54.3	15	9	US-09-504-231A-904	Sequence 904, Appl
C 259	11.6	55.2	38	15	US-10-156-306-5538	Sequence 5538, Ap	C 332	11.4	54.3	15	9	US-09-274-553D-904	Sequence 904, Appl
C 260	11.6	55.2	38	15	US-10-156-306-5615	Sequence 5615, Ap	C 333	11.4	54.3	19	9	US-09-969-373-4574	Sequence 4574, Ap
C 261	11.6	55.2	38	15	US-10-156-306-5717	Sequence 5717, Ap	C 334	11.4	54.3	22	15	US-10-296-995-93	Sequence 93, Appl
C 262	11.6	55.2	38	15	US-10-157-580A-88	Sequence 88, Appl	C 335	11.4	54.3	23	15	US-10-214-932-14	Sequence 14, Appl
C 263	11.6	55.2	38	15	US-10-230-006-863	Sequence 863, Appl	C 336	11.4	54.3	23	16	US-10-474-290-6	Sequence 6, Appl
C 264	11.6	55.2	38	15	US-10-230-006-873	Sequence 873, Appl	C 337	11.4	54.3	24	10	US-09-940-185-2381	Sequence 2381, Ap
C 265	11.6	55.2	38	15	US-10-230-006-887	Sequence 887, Appl	C 338	11.4	54.3	25	14	US-10-215-112-3435	Sequence 3435, Ap
C 266	11.6	55.2	38	15	US-10-230-006-896	Sequence 896, Appl	C 339	11.4	54.3	25	14	US-10-215-112-5874	Sequence 5874, Ap
C 267	11.6	55.2	38	15	US-10-230-006-930	Sequence 930, Appl	C 340	11.4	54.3	25	14	US-10-215-112-10677	Sequence 10677, A
C 268	11.6	55.2	38	15	US-10-230-006-970	Sequence 970, Appl	C 341	11.4	54.3	25	15	US-10-098-2638-34732	Sequence 34732, A
C 269	11.6	55.2	38	15	US-10-230-006-1002	Sequence 1002, Ap	C 342	11.4	54.3	25	15	US-10-098-2638-56624	Sequence 56624, A
C 270	11.6	55.2	38	15	US-10-230-006-1051	Sequence 1051, Ap	C 343	11.4	54.3	25	15	US-10-098-2638-69290	Sequence 69290, A
C 271	11.6	55.2	38	15	US-10-230-006-1058	Sequence 1058, Ap	C 344	11.4	54.3	25	15	US-10-098-2638-71594	Sequence 71594, A
C 272	11.6	55.2	38	15	US-10-230-006-1108	Sequence 1108, Ap	C 345	11.4	54.3	25	15	US-10-098-2638-89565	Sequence 89565, A
C 273	11.6	55.2	38	15	US-10-430-882-1245	Sequence 1245, Ap	C 346	11.4	54.3	25	15	US-10-098-2638-89566	Sequence 89566, A
C 274	11.6	55.2	38	15	US-10-430-882-1307	Sequence 1307, Ap	C 347	11.4	54.3	25	15	US-10-098-2638-104298	Sequence 104298, A
C 275	11.6	55.2	38	15	US-10-430-882-1337	Sequence 1337, Ap	C 348	11.4	54.3	25	15	US-10-098-2638-10438	Sequence 104438,
C 276	11.6	55.2	38	15	US-10-430-882-1379	Sequence 1379, Ap	C 349	11.4	54.3	25	15	US-10-098-2638-110567	Sequence 110567,
C 277	11.6	55.2	38	15	US-10-430-882-1404	Sequence 1404, Ap	C 350	11.4	54.3	25	15	US-10-098-2638-121446	Sequence 121446,
C 278	11.6	55.2	38	15	US-10-430-882-1411	Sequence 1411, Ap	C 351	11.4	54.3	26	9	US-09-895-141-8	Sequence 8, Appl
C 279	11.6	55.2	38	15	US-10-430-882-1465	Sequence 1465, Ap	C 352	11.4	54.3	27	10	US-09-877-705A-11	Sequence 11, Appl
C 280	11.6	55.2	38	16	US-10-342-902-3450	Sequence 3450, Ap	C 353	11.4	54.3	27	10	US-09-877-705A-12	Sequence 12, Appl
C 281	11.6	55.2	38	16	US-10-342-902-3564	Sequence 3564, Ap	C 354	11.4	54.3	27	10	US-09-947-274-11	Sequence 11, Appl
C 282	11.6	55.2	38	16	US-10-342-902-3569	Sequence 3569, Ap	C 355	11.4	54.3	27	10	US-09-947-274-12	Sequence 12, Appl
C 283	11.6	55.2	38	16	US-10-342-902-3604	Sequence 3604, Ap	C 356	11.4	54.3	27	10	US-09-877-738A-11	Sequence 11, Appl
C 284	11.6	55.2	38	16	US-10-342-902-3684	Sequence 3684, Ap	C 357	11.4	54.3	27	10	US-09-877-738A-12	Sequence 12, Appl
C 285	11.6	55.2	38	16	US-10-342-902-3836	Sequence 3836, Ap	C 358	11.4	54.3	27	12	US-09-877-403A-11	Sequence 11, Appl
C 286	11.6	55.2	38	16	US-10-342-902-3891	Sequence 3891, Ap	C 359	11.4	54.3	27	12	US-09-877-403A-12	Sequence 12, Appl
C 287	11.6	55.2	38	16	US-10-138-674-13690	Sequence 13690, A	C 360	11.4	54.3	27	15	US-10-057-810-11	Sequence 11, Appl
C 288	11.6	55.2	38	16	US-10-138-674-14351	Sequence 14351, A	C 361	11.4	54.3	27	15	US-10-057-810-12	Sequence 12, Appl
C 289	11.6	55.2	38	16	US-10-138-674-14432	Sequence 14432, A	C 362	11.4	54.3	27	15	US-10-057-828-11	Sequence 11, Appl
C 290	11.6	55.2	38	16	US-10-138-674-14657	Sequence 14657, A	C 363	11.4	54.3	27	15	US-10-057-828-12	Sequence 12, Appl
C 291	11.6	55.2	38	16	US-10-138-674-14673	Sequence 14673, A	C 364	11.4	54.3	27	17	US-10-779-595-11	Sequence 11, Appl
C 292	11.6	55.2	38	16	US-10-138-674-15466	Sequence 15466, A	C 365	11.4	54.3	27	17	US-10-779-595-12	Sequence 12, Appl
C 293	11.6	55.2	38	17	US-10-287-949A-13690	Sequence 13690, A	C 366	11.4	54.3	28	14	US-10-066-007-31	Sequence 31, Appl
C 294	11.6	55.2	38	17	US-10-287-949A-14351	Sequence 14351, A	C 367	11.2	53.3	18	18	US-10-740-926-406	Sequence 406, Appl
C 295	11.6	55.2	38	17	US-10-287-949A-14432	Sequence 14432, A	C 368	11.2	53.3	18	18	US-10-740-926-436	Sequence 436, Appl
C 296	11.6	55.2	38	17	US-10-287-949A-14657	Sequence 14657, A	C 369	11.2	53.3	20	17	US-10-319-914-77	Sequence 77, Appl
C 297	11.6	55.2	38	17	US-10-287-949A-15466	Sequence 15466, A	C 370	11.2	53.3	20	17	US-10-319-914-155	Sequence 155, Appl
C 298	11.6	55.2	38	17	US-10-287-949A-15466	Sequence 15466, A	C 371	11.2	53.3	25	17	US-10-619-739-322	Sequence 322, Appl
C 299	11.6	55.2	38	17	US-10-287-949A-15727	Sequence 15727, A	C 372	11.2	53.3	25	14	US-10-215-112-308	Sequence 308, Appl
C 300	11.6	55.2	38	17	US-10-712-672-3204	Sequence 3204, Ap	C 373	11.2	53.3	25	14	US-10-215-112-8911	Sequence 8911, Ap
C 301	11.6	55.2	38	17	US-10-712-672-3228	Sequence 3228, Ap	C 374	11.2	53.3	25	14	US-10-215-112-9916	Sequence 9916, Ap
C 302	11.6	55.2	38	17	US-10-712-672-3234	Sequence 3234, Ap	C 375	11.2	53.3	25	14	US-10-215-112-10028	Sequence 10028, A
C 303	11.6	55.2	38	17	US-10-712-672-3242	Sequence 3242, Ap	C 376	11.2	53.3	25	15	US-10-098-2638-1018	Sequence 1018, Ap
C 304	11.6	55.2	38	17			C 377	11.2	53.3	25	15	US-10-098-2638-2080	Sequence 2080, Ap

378	11.2	53.3	25	15	US-10-098-263B-9678	Sequence 9678, Ap	451	11	52.4	24	9	US-09-993-687-459	Sequence 459, App
c 379	11.2	53.3	25	15	US-10-098-263B-11931	Sequence 11931, A	452	11	52.4	24	10	US-09-989-734-459	Sequence 459, App
c 380	11.2	53.3	25	15	US-10-098-263B-26773	Sequence 26773, A	453	11	52.4	24	10	US-09-997-653-459	Sequence 459, App
c 381	11.2	53.3	25	15	US-10-098-263B-30572	Sequence 30572, A	454	11	52.4	24	10	US-09-989-724-459	Sequence 459, App
c 382	11.2	53.3	25	15	US-10-098-263B-34409	Sequence 34409, A	455	11	52.4	24	10	US-09-989-728-459	Sequence 459, App
c 383	11.2	53.3	25	15	US-10-098-263B-34906	Sequence 34906, A	456	11	52.4	24	10	US-09-990-441-459	Sequence 459, App
c 384	11.2	53.3	25	15	US-10-098-263B-36180	Sequence 36180, A	457	11	52.4	24	10	US-09-993-667-459	Sequence 459, App
c 385	11.2	53.3	25	15	US-10-098-263B-36180	Sequence 36180, A	458	11	52.4	24	10	US-09-997-428-459	Sequence 459, App
c 386	11.2	53.3	25	15	US-10-098-263B-44094	Sequence 44094, A	459	11	52.4	24	10	US-09-997-666-459	Sequence 459, App
c 387	11.2	53.3	25	15	US-10-098-263B-59261	Sequence 59261, A	460	11	52.4	24	10	US-09-990-438-459	Sequence 459, App
c 388	11.2	53.3	25	15	US-10-098-263B-71007	Sequence 71007, A	461	11	52.4	24	10	US-09-990-562-459	Sequence 459, App
c 389	11.2	53.3	25	15	US-10-098-263B-72284	Sequence 72284, A	462	11	52.4	24	10	US-09-990-711-459	Sequence 459, App
c 390	11.2	53.3	25	15	US-10-098-263B-75160	Sequence 75160, A	463	11	52.4	24	10	US-09-989-726-459	Sequence 459, App
c 391	11.2	53.3	25	15	US-10-098-263B-75762	Sequence 75762, A	464	11	52.4	24	10	US-09-998-156-459	Sequence 459, App
c 392	11.2	53.3	25	15	US-10-098-263B-121458	Sequence 121458, A	465	11	52.4	24	10	US-09-990-437-459	Sequence 459, App
c 393	11.2	53.3	25	15	US-10-098-263B-122026	Sequence 122026, A	466	11	52.4	24	10	US-09-991-157-459	Sequence 459, App
c 394	11.2	53.3	25	15	US-10-098-263B-128569	Sequence 128569, A	467	11	52.4	24	10	US-09-997-514-459	Sequence 459, App
c 395	11.2	53.3	25	15	US-10-098-263B-128570	Sequence 128570, A	468	11	52.4	24	10	US-09-997-573-459	Sequence 459, App
c 396	11.2	53.3	29	18	US-10-471-868-23	Sequence 23, Appl	469	11	52.4	24	10	US-09-991-172-459	Sequence 459, App
c 397	11.2	53.3	31	9	US-09-801-274-807	Sequence 807, App	470	11	52.4	24	10	US-09-990-726-459	Sequence 459, App
c 398	11.2	53.3	31	10	US-09-961-077-388	Sequence 388, App	471	11	52.4	24	10	US-09-997-559-459	Sequence 459, App
c 399	11.2	53.3	34	17	US-10-038-520-3	Sequence 3, Appl	472	11	52.4	24	10	US-09-997-601-459	Sequence 459, App
c 400	11.2	53.3	37	9	US-09-864-785-1839	Sequence 1839, Ap	473	11	52.4	24	10	US-09-990-443-459	Sequence 459, App
c 401	11.2	53.3	37	9	US-09-864-785-1839	Sequence 1839, Ap	474	11	52.4	24	10	US-09-991-854-459	Sequence 459, App
c 402	11.2	53.3	37	10	US-09-927-046-3665	Sequence 3665, Ap	475	11	52.4	24	10	US-09-997-628-459	Sequence 459, App
c 403	11.2	53.3	37	10	US-09-848-754A-6432	Sequence 6432, Ap	476	11	52.4	24	10	US-09-997-683-459	Sequence 459, App
c 404	11.2	53.3	37	16	US-10-138-674-20489	Sequence 20489, A	477	11	52.4	24	10	US-09-989-729A-459	Sequence 459, App
c 405	11.2	53.3	37	16	US-10-138-674-20600	Sequence 20600, A	478	11	52.4	24	10	US-09-997-349-459	Sequence 459, App
c 406	11.2	53.3	37	16	US-10-138-674-20710	Sequence 20710, A	479	11	52.4	24	10	US-09-997-440-459	Sequence 459, App
c 407	11.2	53.3	37	17	US-10-287-949A-20489	Sequence 20489, A	480	11	52.4	24	10	US-09-990-440-459	Sequence 459, App
c 408	11.2	53.3	37	17	US-10-287-949A-20600	Sequence 20600, A	481	11	52.4	24	10	US-09-997-857-459	Sequence 459, App
c 409	11.2	53.3	37	17	US-10-287-949A-20710	Sequence 20710, A	482	11	52.4	24	10	US-09-993-469-459	Sequence 459, App
c 410	11.2	53.3	38	9	US-09-874-547-65	Sequence 65, Appl	483	11	52.4	24	10	US-09-997-542-459	Sequence 459, App
c 411	11.2	53.3	39	16	US-10-345-410-2	Sequence 2, Appl	484	11	52.4	24	10	US-09-993-748-459	Sequence 459, App
c 412	11.2	53.3	40	9	US-09-815-980-3	Sequence 3, Appl	485	11	52.4	24	10	US-09-990-437-459	Sequence 459, App
c 413	11.2	53.3	40	9	US-09-815-980-4	Sequence 4, Appl	486	11	52.4	24	10	US-09-990-427-459	Sequence 459, App
c 414	11.2	53.3	45	10	US-09-791-153A-121	Sequence 121, App	487	11	52.4	24	10	US-09-989-328-459	Sequence 459, App
c 415	11.2	53.3	48	10	US-09-927-046-5230	Sequence 5230, Ap	488	11	52.4	24	10	US-09-993-583-459	Sequence 459, App
c 416	11.2	53.3	48	10	US-09-930-423-4525	Sequence 4525, Ap	489	11	52.4	24	10	US-09-941-992-459	Sequence 459, App
c 417	11.2	53.3	48	10	US-09-745-237A-4525	Sequence 4525, Ap	490	11	52.4	24	10	US-09-992-521-459	Sequence 459, App
c 418	11.2	53.3	50	16	US-10-131-827-6230	Sequence 6230, Ap	491	11	52.4	24	10	US-09-997-333-459	Sequence 459, App
c 419	11.2	53.3	50	16	US-10-690-487-43	Sequence 43, Appl	492	11	52.4	24	10	US-09-997-384-459	Sequence 459, App
c 420	11.2	53.3	50	18	US-10-690-487-44	Sequence 44, Appl	493	11	52.4	24	10	US-09-940-185-3246	Sequence 3246, Ap
c 421	11	52.4	17	16	US-10-138-674-3829	Sequence 3829, Ap	494	11	52.4	24	10	US-09-998-041-459	Sequence 459, App
c 422	11	52.4	17	16	US-10-138-674-3830	Sequence 3830, Ap	495	11	52.4	24	10	US-09-997-585-459	Sequence 459, App
c 423	11	52.4	17	17	US-10-287-949A-3829	Sequence 3829, Ap	496	11	52.4	24	10	US-09-997-614-459	Sequence 459, App
c 424	11	52.4	20	16	US-10-287-949A-3830	Sequence 3830, Ap	497	11	52.4	24	10	US-09-989-862-459	Sequence 459, App
c 425	11	52.4	20	16	US-10-349-143-6875	Sequence 6875, Ap	498	11	52.4	24	10	US-09-997-529-459	Sequence 459, App
c 426	11	52.4	20	16	US-10-289-762-5503	Sequence 5503, Ap	499	11	52.4	24	10	US-09-989-725-459	Sequence 459, App
c 427	11	52.4	22	15	US-10-270-313-4	Sequence 4, Appl	500	11	52.4	24	10	US-09-991-150-459	Sequence 459, App
c 428	11	52.4	24	9	US-09-823-936-7	Sequence 7, Appl	501	11	52.4	24	10	US-09-997-641-459	Sequence 459, App
c 429	11	52.4	24	9	US-09-823-936-8	Sequence 8, Appl	502	11	52.4	24	10	US-09-989-733-459	Sequence 459, App
c 430	11	52.4	24	9	US-09-989-722-459	Sequence 459, App	503	11	52.4	24	10	US-09-992-643-459	Sequence 459, App
c 431	11	52.4	24	9	US-09-989-723-459	Sequence 459, App	504	11	52.4	24	15	US-10-286-140-7	Sequence 7, Appl
c 432	11	52.4	24	9	US-09-989-729-459	Sequence 459, App	505	11	52.4	24	15	US-10-286-140-8	Sequence 8, Appl
c 433	11	52.4	24	9	US-09-989-727-459	Sequence 459, App	506	11	52.4	24	16	US-10-617-038-143	Sequence 143, App
c 434	11	52.4	24	9	US-09-989-731-459	Sequence 459, App	507	11	52.4	24	17	US-10-645-695-6	Sequence 6, Appl
c 435	11	52.4	24	9	US-09-755-836-6	Sequence 6, Appl	508	11	52.4	24	17	US-10-645-695-7	Sequence 7, Appl
c 436	11	52.4	24	9	US-09-755-836-7	Sequence 7, Appl	509	11	52.4	24	17	US-10-215-112-13237	Sequence 13237, A
c 437	11	52.4	24	9	US-09-989-732-459	Sequence 459, App	510	11	52.4	25	14	US-10-215-112-13363	Sequence 13363, A
c 438	11	52.4	24	9	US-09-991-073-459	Sequence 459, App	511	11	52.4	25	14	US-10-215-112-13363	Sequence 13363, A
c 439	11	52.4	24	9	US-09-990-442-459	Sequence 459, App	512	11	52.4	25	15	US-10-098-263B-4984	Sequence 4984, Ap
c 440	11	52.4	24	9	US-09-991-163-459	Sequence 459, App	513	11	52.4	25	15	US-10-098-263B-14662	Sequence 14662, A
c 441	11	52.4	24	9	US-09-993-604-459	Sequence 459, App	514	11	52.4	25	15	US-10-098-263B-16956	Sequence 16956, A
c 442	11	52.4	24	9	US-09-990-456-459	Sequence 459, App	515	11	52.4	25	15	US-10-098-263B-19771	Sequence 19771, A
c 443	11	52.4	24	9	US-09-989-721-459	Sequence 459, App	516	11	52.4	25	15	US-10-098-263B-25743	Sequence 25743, A
c 444	11	52.4	24	9	US-09-992-598-459	Sequence 459, App	517	11	52.4	25	15	US-10-098-263B-28673	Sequence 28673, A
c 445	11	52.4	24	9	US-09-989-293A-459	Sequence 459, App	518	11	52.4	25	15	US-10-098-263B-28857	Sequence 28857, A
c 446	11	52.4	24	9	US-09-989-735-459	Sequence 459, App	519	11	52.4	25	15	US-10-098-263B-31842	Sequence 31842, A
c 447	11	52.4	24	9	US-09-990-444-459	Sequence 459, App	520	11	52.4	25	15	US-10-098-263B-74355	Sequence 74355, A
c 448	11	52.4	24	9	US-09-991-181-459	Sequence 459, App	521	11	52.4	25	15	US-10-098-263B-75258	Sequence 75258, A
c 449	11	52.4	24	9	US-09-989-730-459	Sequence 459, App	522	11	52.4	25	15	US-10-098-263B-86878	Sequence 86878, A
c 450	11	52.4	24	9	US-09-990-436-459	Sequence 459, App	523	11	52.4	25	15	US-10-098-263B-90842	Sequence 90842, A

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c 525	11	52.4	25	15	US-10-098-263B-96360	Sequence 96360, A	598	11	52.4	37	10	US-09-848-754A-6272	Sequence 6272, Ap
c 526	11	52.4	25	15	US-10-098-263B-100534	Sequence 100534, A	599	11	52.4	37	10	US-09-827-395A-1813	Sequence 1813, Ap
527	11	52.4	25	15	US-10-098-263B-112398	Sequence 112398, A	600	11	52.4	37	15	US-10-156-306-2614	Sequence 2614, Ap
528	11	52.4	28	16	US-10-312-273-525	Sequence 525, App	601	11	52.4	37	15	US-10-156-306-6035	Sequence 6035, Ap
c 529	11	52.4	32	9	US-09-992-901-15	Sequence 15, Appl	602	11	52.4	37	15	US-10-156-306-6240	Sequence 6240, Ap
c 530	11	52.4	33	9	US-09-504-231A-3131	Sequence 3131, Ap	603	11	52.4	37	15	US-10-230-006-1551	Sequence 1551, Ap
c 531	11	52.4	33	9	US-09-274-553D-3131	Sequence 3131, Ap	604	11	52.4	37	15	US-10-230-006-1563	Sequence 1563, Ap
c 532	11	52.4	35	9	US-09-864-785-3828	Sequence 3828, Ap	605	11	52.4	37	15	US-10-230-006-1606	Sequence 1606, Ap
c 533	11	52.4	35	9	US-09-864-785-3830	Sequence 3830, Ap	606	11	52.4	37	15	US-10-430-882-1813	Sequence 1813, Ap
c 534	11	52.4	36	9	US-09-504-231A-1645	Sequence 1645, Ap	c 607	11	52.4	37	16	US-10-342-902-6277	Sequence 6277, Ap
c 535	11	52.4	36	9	US-09-504-231A-1682	Sequence 1682, Ap	c 608	11	52.4	37	16	US-10-342-902-6373	Sequence 6373, Ap
c 536	11	52.4	36	9	US-09-504-231A-1808	Sequence 1808, Ap	c 609	11	52.4	37	16	US-10-138-674-18727	Sequence 18727, A
c 537	11	52.4	36	9	US-09-504-231A-1894	Sequence 1894, Ap	610	11	52.4	37	16	US-10-138-674-18892	Sequence 18892, A
c 538	11	52.4	36	9	US-09-504-231A-1980	Sequence 1980, Ap	611	11	52.4	37	16	US-10-138-674-18891	Sequence 18891, A
c 539	11	52.4	36	9	US-09-504-231A-2001	Sequence 2001, Ap	612	11	52.4	37	16	US-10-138-674-20186	Sequence 20186, A
c 540	11	52.4	36	9	US-09-504-231A-2052	Sequence 2052, Ap	613	11	52.4	37	16	US-10-138-674-20186	Sequence 20624, A
c 541	11	52.4	36	9	US-09-504-231A-2101	Sequence 2101, Ap	614	11	52.4	37	16	US-10-138-674-20731	Sequence 20731, A
c 542	11	52.4	36	9	US-09-504-231A-2174	Sequence 2174, Ap	615	11	52.4	37	16	US-10-138-674-20731	Sequence 20731, A
c 543	11	52.4	36	9	US-09-504-231A-2184	Sequence 2184, Ap	616	11	52.4	37	16	US-10-138-674-20759	Sequence 20759, A
c 544	11	52.4	36	9	US-09-504-231A-2186	Sequence 2186, Ap	617	11	52.4	37	17	US-10-287-949A-18727	Sequence 18727, A
c 545	11	52.4	36	9	US-09-504-231A-2190	Sequence 2190, Ap	618	11	52.4	37	17	US-10-287-949A-18872	Sequence 18872, A
c 546	11	52.4	36	9	US-09-504-231A-2378	Sequence 2378, Ap	619	11	52.4	37	17	US-10-287-949A-18991	Sequence 18991, A
c 547	11	52.4	36	9	US-09-504-231A-2384	Sequence 2384, Ap	620	11	52.4	37	17	US-10-287-949A-20186	Sequence 20186, A
c 548	11	52.4	36	9	US-09-504-231A-2458	Sequence 2458, Ap	621	11	52.4	37	17	US-10-287-949A-20624	Sequence 20624, A
c 549	11	52.4	36	9	US-09-504-231A-2487	Sequence 2487, Ap	622	11	52.4	37	17	US-10-287-949A-20731	Sequence 20731, A
c 550	11	52.4	36	9	US-09-504-231A-2513	Sequence 2513, Ap	623	11	52.4	37	17	US-10-287-949A-20743	Sequence 20743, A
c 551	11	52.4	36	9	US-09-504-231A-2618	Sequence 2618, Ap	624	11	52.4	37	17	US-10-287-949A-20759	Sequence 20759, A
c 552	11	52.4	36	9	US-09-274-553D-1645	Sequence 1645, Ap	c 625	11	52.4	37	17	US-10-669-841-10936	Sequence 10936, A
c 553	11	52.4	36	9	US-09-274-553D-1682	Sequence 1682, Ap	c 626	11	52.4	37	17	US-10-669-841-10936	Sequence 10936, A
c 554	11	52.4	36	9	US-09-274-553D-1808	Sequence 1808, Ap	627	11	52.4	38	9	US-09-874-547-75	Sequence 75, Appl
c 555	11	52.4	36	9	US-09-274-553D-1894	Sequence 1894, Ap	628	11	52.4	38	9	US-09-874-547-79	Sequence 79, Appl
c 556	11	52.4	36	9	US-09-274-553D-1980	Sequence 1980, Ap	629	11	52.4	38	9	US-09-874-547-81	Sequence 81, Appl
c 557	11	52.4	36	9	US-09-274-553D-2001	Sequence 2001, Ap	c 630	11	52.4	38	9	US-09-864-785-721	Sequence 721, Appl
c 558	11	52.4	36	9	US-09-274-553D-2052	Sequence 2052, Ap	c 631	11	52.4	38	9	US-09-864-785-771	Sequence 771, Appl
c 559	11	52.4	36	9	US-09-274-553D-2101	Sequence 2101, Ap	c 632	11	52.4	38	9	US-09-864-785-775	Sequence 775, Appl
c 560	11	52.4	36	9	US-09-274-553D-2174	Sequence 2174, Ap	c 633	11	52.4	38	9	US-09-864-785-787	Sequence 787, Appl
c 561	11	52.4	36	9	US-09-274-553D-2184	Sequence 2184, Ap	c 634	11	52.4	38	9	US-09-864-785-910	Sequence 910, Appl
c 562	11	52.4	36	9	US-09-274-553D-2186	Sequence 2186, Ap	c 635	11	52.4	38	9	US-09-864-785-932	Sequence 932, Appl
c 563	11	52.4	36	9	US-09-274-553D-2190	Sequence 2190, Ap	c 636	11	52.4	38	9	US-09-864-785-951	Sequence 951, Appl
c 564	11	52.4	36	9	US-09-274-553D-2378	Sequence 2378, Ap	c 637	11	52.4	38	9	US-09-864-785-990	Sequence 990, Appl
c 565	11	52.4	36	9	US-09-274-553D-2384	Sequence 2384, Ap	c 638	11	52.4	38	9	US-09-864-785-1027	Sequence 1027, Appl
c 566	11	52.4	36	9	US-09-274-553D-2458	Sequence 2458, Ap	c 639	11	52.4	38	9	US-09-864-785-1030	Sequence 1030, Appl
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c 569	11	52.4	36	9	US-09-274-553D-2618	Sequence 2618, Ap	c 642	11	52.4	38	9	US-09-864-785-1082	Sequence 1082, Appl
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571	11	52.4	36	10	US-09-825-805-1494	Sequence 1494, Ap	c 644	11	52.4	38	9	US-09-864-785-1138	Sequence 1138, Appl
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c 573	11	52.4	36	16	US-10-420-194-565	Sequence 565, App	c 646	11	52.4	38	9	US-09-864-785-1196	Sequence 1196, Appl
c 574	11	52.4	36	16	US-10-420-194-573	Sequence 573, App	c 647	11	52.4	38	9	US-09-864-785-1198	Sequence 1198, Appl
c 575	11	52.4	36	16	US-10-420-194-585	Sequence 585, App	c 648	11	52.4	38	9	US-09-864-785-1205	Sequence 1205, Appl
c 576	11	52.4	36	16	US-10-420-194-587	Sequence 587, App	c 649	11	52.4	38	9	US-09-864-785-1229	Sequence 1229, Appl
c 577	11	52.4	36	16	US-10-420-194-602	Sequence 602, App	c 650	11	52.4	38	9	US-09-864-785-1276	Sequence 1276, Appl
c 578	11	52.4	36	16	US-10-420-194-614	Sequence 614, App	c 651	11	52.4	38	9	US-09-864-785-1290	Sequence 1290, Appl
c 579	11	52.4	36	16	US-10-420-194-634	Sequence 634, App	c 652	11	52.4	38	9	US-09-864-785-1295	Sequence 1295, Appl
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c 582	11	52.4	37	9	US-09-504-231A-3192	Sequence 3192, Ap	c 655	11	52.4	38	9	US-09-864-785-1387	Sequence 1387, Appl
c 583	11	52.4	37	9	US-09-504-231A-3198	Sequence 3198, Ap	c 656	11	52.4	38	9	US-09-864-785-1389	Sequence 1389, Appl
c 584	11	52.4	37	9	US-09-504-231A-3206	Sequence 3206, Ap	c 657	11	52.4	38	9	US-09-864-785-1401	Sequence 1401, Appl
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586	11	52.4	37	9	US-09-864-785-1891	Sequence 1891, Ap	c 659	11	52.4	38	10	US-09-730-289B-2407	Sequence 2407, Appl
587	11	52.4	37	9	US-09-864-785-1979	Sequence 1979, Ap	c 660	11	52.4	38	10	US-09-730-289B-2438	Sequence 2438, Appl
c 588	11	52.4	37	9	US-09-864-785-3829	Sequence 3829, Ap	c 661	11	52.4	38	10	US-09-730-289B-2496	Sequence 2496, Appl
c 589	11	52.4	37	9	US-09-864-785-3853	Sequence 3853, Ap	c 662	11	52.4	38	10	US-09-730-289B-2563	Sequence 2563, Appl
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c 594	11	52.4	37	10	US-09-877-478-6373	Sequence 6373, Ap	c 667	11	52.4	38	10	US-09-780-533A-2763	Sequence 2763, Appl
c 595	11	52.4	37	10	US-09-848-754A-5984	Sequence 5984, Ap	c 668	11	52.4	38	10	US-09-780-533A-2792	Sequence 2792, Appl
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c 671	11	52.4	38	10	US-09-780-533A-3451	Sequence 3451, Ap	c 744	11	52.4	38	10	US-09-877-478-3862	Sequence 3862, Ap
c 672	11	52.4	38	10	US-09-780-533A-3474	Sequence 3474, Ap	c 745	11	52.4	38	10	US-09-877-478-3898	Sequence 3898, Ap
c 673	11	52.4	38	10	US-09-780-533A-3488	Sequence 3488, Ap	c 746	11	52.4	38	10	US-09-877-478-3904	Sequence 3904, Ap
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c 681	11	52.4	38	10	US-09-780-533A-3732	Sequence 3732, Ap	c 754	11	52.4	38	10	US-09-848-754A-4465	Sequence 4465, Ap
c 682	11	52.4	38	10	US-09-780-533A-3770	Sequence 3770, Ap	c 755	11	52.4	38	10	US-09-848-754A-4606	Sequence 4606, Ap
c 683	11	52.4	38	10	US-09-780-533A-3779	Sequence 3779, Ap	c 756	11	52.4	38	10	US-09-848-754A-4670	Sequence 4670, Ap
c 684	11	52.4	38	10	US-09-780-533A-3861	Sequence 3861, Ap	c 757	11	52.4	38	10	US-09-848-754A-4705	Sequence 4705, Ap
c 685	11	52.4	38	10	US-09-780-533A-3871	Sequence 3871, Ap	c 758	11	52.4	38	10	US-09-848-754A-4799	Sequence 4799, Ap
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c 687	11	52.4	38	10	US-09-780-533A-3893	Sequence 3893, Ap	c 760	11	52.4	38	10	US-09-848-754A-4896	Sequence 4896, Ap
c 688	11	52.4	38	10	US-09-780-533A-3950	Sequence 3950, Ap	c 761	11	52.4	38	10	US-09-848-754A-4926	Sequence 4926, Ap
c 689	11	52.4	38	10	US-09-780-533A-3974	Sequence 3974, Ap	c 762	11	52.4	38	10	US-09-848-754A-4946	Sequence 4946, Ap
c 690	11	52.4	38	10	US-09-780-533A-4009	Sequence 4009, Ap	c 763	11	52.4	38	10	US-09-848-754A-4990	Sequence 4990, Ap
c 691	11	52.4	38	10	US-09-780-533A-4020	Sequence 4020, Ap	c 764	11	52.4	38	10	US-09-848-754A-5030	Sequence 5030, Ap
c 692	11	52.4	38	10	US-09-780-533A-4035	Sequence 4035, Ap	c 765	11	52.4	38	10	US-09-848-754A-5030	Sequence 5030, Ap
c 693	11	52.4	38	10	US-09-780-533A-4039	Sequence 4039, Ap	c 766	11	52.4	38	10	US-09-848-754A-5107	Sequence 5107, Ap
c 694	11	52.4	38	10	US-09-780-533A-4062	Sequence 4062, Ap	c 767	11	52.4	38	10	US-09-848-754A-5143	Sequence 5143, Ap
c 695	11	52.4	38	10	US-09-780-533A-4068	Sequence 4068, Ap	c 768	11	52.4	38	10	US-09-848-754A-5165	Sequence 5165, Ap
c 696	11	52.4	38	10	US-09-780-533A-4086	Sequence 4086, Ap	c 769	11	52.4	38	10	US-09-848-754A-5182	Sequence 5182, Ap
c 697	11	52.4	38	10	US-09-780-533A-4118	Sequence 4118, Ap	c 770	11	52.4	38	10	US-09-848-754A-5196	Sequence 5196, Ap
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c 699	11	52.4	38	10	US-09-780-533A-4214	Sequence 4214, Ap	c 772	11	52.4	38	10	US-09-848-754A-5275	Sequence 5275, Ap
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c 701	11	52.4	38	10	US-09-927-046-2493	Sequence 2493, Ap	c 774	11	52.4	38	10	US-09-848-754A-5308	Sequence 5308, Ap
c 702	11	52.4	38	10	US-09-927-046-2818	Sequence 2818, Ap	c 775	11	52.4	38	10	US-09-848-754A-5321	Sequence 5321, Ap
c 703	11	52.4	38	10	US-09-927-046-2833	Sequence 2833, Ap	c 776	11	52.4	38	10	US-09-848-754A-5359	Sequence 5359, Ap
c 704	11	52.4	38	10	US-09-927-046-2856	Sequence 2856, Ap	c 777	11	52.4	38	10	US-09-848-754A-5473	Sequence 5473, Ap
c 705	11	52.4	38	10	US-09-927-046-2931	Sequence 2931, Ap	c 778	11	52.4	38	10	US-09-848-754A-5490	Sequence 5490, Ap
c 706	11	52.4	38	10	US-09-927-046-2995	Sequence 2995, Ap	c 779	11	52.4	38	10	US-09-848-754A-5490	Sequence 5490, Ap
c 707	11	52.4	38	10	US-09-927-046-3018	Sequence 3018, Ap	c 780	11	52.4	38	10	US-09-848-754A-5566	Sequence 5566, Ap
c 708	11	52.4	38	10	US-09-927-046-3080	Sequence 3080, Ap	c 781	11	52.4	38	10	US-09-848-754A-5566	Sequence 5566, Ap
c 709	11	52.4	38	10	US-09-927-046-3116	Sequence 3116, Ap	c 782	11	52.4	38	10	US-09-848-754A-5673	Sequence 5673, Ap
c 710	11	52.4	38	10	US-09-927-046-3124	Sequence 3124, Ap	c 783	11	52.4	38	10	US-09-848-754A-5679	Sequence 5679, Ap
c 711	11	52.4	38	10	US-09-927-046-3140	Sequence 3140, Ap	c 784	11	52.4	38	10	US-09-848-754A-5721	Sequence 5721, Ap
c 712	11	52.4	38	10	US-09-927-046-3190	Sequence 3190, Ap	c 785	11	52.4	38	10	US-09-848-754A-5734	Sequence 5734, Ap
c 713	11	52.4	38	10	US-09-927-046-3203	Sequence 3203, Ap	c 786	11	52.4	38	10	US-09-848-754A-5750	Sequence 5750, Ap
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c 716	11	52.4	38	10	US-09-927-046-3382	Sequence 3382, Ap	c 789	11	52.4	38	10	US-09-848-754A-5811	Sequence 5811, Ap
c 717	11	52.4	38	10	US-09-877-478-2820	Sequence 2820, Ap	c 790	11	52.4	38	10	US-09-848-754A-5811	Sequence 5811, Ap
c 718	11	52.4	38	10	US-09-877-478-2852	Sequence 2852, Ap	c 791	11	52.4	38	10	US-09-848-754A-5854	Sequence 5854, Ap
c 719	11	52.4	38	10	US-09-877-478-2855	Sequence 2855, Ap	c 792	11	52.4	38	10	US-09-776-474-1667	Sequence 1667, Ap
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c 721	11	52.4	38	10	US-09-877-478-3247	Sequence 3247, Ap	c 794	11	52.4	38	10	US-09-776-474-1734	Sequence 1734, Ap
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ALIGNMENTS

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; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify
; OTHER INFORMATION: principle
US-10-087-631B-2
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; Sequence 17, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify
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US-10-087-631B-17/c
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; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2003-04-17
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGCGTACGGTCTTAATGACCG 21
      |||
DB      1 TCGCGTACGGTCTTAATGACCG 21

RESULT 4
US-10-419-022-17/c
; Sequence 17, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial sequence to exemplify
; OTHER INFORMATION: principle
US-10-419-022-17/c
Query Match      100.0%; Score 21; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGCGTACGGTCTTAATGACCG 21
      |||
DB      1 TCGCGTACGGTCTTAATGACCG 21
```


FILE REFERENCE: 1803-335-999
CURRENT APPLICATION NUMBER: US/10/419,022
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/10/087,631B
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence to exemplify principle
US-10-419-022-17

Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGCGTACGGTCTAATGACCG 21
Db 21 TCGCGTACGGTCTAATGACCG 1

RESULT 5
US-10-098-263B-56047/c
Sequence 56047, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 56047
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-56047

Query Match 67.6%; Score 14.2; DB 15; Length 25;
Best Local Similarity 84.2%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TCGCGTACGGTCTAATGAC 19
Db 24 TCGACACGGTCTAATGAC 6

RESULT 6
US-09-374-046A-218/c
Sequence 218, Application US/09374046A
Publication No. US20030096951A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: GI 6075-83A
CURRENT APPLICATION NUMBER: US/09/374,046A
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: biotinylated phosphoramidite residue
US-09-374-046A-218

Query Match 64.8%; Score 13.6; DB 10; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TCGCGTACGGTCTAATGACC 20
Db 24 TGGAGTACTGCTTATGACC 5

RESULT 7
US-10-616-263-218/c
Sequence 218, Application US/10616263
Publication No. US20040038276A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000103.5
CURRENT APPLICATION NUMBER: US/10/616,263
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 218
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: oligonucleotide
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)
OTHER INFORMATION: biotinylated phosphoramidite residue
US-10-616-263-218

Query Match 64.8%; Score 13.6; DB 16; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 TCGCGTACGGTCTAATGACC 20
Db 24 TGGAGTACTGCTTATGACC 5

RESULT 8

```
US-10-138-674-20182
; Sequence 20182, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20182

Query Match          64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
   |||:|:|:|:|:|
Db 18 CGAGUGAGGUCUACUGACCG 37

RESULT 9
US-10-138-674-20479
; Sequence 20479, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20479

Query Match          64.8%; Score 13.6; DB 16; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
   |||:|:|:|:|:|
Db 18 CGAGUGAGGUCUACUGACCG 37

RESULT 10
US-10-287-949A-20182
; Sequence 20182, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
```

```
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20182
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20182

Query Match          64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
   |||:|:|:|:|:|
Db 18 CGAGUGAGGUCUACUGACCG 37

RESULT 11
US-10-287-949A-20479
; Sequence 20479, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20479
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20479

Query Match          64.8%; Score 13.6; DB 17; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACCG 21
   |||:|:~|:|:|:|
Db 18 CGAGUGAGGUCUACUGACCG 37

RESULT 12
US-10-098-263B-9436
; Sequence 9436, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
```

; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 9436
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-9436

Query Match 63.8%; Score 13.4; DB 15; Length 25;
Best Local Similarity 93.3%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GTACGGTCTAATGAC 19
||| ||||| |||||
Db 4 GTACAGTCTAATGAC 18

RESULT 13
US-10-098-263B-88235/c
; Sequence 88235, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88235
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88235

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGA 18
||| ||||| |||||
Db 24 TCCCGTAAGGTCATTGA 7

RESULT 14
US-10-098-263B-88853/c
; Sequence 88853, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 88853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-88853

Query Match 62.9%; Score 13.2; DB 15; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATGA 18
||| ||||| |||||

Db 25 TCCCGTAAGGTCATTGA 8

RESULT 15
US-10-098-263B-71593
; Sequence 71593, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71593
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71593

Query Match 61.9%; Score 13; DB 15; Length 25;
Best Local Similarity 76.2%; Pred. No. 3.8e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACCG 21
||| ||||| |||||
Db 1 TCTCGTACGGACTACCCACCG 21

RESULT 16
US-10-098-263B-71008/c
; Sequence 71008, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 71008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-71008

Query Match 61.0%; Score 12.8; DB 15; Length 25;
Best Local Similarity 87.5%; Pred. No. 4.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGTACGGTCTAATGAC 19
||| ||||| |||||
Db 20 CGTACGGTCAATGAC 5

RESULT 17
US-10-098-263B-25744/c
; Sequence 25744, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

```

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 25744
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-25744

```

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 |||||
Db 25 GCGTTCCGGTCTAAGGACG 7

```

RESULT 18
US-10-098-263B-5604B/c
; Sequence 5604B, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 5604B
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-5604B

```

```
Query Match          . 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 TCGCGTACGGTCTAATGAC 19
||| ||||| |||||
Db 24 TCGAACACGGTGTAAATGAC 6

```

RESULT 19
US-10-098-263B-118819
; Sequence 118819, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118819
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-118819

```

Query Match	60.0%	Score 12.6;	DB 15;	Length 25;
Best Local Similarity	78.9%;	Pred. No. 6.3e+03;		
Matches 15; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
 | | | | | | | | | |
Db 3 GTGTGCGGTCGAATGACAG 21

```

RESULT 20
US-10-098-263B-118820
; Sequence 118820, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118820
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118820

```

Query Match 60.0%; Score 12.6; DB 15; Length 25;
Best Local Similarity 78.9%; Pred. No. 6.3e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GCGTACGGTCTAATGACCG 21
| | | | | | | | | |
Db 3 GTGTGCGGTCCAATGACAG 21

```

RESULT 21
US-09-864-785-3885
; Sequence 3885, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MHB00-813-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3885
; LENGTH: 36
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(4)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (18)..(23)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (25)..(26)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (28)..(35)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-Amino
; NAME/KEY: misc feature
; LOCATION: (27)..(27)

```

; OTHER INFORMATION: 2'-deoxy-2'-Amino
; NAME/KEY: misc_feature
; LOCATION: (36)..(36)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-864-785-3885

Query Match 60.0%; Score 12.6; DB 9; Length 36;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
|||.|||.|||.|||
DB 17 CGAGUGAGGUCUAUGGCC 35

RESULT 22

US-09-864-785-1812
; Sequence 1812, Application US/09864785
; Patent No. US20020177568A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Draper, Ken

; APPLICANT: McSwiggen, Jim

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Levels of NF-Kappa B

; FILE REFERENCE: 400/022 (MBH800-812-D)

; CURRENT APPLICATION NUMBER: US/09/864,785

; CURRENT FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 3929

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1812

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid

US-09-864-785-1812

Query Match 60.0%; Score 12.6; DB 9; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
|||.|||.|||.|||
DB 18 CGAGUGAGGUCUAUGGCC 36

RESULT 23

US-09-740-332-9583/c
; Sequence 9583, Application US/09740332
; Publication No. US20030125270A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Hepatitis C Virus Infection

; FILE REFERENCE: RPI 400/003

; CURRENT APPLICATION NUMBER: US/09/740,332

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9704

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9583

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (37)..(37)

; OTHER INFORMATION: n is an inverted deoxyabasic moiety

; NAME/KEY: misc_feature

; LOCATION: (30)..(30)

; OTHER INFORMATION: n is inosine

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; NAME/KEY: misc_feature

; LOCATION: (1)..(7)
; OTHER INFORMATION: 2'-O-methyl derivative
; NAME/KEY: misc_feature
; LOCATION: (15)..(26)
; OTHER INFORMATION: 2'-O-methyl derivative
; NAME/KEY: misc_feature
; LOCATION: (31)..(36)
; OTHER INFORMATION: 2'-O-methyl derivative
US-09-740-332-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
DB 34 TCGCNTTCGGCCTAACGCC 15

RESULT 24

US-09-817-879-9583/c

; Sequence 9583, Application US/09817879

; Publication No. US20030171311A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals Inc.

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

; FILE REFERENCE: Hepatitis C Virus Infection

; CURRENT APPLICATION NUMBER: US/09/817,879

; CURRENT FILING DATE: 2001-03-26

; NUMBER OF SEQ ID NOS: 9703

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9583

; LENGTH: 37

; TYPE: RNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (37)..(37)

; OTHER INFORMATION: n is an inverted deoxyabasic moiety

; NAME/KEY: misc_feature

; LOCATION: (30)..(30)

; OTHER INFORMATION: n is inosine

; NAME/KEY: misc_feature

; LOCATION: (1)..(7)

; OTHER INFORMATION: 2'-O-methyl derivative

; NAME/KEY: misc_feature

; LOCATION: (15)..(26)

; OTHER INFORMATION: 2'-O-methyl derivative

; NAME/KEY: misc_feature

; LOCATION: (31)..(36)

; OTHER INFORMATION: 2'-O-methyl derivative

US-09-817-879-9583

Query Match 60.0%; Score 12.6; DB 10; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
||||| ||||| ||||| |||||
DB 34 TCGCNTTCGGCCTAACGCC 15

RESULT 25

US-10-138-674-18225

; Sequence 18225, Application US/10138674

; Publication No. US20040077565A1

; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

```
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18225
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18225

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 63.2%; Pred. No. 6.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        |||:|:|:|:|:|:|
Db      18 CGAGUGAGGCUAAGACC 36

RESULT 26
US-10-138-674-18462
/ Sequence 18462, Application US/10138674
/ Publication No. US20040077565A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18462
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-18462

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        |||:|:|:|:|:|:|
Db      18 CGAGUGAGGCUAAGACC 36

RESULT 27
US-10-138-674-20525
/ Sequence 20525, Application US/10138674
/ Publication No. US20040077565A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/138,674
/ CURRENT FILING DATE: 2002-05-03
```

```
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20525
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-20525

Query Match          60.0%; Score 12.6; DB 16; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        |||:|:|:|:|:|:|
Db      18 CGAGUGAGGCUAAGACC 36

RESULT 28
US-10-287-949A-18225
/ Sequence 18225, Application US/10287949A
/ Publication No. US20040102389A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/287,949A
/ CURRENT FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18225
/ LENGTH: 37
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18225

Query Match          60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 63.2%; Pred. No. 6.5e+03;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 CGCGTACGGTCTAATGACC 20
        |||:|:~|:|:|:|:|
Db      18 CGAGUGAGGCUAAGACC 36

RESULT 29
US-10-287-949A-18462
/ Sequence 18462, Application US/10287949A
/ Publication No. US20040102389A1
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
/ FILE REFERENCE: MBH00-876-N (400/049)
/ CURRENT APPLICATION NUMBER: US/10/287,949A
/ CURRENT FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 20822
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 18462
/ LENGTH: 37
/ TYPE: RNA
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-18462

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
DB 18 CGAGUGAGGCUAAUACACC 36

RESULT 30
US-10-287-949A-20525
Sequence 20525, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MEBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20525
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-20525

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 57.9%; Pred. No. 6.5e+03;
Matches 11; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGACC 20
DB 18 CGAGUGAGGCUAAUACACC 36

RESULT 31
US-10-669-841-16128/c
Sequence 16128, Application US/10669841
Publication No. US20040127446A1
GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.
APPLICANT: Lawrence, Blatt
APPLICANT: Dennis, Macejak
APPLICANT: James, McSwiggen
APPLICANT: David, Morrissey
APPLICANT: Pamela, Pavco
APPLICANT: Patrice, Lee
APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts
TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEP
FILE REFERENCE: 400/042US (MEBH02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841
CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059
PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 60/337,055
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321
PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16128
LENGTH: 37
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(37)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (30)..(30)
OTHER INFORMATION: n is inosine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(7)
OTHER INFORMATION: 2'-O-Methyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(26)
OTHER INFORMATION: 2'-O-Methyl
FEATURE:
NAME/KEY: misc_feature
LOCATION: (31)..(36)
OTHER INFORMATION: 2'-O-Methyl
US-10-669-841-16128

Query Match 60.0%; Score 12.6; DB 17; Length 37;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAATGACC 20
DB 34 TCGCNTTCGGCCTAACGGCC 15

RESULT 32
US-09-874-547-83
Sequence 83, Application US/09874547
Patent No. US20020058269A1
GENERAL INFORMATION:
APPLICANT: No. US20020058269A1k, Steffen
APPLICANT: Kassner, Paul D.
APPLICANT: Zyomyx, Inc.
TITLE OF INVENTION: Screening of Phage Displayed Peptides
TITLE OF INVENTION: Without Clearing of the Cell Culture
FILE REFERENCE: 020144-001110US
CURRENT APPLICATION NUMBER: US/09/874,547
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/209,503
PRIOR FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 83
LENGTH: 38


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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: I)- MVK24
US-09-874-547-83

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 78.9%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGGTACGGTCTAATGACC 20
    ||||| ||| ||||| |||
Db 12 CGCGGACATTGTAATGACC 30

RESULT 33
US-09-864-785-1169/c
; Sequence 1169, Application US/09864785
; Publication No. US20020177569A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1169
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-864-785-1169

Query Match          60.0%; Score 12.6; DB 9; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||||| |||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 34
US-09-780-533A-3557/c
; Sequence 3557, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO.3557
; LENGTH: 38
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3557

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||||| |||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 35
US-09-780-533A-3581/c
; Sequence 3581, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3581
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3581

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATGACC 20
    ||||| ||| ||||| |||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 36
US-09-927-046-3026/c
; Sequence 3026, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; TITLE OF INVENTION: Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
```

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3026
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3026

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 37
US-09-927-046-3197/c
; Sequence 3197, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwigen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3197
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-927-046-3197

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 38
US-09-927-478-3468/c
; Sequence 3468, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
```

```
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3468
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3468

Query Match          60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACC 20
    ||||| ||||| ||||| |||||
Db 35 TCGCNTTCGGCCTAACGGCC 16

RESULT 39
US-09-877-478-3764/c
; Sequence 3764, Application US/09877478
; Publication No. US20030068301A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: MBH00-845-H (400/029)
; CURRENT APPLICATION NUMBER: US/09/877,478
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 08/433,993
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 08/434,504
; PRIOR FILING DATE: 1995-05-04
; PRIOR APPLICATION NUMBER: US 09/436,430
; PRIOR FILING DATE: 1999-11-08
; NUMBER OF SEQ ID NOS: 6586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3764
; LENGTH: 38
```

```

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-877-478-3764

```

Query Match 60.0%; Score 12.6; DB 10; Length 38;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0

1 TCGCGTACGGTCTAATGACC 20
35 TCGCNTTCGGCCTAACGGCC 16

```

RESULT 40
US-09-848-754A-5094/c
; Sequence 5094, Application US/09848754A
; Publication NO. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
; FILE REFERENCE: MBH00-958-I (406/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5094
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-848-754A-5094

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Query Match	60.0%;	Score 12.6;	DB 10;	Length 38;
Best Local Similarity	75.0%;	Pred. No. 6.5e+03;		
Matches 15;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;

Qy 1 TCGCGTACGGTCTAATGACC 20
Db 35 TCGCNTTCGGCCTAACGGCC 16

Search completed: November 24, 2004, 03:42:04
Job time : 108.572 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1006.82 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-2

Perfect score: 21
Sequence: 1 tcgcgtacggtctaatgacg 21

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12.6	60.0	32	9	TA199C08P
2	12.2	58.1	50	1	AW004201
3	12	57.1	33	6	CF338319
4	11.6	55.2	36	5	BO592384
5	11.6	55.2	43	8	BH903257
6	11.4	54.3	29	9	CL660557
7	11.4	54.3	39	9	CL293866
8	11.4	54.3	50	1	AU106620
9	11.4	54.3	50	1	AU106620
10	11.2	53.3	31	8	BH615074
11	11.2	53.3	43	9	CL303319
12	11.2	53.3	45	9	CL287629
13	11.2	53.3	45	9	BX650703
14	11.2	53.3	46	8	AZ583945
15	11.2	53.3	49	9	CG774856
16	11	52.4	42	9	AL754718
17	11	52.4	47	9	AL939959
18	11	52.4	48	8	BH895527
19	10.8	51.4	32	4	BI233057
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21	10.8	51.4	36	8	BH810143
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23	10.8	51.4	44	9	CL524591
24	10.8	51.4	45	9	AG192385

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38	50.5	10.6	27	8	AZ492641
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46	50.5	10.6	31	8	AZ769367
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99	9.8	46.7	38	1	AJ803928	AJ803928	BZ289706	c 172	9.4	44.8	31	1	AU266472	AU266472	ARabidops
100	9.8	46.7	39	8	BZ289706	BZ289706	CC053623	c 173	9.4	44.8	31	9	AL947428	AL947428	ARabidops
101	9.8	46.7	39	8	CC053623	CC053623	CC053623	c 174	9.4	44.8	33	9	EX530768	EX530768	ARabidops
102	9.8	46.7	40	5	BX564806	BX564806	BZ287846	c 175	9.4	44.8	34	1	AI168400	AI168400	qa25e03.s
103	9.8	46.7	40	8	BZ287846	BZ287846	SALK 0212	c 176	9.4	44.8	34	1	AI185295	AI185295	qa25b09.s
104	9.8	46.7	40	9	AL759372	AL759372	ARabidops	c 177	9.4	44.8	34	1	AU007062	AU007062	AU007062
105	9.8	46.7	41	8	BH863752	BH863752	SALK 0944	c 178	9.4	44.8	34	8	BH911674	BH911674	SALK 0714
106	9.8	46.7	41	8	BH863753	BH863753	SALK 0944	c 179	9.4	44.8	35	8	AZ591995	AZ591995	1M0402F06
107	9.8	46.7	41	8	BH864990	BH864990	SALK 0972	c 180	9.4	44.8	35	8	AZ591995	AZ591995	1M0402F06
108	9.8	46.7	42	6	CD530457	CD530457	06G12 Ara	c 181	9.4	44.8	35	9	CG709475	CG709475	1119013cl
109	9.8	46.7	43	1	AI196640	AI196640	ui53d01.y	c 182	9.4	44.8	36	9	BX535278	BX535278	ARabidops
110	9.8	46.7	44	9	TA30E12Q	TA30E12Q	T. brucei	c 183	9.4	44.8	36	9	TA38H05P	TA38H05P	ARabidops
111	9.8	46.7	44	9	CL528344	CL528344	ASV25C07	c 184	9.4	44.8	37	9	DR68G5T	DR68G5T	Danio rer
112	9.8	46.7	45	8	BZ384047	BZ384047	SALK 1349	c 185	9.4	44.8	37	9	TA35D05P	TA35D05P	T. brucei
113	9.8	46.7	45	9	CL002876	CL002876	02S0169-0	c 186	9.4	44.8	37	9	CG797773	CG797773	SALK 1453
114	9.8	46.7	46	1	AA736376	AA736376	zg7fa12.s	c 187	9.4	44.8	38	5	BX559481	BX559481	EX559481
115	9.8	46.7	46	8	BZ770587	BZ770587	SALK 1435	c 188	9.4	44.8	38	9	CNS07FAG	CNS07FAG	Anopheles
116	9.8	46.7	46	8	CC027411	CC027411	3591_1_5	c 189	9.4	44.8	39	9	BX650160	BX650160	ARabidops
117	9.8	46.7	47	9	AL758197	AL758197	ARabidops	c 190	9.4	44.8	39	9	TA380H06P	TA380H06P	T. brucei
118	9.8	46.7	48	1	AI313698	AI313698	EST010 Mo	c 191	9.4	44.8	39	9	CG796635	CG796635	SALK 1362
119	9.8	46.7	49	1	AI359268	AI359268	qy2c06.x	c 192	9.4	44.8	40	8	BH900955	BH900955	KG07812-3
120	9.8	46.7	49	1	AA124225	AA124225	mp98d08.f	c 193	9.4	44.8	40	9	CR361442	CR361442	ARabidops
121	9.8	46.7	49	1	AV833344	AV833344	AV833344	c 194	9.4	44.8	41	5	BUE37476	BUE37476	mgcw003xj
122	9.8	46.7	49	6	CO0961	CO0961	HUMGS00331	c 195	9.4	44.8	42	8	AZ806216	AZ806216	2M068D09
123	9.8	46.7	49	9	CR402941	CR402941	ARabidops	c 196	9.4	44.8	42	9	TA157C05P	TA157C05P	T. brucei
124	9.8	46.7	49	9	CR402942	CR402942	ARabidops	c 197	9.4	44.8	42	9	CL265604	CL265604	02S0166-0
125	9.8	46.7	50	1	AU104155	AU104155	AU104155	c 198	9.4	44.8	42	9	AG204866	AG204866	Pan trogl
126	9.8	46.7	50	1	AU105980	AU105980	AU105980	c 199	9.4	44.8	43	2	BF163929	BF163929	601772256
127	9.8	46.7	50	1	AU106625	AU106625	AU106625	c 200	9.4	44.8	44	4	B1829988	B1829988	603080234
128	9.8	46.7	50	9	BX945487	BX945487	ARabidops	c 201	9.4	44.8	44	8	AZ622559	AZ622559	1M0459P24
129	9.6	45.7	24	4	BM397712	BM397712	5009-0-35	c 202	9.4	44.8	44	8	CC455081	CC455081	SALK 0476
130	9.6	45.7	25	8	CC458426	CC458426	SALK 1187	c 203	9.4	44.8	44	9	AJ622264	AJ622264	Drosophil
131	9.6	45.7	27	9	TA143H1P	TA143H1P	T. brucei	c 204	9.4	44.8	44	9	CG797754	CG797754	SALK 1453
132	9.6	45.7	30	8	BH849994	BH849994	SALK 0706	c 205	9.4	44.8	45	1	AV970560	AV970560	AV970560
133	9.6	45.7	31	1	AU258240	AU258240	AU258240	c 206	9.4	44.8	45	8	BH908303	BH908303	SALK 0471
134	9.6	45.7	31	7	D18722	D18722	MUSGS01784	c 207	9.4	44.8	46	8	BH902367	BH902367	SALK 0917
135	9.6	45.7	31	8	BH810158	BH810158	SALK 0414	c 208	9.4	44.8	47	6	CB305190	CB305190	3'EST-NF1
136	9.6	45.7	34	9	TA124F07P	TA124F07P	T. brucei	c 209	9.4	44.8	47	9	CG466461	CG466461	01S0600-0
137	9.6	45.7	35	2	BE275280	BE275280	601122119	c 210	9.4	44.8	48	2	B738353	B738353	601572748
138	9.6	45.7	38	8	BH613959	BH613959	SALK 0352	c 211	9.4	44.8	48	4	B083470	B083470	BJ083470
139	9.6	45.7	40	8	BJ060137	BJ060137	BJ060137	c 212	9.4	44.8	48	5	B0582005	B0582005	195 Cryct
140	9.6	45.7	40	8	BH911408	BH911408	SALK 0684	c 213	9.4	44.8	48	8	AQ026317	AQ026317	113034A6
141	9.6	45.7	40	9	TA71C08Q	TA71C08Q	T. brucei	c 214	9.4	44.8	48	8	AQ026317	AQ026317	113034A6
142	9.6	45.7	41	7	CN755514	CN755514	ID0AA16A	c 215	9.4	44.8	48	8	BH865457	BH865457	SALK 0985
143	9.6	45.7	41	8	BH908133	BH908133	SALK 0458	c 216	9.4	44.8	48	8	BH866365	BH866365	SALK 1012
144	9.6	45.7	41	9	CNS07FEE	CNS07FEE	Anopheles	c 217	9.4	44.8	48	9	EX204287	EX204287	Danio rer
145	9.6	45.7	42	9	AL763403	AL763403	ARabidops	c 218	9.4	44.8	48	9	CR399068	CR399068	ARabidops
146	9.6	45.7	43	9	AG217405	AG217405	Drosophil	c 219	9.4	44.8	48	9	CG808438	CG808438	1118092D1
147	9.6	45.7	44	8	BH172536	BH172536	SALK 0058	c 220	9.4	44.8	49	4	BJ040441	BJ040441	BJ040441
148	9.6	45.7	44	8	BH214294	BH214294	SALK 0105	c 221	9.4	44.8	49	9	AL771898	AL771898	ARabidops
149	9.6	45.7	44	8	BH252344	BH252344	SALK 0131	c 222	9.4	44.8	49	9	TA101C02Q	TA101C02Q	T. brucei
150	9.6	45.7	44	8	BH612495	BH612495	SALK 0328	c 223	9.4	44.8	49	9	CG705752	CG705752	01S0585-0
151	9.6	45.7	44	8	BH635702	BH635702	1008007C1	c 224	9.4	44.8	50	1	AU103207	AU103207	AU103207
152	9.6	45.7	44	8	BH752299	BH752299	SALK 0140	c 225	9.4	44.8	50	1	AU103418	AU103418	AU103418
153	9.6	45.7	44	9	DR102GGG	DR102GGG	Danio rer	c 226	9.4	44.8	50	1	AU103989	AU103989	AU103989
154	9.6	45.7	45	8	CC023725	CC023725	3591_1_36	c 227	9.4	44.8	50	1	AU104834	AU104834	AU104834
155	9.6	45.7	46	7	CN758478	CN758478	ID0AA22B	c 228	9.4	44.8	50	1	AU104848	AU104848	AU104848
156	9.6	45.7	46	8	BH610910	BH610910	SALK 0182	c 229	9.4	44.8	50	1	AU106578	AU106578	AU106578
157	9.6	45.7	46	9	AB081994	AB081994	Drosophil	c 230	9.4	44.8	50	1	AU106591	AU106591	AU106591
158	9.6	45.7	47	9	CL523386	CL523386	SAW7D03 F	c 231	9.4	44.8	50	1	AU107230	AU107230	AU107230
159	9.6	45.7	48	8	BH253356	BH253356	602362952	c 232	9.4	44.8	50	2	AM630853	AM630853	hnh8e07.y
160	9.6	45.7	48	8	BH251093	BH251093	SALK 0109	c 233	9.4	44.8	50	4	BI708333	BI708333	ft4c02.y
161	9.6	45.7	48	8	BH611118	BH611118	SALK 0299	c 234	9.4	44.8	50	7	CF641166	CF641166	D36_E05 F
162	9.6	45.7	48	9	TA194C12Q	TA194C12Q	T. brucei	c 235	9.4	44.8	50	9	AJ588199	AJ588199	ARabidops
163	9.6	45.7	50	1	AU102458	AU102458	AU102458	c 236	9.4	44.8	50	9	TA154F10Q	TA154F10Q	1M0124J02
164	9.6	45.7	50	1	AU103408	AU103408	AU103408	c 237	9.2	43.8	22	8	AZ372259	AZ372259	1M0332N13
165	9.6	45.7	50	1	AU106624	AU106624	AU106624	c 238	9.2	43.8	22	8	AZ496170	AZ496170	2M0336N05
166	9.6	45.7	50	1	AV969171	AV969171	AV969171	c 239	9.2	43.8	23	8	AZ840154	AZ840154	2M0336N05
167	9.6	45.7	50	4	BG222716	BG222716	nah37e07.	c 240	9.2	43.8	25	1	AI000280	AI000280	ov10e04.s
168	9.4	44.8	27	8	AZ794090	AZ794090	2M0047O09	c 241	9.2	43.8	26	9	AJ595210	AJ595210	ARabidops
169	9.4	44.8	27	8	BZ378105	BZ378105	SALK 1071	c 242	9.2	43.8	27	1	AU254174	AU254174	AU254174
170	9.4	44.8	29	1	AU007063	AU007063	AU007063	c 243	9.2	43.8	27	7	D18735	D18735	MUSGS01797

C 244	9.2	43.8	27	8	A2427088	AZ427088	1M0208B24	317	9.2	43.8	50	1	AU105480	AU105480
C 245	9.2	43.8	27	8	A2810485	AZ810485	2M0076H05	318	9.2	43.8	50	1	AU108048	AU108048
C 246	9.2	43.8	28	8	A2441205	AZ441205	1M0232B10	319	9.2	43.8	50	5	BX722422	BX722422
C 247	9.2	43.8	29	1	AJ674160	AJ674160	AJ674160	C 320	9.2	43.8	50	7	CR437050	CR437050
C 248	9.2	43.8	29	9	AJ594026	AJ594026	Arabidops	321	9.2	43.8	50	9	BX977848	BX977848
C 249	9.2	43.8	29	9	AG198112	AG198112	Pan trogl	322	9.2	43.8	50	9	CR209280	CR209280
C 250	9.2	43.8	30	7	CF543220	CF543220	S014680-0	323	9.2	43.8	50	9	CL519142	CL519142
C 251	9.2	43.8	30	8	A2431038	AZ431038	1M0215I15	C 324	9.2	43.8	50	9	CL519142	CL519142
C 252	9.2	43.8	30	8	B2762449	BZ762449	SALK 1047	325	9.2	43.8	50	9	AZ592202	AZ592202
C 253	9.2	43.8	30	9	CG714388	CG714388	1119036D1	C 326	9.2	43.8	50	21	TA390C02P	TA390C02P
C 254	9.2	43.8	32	8	AZ765095	AZ765095	1M0561A22	327	9.2	43.8	50	23	AZ818662	AZ818662
C 255	9.2	43.8	33	9	DNE545578	AJ545578	Drosophil	328	9.2	43.8	50	23	AZ826455	AZ826455
C 256	9.2	43.8	34	1	AI125992	AI125992	qc4ed12.x	329	9.2	43.8	50	24	CO785230	CO785230
C 257	9.2	43.8	34	8	BH907363	BH907363	SALK 0397	330	9.2	43.8	50	25	AZ605844	AZ605844
C 258	9.2	43.8	34	8	B288240	BZ88240	SALK 0216	331	9.2	43.8	50	25	AZ655084	AZ655084
C 259	9.2	43.8	35	9	AZ820699	AZ820699	2M0093L02	332	9.2	43.8	50	25	CG114033	CG114033
C 260	9.2	43.8	35	9	TA103A09Q	AL460518	T. brucei	333	9.2	43.8	50	25	CG723016	CG723016
C 261	9.2	43.8	37	9	DR10838	AL744370	Danio rer	334	9.2	43.8	50	27	AZ831609	AZ831609
C 262	9.2	43.8	38	1	AU260238	AU260238	AU260238	C 335	9.2	43.8	50	27	AJ587528	AJ587528
C 263	9.2	43.8	38	8	AZ659279	AZ659279	1M0536L02	336	9.2	43.8	50	27	TA383D12Q	TA383D12Q
C 264	9.2	43.8	39	8	BH809708	BH809708	SALK 0050	337	9.2	43.8	50	27	CG13831	CG13831
C 265	9.2	43.8	39	8	BH908228	BH908228	SALK 0465	338	9.2	43.8	50	28	AI573848	AI573848
C 266	9.2	43.8	40	8	B2589975	BZ589975	3590_1_73	C 339	9.2	43.8	50	28	AJ795430	AJ795430
C 267	9.2	43.8	40	9	CL522373	CL522373	DAL2H04 F	C 340	9.2	43.8	50	28	AZ780159	AZ780159
C 268	9.2	43.8	41	1	AA253540	AZ253540	SWPFCAL43	C 341	9.2	43.8	50	29	AH46511	AH46511
C 269	9.2	43.8	41	8	AZ774470	AZ774470	2M0003P13	342	9.2	43.8	50	31	AU266417	AU266417
C 270	9.2	43.8	41	8	B2765629	BZ765629	SALK 1319	C 343	9.2	43.8	50	31	CF335931	CF335931
C 271	9.2	43.8	41	9	TA151G10Q	AL473068	T. brucei	344	9.2	43.8	50	31	BZ382978	BZ382978
C 272	9.2	43.8	42	8	AZ666806	AZ666806	1M0549N10	C 345	9.2	43.8	50	31	BX893918	BX893918
C 273	9.2	43.8	43	1	AA815634	AA815634	vt03d02.r	C 346	9.2	43.8	50	31	TA65G01Q	TA65G01Q
C 274	9.2	43.8	43	1	AA921653	AA921653	VY22d03.r	347	9.2	43.8	50	32	CD534487	CD534487
C 275	9.2	43.8	44	8	AZ646714	AZ646714	1M0512D21	C 348	9.2	43.8	50	32	AZ491344	AZ491344
C 276	9.2	43.8	45	9	TA372A04P	AL496098	T. brucei	349	9.2	43.8	50	32	AZ799655	AZ799655
C 277	9.2	43.8	45	9	CG892752	CG892752	01S0617-0	C 350	9.2	43.8	50	32	BZ358744	BZ358744
C 278	9.2	43.8	46	1	AI884160	AI884160	fc74e12.x	C 351	9.2	43.8	50	32	AJ590509	AJ590509
C 279	9.2	43.8	46	1	AA625631	AA625631	ad10d01.s	C 352	9.2	43.8	50	33	AJ647516	AJ647516
C 280	9.2	43.8	46	9	AJ591587	AJ591587	Arabidops	C 353	9.2	43.8	50	33	BH849814	BH849814
C 281	9.2	43.8	46	9	CR360032	CR360032	Arabidops	354	9.2	43.8	50	33	CG722737	CG722737
C 282	9.2	43.8	47	4	BI089840	BI089840	602855085	355	9.2	43.8	50	33	BH251010	BH251010
C 283	9.2	43.8	47	8	AQ026076	AQ026076	1(2)k1420	356	9.2	43.8	50	35	BH253542	BH253542
C 284	9.2	43.8	47	8	BH813914	BH813914	SALK 0654	357	9.2	43.8	50	35	BH613670	BH613670
C 285	9.2	43.8	47	8	BH846892	BH846892	SALK_0110	358	9.2	43.8	50	35	BH617331	BH617331
C 286	9.2	43.8	47	9	DNE545407	AU545407	Drosophil	359	9.2	43.8	50	35	BH617681	BH617681
C 287	9.2	43.8	47	9	AG197950	AG197950	Pan trogl	360	9.2	43.8	50	35	BH618593	BH618593
C 288	9.2	43.8	48	4	BJ083470	BJ083470	Arabidops	361	9.2	43.8	50	35	BH751605	BH751605
C 289	9.2	43.8	48	9	CR358002	CR358002	Arabidops	362	9.2	43.8	50	35	BH753496	BH753496
C 290	9.2	43.8	49	1	AA109169	AA109169	mp38f04.r	C 363	9.2	43.8	50	35	BH854633	BH854633
C 291	9.2	43.8	49	4	BG292262	BG292262	602386710	C 364	9.2	43.8	50	35	TA248D10Q	TA248D10Q
C 292	9.2	43.8	49	4	BI760726	BI760726	603044726	C 365	9.2	43.8	50	36	T61825	T61825
C 293	9.2	43.8	49	8	CG325828	CG325828	RRG292_Ba	366	9.2	43.8	50	36	BH751713	BH751713
C 294	9.2	43.8	49	9	CG779221	CG779221	1123032D0	367	9.2	43.8	50	36	CG713884	CG713884
C 295	9.2	43.8	49	9	AG190566	AG190566	Pan trogl	368	9.2	43.8	50	36	CG714202	CG714202
C 296	9.2	43.8	50	1	AI920149	AI920149	1679_Pine	369	9.2	43.8	50	36	CG714303	CG714303
C 297	9.2	43.8	50	1	AU102923	AU102923	AU102923	370	9.2	43.8	50	36	AU010468	AU010468
C 298	9.2	43.8	50	1	AU102930	AU102930	AU102930	371	9.2	43.8	50	37	AU010469	AU010469
C 299	9.2	43.8	50	1	AU102933	AU102933	AU102933	372	9.2	43.8	50	37	BH211687	BH211687
C 300	9.2	43.8	50	1	AU102934	AU102934	AU102934	373	9.2	43.8	50	37	BH212711	BH212711
C 301	9.2	43.8	50	1	AU102935	AU102935	AU102935	374	9.2	43.8	50	37	BH213109	BH213109
C 302	9.2	43.8	50	1	AU102936	AU102936	AU102936	375	9.2	43.8	50	37	BH254171	BH254171
C 303	9.2	43.8	50	1	AU102937	AU102937	AU102937	376	9.2	43.8	50	37	BH612755	BH612755
C 304	9.2	43.8	50	1	AU102947	AU102947	AU102947	377	9.2	43.8	50	37	BH613685	BH613685
C 305	9.2	43.8	50	1	AU102948	AU102948	AU102948	378	9.2	43.8	50	37	BH613909	BH613909
C 306	9.2	43.8	50	1	AU102954	AU102954	AU102954	379	9.2	43.8	50	37	BH613940	BH613940
C 307	9.2	43.8	50	1	AU103589	AU103589	AU103589	380	9.2	43.8	50	37	BH617568	BH617568
C 308	9.2	43.8	50	1	AU104153	AU104153	AU104153	381	9.2	43.8	50	37	BH617569	BH617569
C 309	9.2	43.8	50	1	AU104179	AU104179	AU104179	382	9.2	43.8	50	37	BH617569	BH617569
C 310	9.2	43.8	50	1	AU104207	AU104207	AU104207	383	9.2	43.8	50	37	BH633214	BH633214
C 311	9.2	43.8	50	1	AU105472	AU105472	AU105472	384	9.2	43.8	50	37	BH751779	BH751779
C 312	9.2	43.8	50	1	AU105473	AU105473	AU105473	385	9.2	43.8	50	37	BH751802	BH751802
C 313	9.2	43.8	50	1	AU105474	AU105474	AU105474	386	9.2	43.8	50	37	BH791757	BH791757
C 314	9.2	43.8	50	1	AU105475	AU105475	AU105475	C 387	9.2	43.8	50	37	CG711288	CG711288
C 315	9.2	43.8	50	1	AU105476	AU105476	AU105476	388	9.2	43.8	50	37	CG713746	CG713746
C 316	9.2	43.8	50	1	AU105479	AU105479	AU105479	389	9.2	43.8	50	37	CG722734	CG722734

390	9	42.9	37	9	CG724536	CG724536	1119081F0	463	9	42.9	44	8	BH172646	BH172646	SALK_0059
391	9	42.9	38	4	BM400755	BM400755	5009-0-78	464	9	42.9	44	8	BH172689	BH172689	SALK_0060
392	9	42.9	38	8	BH170263	BH170263	SALK_0026	465	9	42.9	44	8	BH173144	BH173144	SALK_0000
393	9	42.9	38	8	BH611224	BH611224	SALK_0304	466	9	42.9	44	8	BH212259	BH212259	SALK_0073
394	9	42.9	38	8	BH612424	BH612424	SALK_0326	467	9	42.9	44	8	BH212377	BH212377	SALK_0075
395	9	42.9	38	8	BH792093	BH792093	SALK_0626	468	9	42.9	44	8	BH212514	BH212514	SALK_0076
396	9	42.9	38	9	CG287919	CG287919	Arabidops	469	9	42.9	44	8	BH213282	BH213282	SALK_0090
397	9	42.9	38	9	CG729929	CG729929	1119116F0	470	9	42.9	44	8	BH251475	BH251475	SALK_0116
398	9	42.9	39	4	BI660394	BI660394	602283080	471	9	42.9	44	8	BH251575	BH251575	SALK_0118
399	9	42.9	39	4	BH212311	BH212311	SALK_0074	472	9	42.9	44	8	BH251615	BH251615	SALK_0118
400	9	42.9	39	8	BH212359	BH212359	SALK_0074	473	9	42.9	44	8	BH251830	BH251830	SALK_0121
401	9	42.9	39	8	BH751820	BH751820	SALK_0506	474	9	42.9	44	8	BH251946	BH251946	SALK_0123
402	9	42.9	39	8	BH751820	BH751820	SALK_0506	475	9	42.9	44	8	BH252164	BH252164	SALK_0128
403	9	42.9	39	9	CG713565	CG713565	1119032D0	476	9	42.9	44	8	BH252206	BH252206	SALK_0129
404	9	42.9	40	1	AI613042	AI613042	ty06h09.X	477	9	42.9	44	8	BH252225	BH252225	SALK_0129
405	9	42.9	40	1	AI805437	AI805437	tx96e03.X	478	9	42.9	44	8	BH252253	BH252253	SALK_0130
406	9	42.9	40	8	BH212182	BH212182	SALK_0072	479	9	42.9	44	8	BH252260	BH252260	SALK_0130
407	9	42.9	40	8	BH212218	BH212218	SALK_0072	480	9	42.9	44	8	BH252306	BH252306	SALK_0135
408	9	42.9	40	8	BH751805	BH751805	SALK_0349	481	9	42.9	44	8	BH252718	BH252718	SALK_0137
409	9	42.9	40	8	BH751840	BH751840	SALK_0504	482	9	42.9	44	8	BH252765	BH252765	SALK_0138
410	9	42.9	40	9	CG796357	CG796357	Arabidops	483	9	42.9	44	8	BH252848	BH252848	SALK_0139
411	9	42.9	40	9	CG729877	CG729877	1119116F0	484	9	42.9	44	8	BH252865	BH252865	SALK_0139
412	9	42.9	40	1	AV834393	AV834393	AV834393	485	9	42.9	44	8	BH253523	BH253523	SALK_0150
413	9	42.9	41	8	AQ025324	AQ025324	EP(X)0362	486	9	42.9	44	8	BH253838	BH253838	SALK_0155
414	9	42.9	41	8	AZ454047	AZ454047	1M0255015	487	9	42.9	44	8	BH254181	BH254181	SALK_0161
415	9	42.9	41	8	AZ454047	AZ454047	1M0255015	488	9	42.9	44	8	BH254446	BH254446	SALK_0165
416	9	42.9	41	8	AZ475800	AZ475800	1M0294G10	489	9	42.9	44	8	BH254727	BH254727	SALK_0171
417	9	42.9	41	8	AZ773365	AZ773365	1M0584A20	490	9	42.9	44	8	BH611523	BH611523	SALK_0310
418	9	42.9	41	8	BH252552	BH252552	SALK_0135	491	9	42.9	44	8	BH611569	BH611569	SALK_0311
419	9	42.9	41	8	BH254298	BH254298	SALK_0163	492	9	42.9	44	8	BH611657	BH611657	SALK_0315
420	9	42.9	41	8	BH610796	BH610796	SALK_0180	493	9	42.9	44	8	BH611723	BH611723	SALK_0316
421	9	42.9	41	8	BH611601	BH611601	SALK_0312	494	9	42.9	44	8	BH611974	BH611974	SALK_0319
422	9	42.9	41	8	BH614048	BH614048	SALK_0353	495	9	42.9	44	8	BH612122	BH612122	SALK_0321
423	9	42.9	41	8	BH749252	BH749252	SALK_0475	496	9	42.9	44	8	BH612168	BH612168	SALK_0322
424	9	42.9	41	8	BH749713	BH749713	SALK_0286	497	9	42.9	44	8	BH612218	BH612218	SALK_0323
425	9	42.9	41	8	BH751659	BH751659	SALK_0504	498	9	42.9	44	8	BH612350	BH612350	SALK_0325
426	9	42.9	41	8	BZ663233	BZ663233	SALK_0268	499	9	42.9	44	8	BH612910	BH612910	SALK_0334
427	9	42.9	41	9	DM5547498	DM5547498	T. brucei	500	9	42.9	44	8	BH613025	BH613025	SALK_0336
428	9	42.9	41	9	TA131C04P	TA131C04P	Arabidops	501	9	42.9	44	8	BH613029	BH613029	SALK_0339
429	9	42.9	42	8	BH611542	BH611542	SALK_0311	502	9	42.9	44	8	BH613233	BH613233	SALK_0339
430	9	42.9	42	8	BH624495	BH624495	1007078G0	503	9	42.9	44	8	BH613425	BH613425	SALK_0342
431	9	42.9	42	8	BH750272	BH750272	SALK_0376	504	9	42.9	44	8	BH613572	BH613572	SALK_0344
432	9	42.9	42	9	AL765989	AL765989	Arabidops	505	9	42.9	44	8	BH617039	BH617039	SALK_0358
433	9	42.9	42	9	CG729941	CG729941	1119116F0	506	9	42.9	44	8	BH617095	BH617095	SALK_0359
434	9	42.9	42	9	CL705862	CL705862	EY00848-3	507	9	42.9	44	8	BH617247	BH617247	SALK_0361
435	9	42.9	43	1	AA928331	AA928331	cm76c12.8	508	9	42.9	44	8	BH617442	BH617442	SALK_0365
436	9	42.9	43	1	AI657864	AI657864	fc14e05.Y	509	9	42.9	44	8	BH617506	BH617506	SALK_0371
437	9	42.9	43	1	AA241931	AA241931	mx28a04.r	510	9	42.9	44	8	BH617771	BH617771	SALK_0377
438	9	42.9	43	1	AA549203	AA549203	vk85d08.s	511	9	42.9	44	8	BH617921	BH617921	SALK_0381
439	9	42.9	43	8	BH173048	BH173048	SALK_0014	512	9	42.9	44	8	BH617944	BH617944	SALK_0381
440	9	42.9	43	8	BH254096	BH254096	SALK_0159	513	9	42.9	44	8	BH618166	BH618166	SALK_0386
441	9	42.9	43	8	BH611286	BH611286	SALK_0306	514	9	42.9	44	8	BH618486	BH618486	SALK_0391
442	9	42.9	43	8	BH611477	BH611477	SALK_0309	515	9	42.9	44	8	BH618549	BH618549	SALK_0392
443	9	42.9	43	8	BH612999	BH612999	SALK_0336	516	9	42.9	44	8	BH633222	BH633222	SALK_0394
444	9	42.9	43	8	BH613221	BH613221	SALK_0339	517	9	42.9	44	8	BH634244	BH634244	SALK_0410
445	9	42.9	43	8	BH617226	BH617226	SALK_0361	518	9	42.9	44	8	BH750166	BH750166	SALK_0416
446	9	42.9	43	8	BH617444	BH617444	SALK_0365	519	9	42.9	44	8	BH750554	BH750554	SALK_0500
447	9	42.9	43	8	BH750703	BH750703	SALK_0422	520	9	42.9	44	8	BH752016	BH752016	SALK_0516
448	9	42.9	44	8	BH168728	BH168728	SALK_0001	521	9	42.9	44	8	BH752121	BH752121	SALK_0517
449	9	42.9	44	8	BH168811	BH168811	SALK_0002	522	9	42.9	44	8	BH752301	BH752301	SALK_0517
450	9	42.9	44	8	BH168944	BH168944	SALK_0003	523	9	42.9	44	8	BH752319	BH752319	SALK_0517
451	9	42.9	44	8	BH168955	BH168955	SALK_0004	524	9	42.9	44	8	BH752330	BH752330	SALK_0517
452	9	42.9	44	8	BH169147	BH169147	SALK_0007	525	9	42.9	44	8	BH752350	BH752350	SALK_0517
453	9	42.9	44	8	BH169189	BH169189	SALK_0014	526	9	42.9	44	8	BH752481	BH752481	SALK_0517
454	9	42.9	44	8	BH169506	BH169506	SALK_0014	527	9	42.9	44	8	BH752619	BH752619	SALK_0517
455	9	42.9	44	8	BH169809	BH169809	SALK_0019	528	9	42.9	44	8	BH908840	BH908840	SALK_0507
456	9	42.9	44	8	BH169920	BH169920	SALK_0020	529	9	42.9	44	8	AL757126	AL757126	Arabidops
457	9	42.9	44	8	BH170451	BH170451	SALK_0029	530	9	42.9	44	9	CG714300	CG714300	SALK_0516
458	9	42.9	44	8	BH171381	BH171381	SALK_0041	531	9	42.9	44	9	CG724480	CG724480	SALK_0516
459	9	42.9	44	8	BH171826	BH171826	SALK_0048	532	9	42.9	44	9	2M0083M04	2M0083M04	
460	9	42.9	44	8	BH172056	BH172056	SALK_0051	533	9	42.9	44	9			
461	9	42.9	44	8	BH172538	BH172538	SALK_0058	534	9	42.9	44	9			
462	9	42.9	44	8				535	9	42.9	45	8			

536	9	42.9	45	8	BH168809	BH168809	SALK_0002	609	9	42.9	48	8	BH172074	BH172074	SALK_0052
537	9	42.9	45	8	BH169016	BH169016	SALK_0004	610	9	42.9	48	8	BH172483	BH172483	SALK_0057
538	9	42.9	45	8	BH169715	BH169715	SALK_0017	611	9	42.9	48	8	BH173104	BH173104	SALK_0013
539	9	42.9	45	8	BH170991	BH170991	SALK_0036	612	9	42.9	48	8	BH211911	BH211911	SALK_0068
540	9	42.9	45	8	BH171160	BH171160	SALK_0038	613	9	42.9	48	8	BH212124	BH212124	SALK_0071
541	9	42.9	45	8	BH172480	BH172480	SALK_0057	614	9	42.9	48	8	BH212192	BH212192	SALK_0072
542	9	42.9	45	8	BH251855	BH251855	SALK_0122	615	9	42.9	48	8	BH212362	BH212362	SALK_0074
543	9	42.9	45	8	BH252041	BH252041	SALK_0124	616	9	42.9	48	8	BH213362	BH213362	SALK_0091
544	9	42.9	45	8	BH252624	BH252624	SALK_0136	617	9	42.9	48	8	BH213445	BH213445	SALK_0092
545	9	42.9	45	8	BH253683	BH253683	SALK_0152	618	9	42.9	48	8	BH213559	BH213559	SALK_0093
546	9	42.9	45	8	BH610643	BH610643	SALK_0177	619	9	42.9	48	8	BH214012	BH214012	SALK_0100
547	9	42.9	45	8	BH613489	BH613489	SALK_0343	620	9	42.9	48	8	BH214058	BH214058	SALK_0101
548	9	42.9	45	8	BH617238	BH617238	SALK_0361	621	9	42.9	48	8	BH251827	BH251827	SALK_0121
549	9	42.9	45	8	BH617343	BH617343	SALK_0363	622	9	42.9	48	8	BH252179	BH252179	SALK_0128
550	9	42.9	45	8	BH617375	BH617375	SALK_0364	623	9	42.9	48	8	BH252272	BH252272	SALK_0130
551	9	42.9	45	8	BH617528	BH617528	SALK_0372	624	9	42.9	48	8	BH253038	BH253038	SALK_0143
552	9	42.9	45	8	BH618005	BH618005	SALK_0383	625	9	42.9	48	8	BH253184	BH253184	SALK_0145
553	9	42.9	45	8	BH618006	BH618006	SALK_0383	626	9	42.9	48	8	BH253291	BH253291	SALK_0147
554	9	42.9	45	8	BH618252	BH618252	SALK_0387	627	9	42.9	48	8	BH253306	BH253306	SALK_0147
555	9	42.9	45	8	BH619123	BH619123	SALK_0402	628	9	42.9	48	8	BH253358	BH253358	SALK_0148
556	9	42.9	45	8	BH749090	BH749090	SALK_0472	629	9	42.9	48	8	BH253833	BH253833	SALK_0155
557	9	42.9	45	8	BH790393	BH790393	SALK_0569	630	9	42.9	48	8	BH254186	BH254186	SALK_0161
558	9	42.9	46	1	A1735034	ase6h04.x		631	9	42.9	48	8	BH254463	BH254463	SALK_0165
559	9	42.9	46	1	A1735034	ase6h04.x		632	9	42.9	48	8	BH254917	BH254917	SALK_0174
560	9	42.9	46	7	H52294	CHR220233.C		633	9	42.9	48	8	BH610731	BH610731	SALK_0179
561	9	42.9	46	8	BH168816	BH168816	SALK_0002	634	9	42.9	48	8	BH610835	BH610835	SALK_0181
562	9	42.9	46	8	BH169680	BH169680	SALK_0017	635	9	42.9	48	8	BH610916	BH610916	SALK_0182
563	9	42.9	46	8	BH172748	BH172748	SALK_0061	636	9	42.9	48	8	BH611306	BH611306	SALK_0306
564	9	42.9	46	8	BH212329	BH212329	SALK_0074	637	9	42.9	48	8	BH611439	BH611439	SALK_0309
565	9	42.9	46	8	BH213521	BH213521	SALK_0093	638	9	42.9	48	8	BH611499	BH611499	SALK_0310
566	9	42.9	46	8	BH252530	BH252530	SALK_0135	639	9	42.9	48	8	BH611861	BH611861	SALK_0318
567	9	42.9	46	8	BH611610	BH611610	SALK_0312	640	9	42.9	48	8	BH612357	BH612357	SALK_0325
568	9	42.9	46	8	BH618888	BH618888	SALK_0399	641	9	42.9	48	8	BH613342	BH613342	SALK_0341
569	9	42.9	46	8	BH641999	BH641999	1008052B0	642	9	42.9	48	8	BH614164	BH614164	SALK_0355
570	9	42.9	46	8	BH747763	BH747763	SALK_0340	643	9	42.9	48	8	BH617377	BH617377	SALK_0364
571	9	42.9	46	8	BH751055	BH751055	SALK_0487	644	9	42.9	48	8	BH617696	BH617696	SALK_0374
572	9	42.9	46	8	BH910540	BH910540	SALK_0601	645	9	42.9	48	8	BH633587	BH633587	SALK_0428
573	9	42.9	46	9	CC887473	CC887473	SALK_1502	646	9	42.9	48	8	BH748267	BH748267	SALK_0450
574	9	42.9	46	9	CG782542	CG782542	1123050H0	647	9	42.9	48	8	BH748292	BH748292	SALK_0451
575	9	42.9	47	8	A2623246	A2623246	1M0460C17	648	9	42.9	48	8	BH748882	BH748882	SALK_0469
576	9	42.9	47	8	A2779546	A2779546	2M0016C09	649	9	42.9	48	8	BH749772	BH749772	SALK_0302
577	9	42.9	47	8	BH169602	BH169602	SALK_0016	650	9	42.9	48	8	BH749892	BH749892	SALK_0303
578	9	42.9	47	8	BH172194	BH172194	SALK_0053	651	9	42.9	48	8	BH750103	BH750103	SALK_0347
579	9	42.9	47	8	BH172688	BH172688	SALK_0060	652	9	42.9	48	8	BH751416	BH751416	SALK_0501
580	9	42.9	47	8	BH213222	BH213222	SALK_0089	653	9	42.9	48	8	BH753224	BH753224	SALK_0199
581	9	42.9	47	8	BH213678	BH213678	SALK_0095	654	9	42.9	48	8	BH753678	BH753678	SALK_0294
582	9	42.9	47	8	BH214187	BH214187	SALK_0103	655	9	42.9	48	8	BH902361	BH902361	SALK_0917
583	9	42.9	47	8	BH252265	BH252265	SALK_0130	656	9	42.9	48	8	B2382688	B2382688	SALK_1186
585	9	42.9	47	8	BH252337	BH252337	SALK_0138	657	9	42.9	48	9	EX286631	EX286631	ArabiDops
586	9	42.9	47	8	BH253852	BH253852	SALK_0155	658	9	42.9	49	1	AA706582	AA706582	ah27b06.8
587	9	42.9	47	8	BH611281	BH611281	SALK_0306	659	9	42.9	49	1	AA726836	AA726836	vu94g12.r
588	9	42.9	47	8	BH611531	BH611531	SALK_0310	660	9	42.9	49	1	AI558595	AI558595	fb68a10.y
589	9	42.9	47	8	BH612570	BH612570	SALK_0329	661	9	42.9	49	1	AI584385	AI584385	fb92h12.x
590	9	42.9	47	8	BH617563	BH617563	SALK_0372	662	9	42.9	49	1	AI883392	AI883392	fc63c06.y
591	9	42.9	47	8	BH618704	BH618704	SALK_0395	663	9	42.9	49	1	A0015938	A0015938	A0013938
592	9	42.9	47	8	BH747945	BH747945	SALK_0397	664	9	42.9	49	5	BQ587334	BQ587334	E012340w-
593	9	42.9	47	8	BH748581	BH748581	SALK_0461	665	9	42.9	49	5	BQ587752	BQ587752	E012340-0
594	9	42.9	47	8	BH752651	BH752651	SALK_0189	666	9	42.9	49	7	X98140	X98140	MMEST49.Mou
595	9	42.9	47	8	BH753401	BH753401	SALK_0287	667	9	42.9	49	8	BH168986	BH168986	SALK_0004
596	9	42.9	47	8	BH851673	BH851673	SALK_0733	668	9	42.9	49	8	BH169475	BH169475	SALK_0014
597	9	42.9	47	9	AL946412	AL946412	ArabiDops	669	9	42.9	49	8	BH170166	BH170166	SALK_0034
598	9	42.9	47	9	CG714468	CG714468	1119036H0	670	9	42.9	49	8	BH170234	BH170234	SALK_0025
599	9	42.9	48	1	AV967257	AV967257	SALK_0006	671	9	42.9	49	8	BH172398	BH172398	SALK_0056
600	9	42.9	48	8	BH169127	BH169127	SALK_0020	672	9	42.9	49	8	BH212186	BH212186	SALK_0072
601	9	42.9	48	8	BH169313	BH169313	SALK_0020	673	9	42.9	49	8	BH212189	BH212189	SALK_0072
602	9	42.9	48	8	BH170421	BH170421	SALK_0028	674	9	42.9	49	8	BH213269	BH213269	SALK_0089
603	9	42.9	48	8	BH170455	BH170455	SALK_0029	675	9	42.9	49	8	BH251862	BH251862	SALK_0122
604	9	42.9	48	8	BH170532	BH170532	SALK_0030	676	9	42.9	49	8	BH252868	BH252868	SALK_0139
605	9	42.9	48	8	BH170799	BH170799	SALK_0033	677	9	42.9	49	8	BH253161	BH253161	SALK_0145
606	9	42.9	48	8	BH171310	BH171310	SALK_0040	678	9	42.9	49	8	BH253743	BH253743	SALK_0153
607	9	42.9	48	8	BH171340	BH171340	SALK_0041	679	9	42.9	49	8	BH253938	BH253938	SALK_0157
608	9	42.9	48	8	BH171719	BH171719	SALK_0047	680	9	42.9	49	8	BH614128	BH614128	SALK_0355
								681	9	42.9	49	8	BH748794	BH748794	SALK_0467

682	9	42.9	49	8	BH752698	SALK_0192	755	8.8	41.9	31	9	AG194290	Pan trogl
683	9	42.9	49	8	BH753750	SALK_0295	756	8.8	41.9	32	8	AZ485865	IM0313H02
684	9	42.9	49	9	AJ596083	Arabidops	757	8.8	41.9	32	8	AZ583239	IM0378K08
685	9	42.9	49	9	CNS007F9C	Arabidops	758	8.8	41.9	32	8	BZ381666	SALK_1170
686	9	42.9	49	9	CR400023	Arabidops	759	8.8	41.9	32	8	BZ383892	SALK_1347
687	9	42.9	50	1	AL802196	AL802196	760	8.8	41.9	32	9	EX656781	Arabidops
688	9	42.9	50	1	AUI102484	AUI102484	761	8.8	41.9	32	9	CR359094	Arabidops
689	9	42.9	50	1	AUI104254	AUI104254	762	8.8	41.9	32	9	CR359095	Arabidops
690	9	42.9	50	1	AUI105296	AUI105296	763	8.8	41.9	32	9	DMES45221	Drosophil
691	9	42.9	50	1	AUI107262	AUI107262	764	8.8	41.9	32	1	AV834380	AV834380
692	9	42.9	50	1	AUI107263	AUI107263	765	8.8	41.9	33	1	B1656215	603283594
693	9	42.9	50	1	AUI107510	AUI107510	766	8.8	41.9	33	7	T89682	Y099F02.s1
694	9	42.9	50	1	AUI107860	AUI107860	767	8.8	41.9	33	8	AZ316728	IM0035A15
695	9	42.9	50	1	AUI107968	AUI107968	768	8.8	41.9	33	8	BZ380694	SALK_1155
696	9	42.9	50	1	AZ108799	AZ108799	769	8.8	41.9	33	8	BZ382892	SALK_1190
697	9	42.9	50	8	BH211702	BH211702	770	8.8	41.9	33	8	CC049737	0190506-0
698	9	42.9	50	8	BH213709	BH213709	771	8.8	41.9	33	9	AJ599957	Arabidops
699	9	42.9	50	8	BH253148	BH253148	772	8.8	41.9	34	8	BZ377896	SALK_1063
700	9	42.9	50	8	BH611167	BH611167	773	8.8	41.9	34	8	BZ380603	SALK_1153
701	9	42.9	50	8	BH612727	BH612727	774	8.8	41.9	34	9	CG723116	CG723116
702	9	42.9	50	8	BH617293	BH617293	775	8.8	41.9	35	8	AZ838159	2M0133C15
703	9	42.9	50	8	BH617418	BH617418	776	8.8	41.9	35	8	BH847051	SALK_0129
704	9	42.9	50	8	BH747393	BH747393	777	8.8	41.9	35	8	BH852456	SALK_0746
705	9	42.9	50	8	BH750106	BH750106	778	8.8	41.9	35	8	BZ378301	SALK_1079
706	9	42.9	50	8	BH753469	BH753469	779	8.8	41.9	35	8	BZ380621	SALK_1154
707	9	42.9	50	8	BX572281	BX572281	780	8.8	41.9	35	8	BZ380790	SALK_1156
708	9	42.9	50	9	CC547498	CC547498	781	8.8	41.9	35	8	BZ383613	SALK_1341
709	9	42.9	50	9	CG711376	CG711376	782	8.8	41.9	35	8	BZ763321	SALK_1162
710	9	42.9	50	9	CG713887	CG713887	783	8.8	41.9	35	8	AL947040	Arabidops
711	9	42.9	50	9	CG894689	CG894689	784	8.8	41.9	35	9	DR31814T	AL980561
712	8.8	41.9	20	1	AU258084	AU258084	785	8.8	41.9	36	8	AQ073401	EP(2)_2212
713	8.8	41.9	21	5	BX566484	BX566484	786	8.8	41.9	36	8	BZ380578	SALK_1153
714	8.8	41.9	21	8	AZ309721	AZ309721	787	8.8	41.9	36	9	TA126A03P	AA9377326
715	8.8	41.9	22	9	TA2309E03P	TA2309E03P	788	8.8	41.9	37	1	AA984865	am62b07.s
716	8.8	41.9	22	9	CL438518	CL438518	789	8.8	41.9	37	1	AA984865	am62b07.s
717	8.8	41.9	22	9	CL670198	CL670198	790	8.8	41.9	37	1	AA142601	ok35d07.s
718	8.8	41.9	22	9	AG195487	AG195487	791	8.8	41.9	37	2	BF122604	BF122604
719	8.8	41.9	23	8	AZ805705	AZ805705	792	8.8	41.9	37	4	BJ049420	BJ049420
720	8.8	41.9	24	7	L32029	L32029	793	8.8	41.9	37	8	AZ653729	IM0037N16
721	8.8	41.9	24	8	AZ469511	AZ469511	794	8.8	41.9	37	8	AZ789498	2M017E07
722	8.8	41.9	24	8	AZ475486	AZ475486	795	8.8	41.9	37	8	AZ863572	2M017E07
723	8.8	41.9	25	1	AJ679528	AJ679528	796	8.8	41.9	37	8	BZ377641	SALK_0986
724	8.8	41.9	25	8	AZ654827	AZ654827	797	8.8	41.9	37	8	BZ377654	SALK_0987
725	8.8	41.9	26	1	AU011509	AU011509	798	8.8	41.9	37	8	BZ377656	SALK_0987
726	8.8	41.9	26	8	AZ427547	AZ427547	800	8.8	41.9	37	8	BZ377658	SALK_0987
727	8.8	41.9	26	8	AZ623173	AZ623173	801	8.8	41.9	37	8	BZ377667	SALK_0987
728	8.8	41.9	26	8	AZ821460	AZ821460	802	8.8	41.9	37	8	BZ377667	SALK_0987
729	8.8	41.9	26	9	TA252D07Q	TA252D07Q	803	8.8	41.9	37	8	BZ377667	SALK_0987
730	8.8	41.9	27	8	AZ347928	AZ347928	804	8.8	41.9	37	8	BZ377667	SALK_0987
731	8.8	41.9	27	9	TA354A04Q	TA354A04Q	805	8.8	41.9	37	8	BZ377667	SALK_0987
732	8.8	41.9	28	1	AI076131	AI076131	806	8.8	41.9	37	8	BZ377667	SALK_0987
733	8.8	41.9	28	8	AZ780159	AZ780159	807	8.8	41.9	37	8	BZ377667	SALK_0987
734	8.8	41.9	28	8	AZ783515	AZ783515	808	8.8	41.9	37	8	BZ377667	SALK_0987
735	8.8	41.9	28	9	TA300B03Q	TA300B03Q	809	8.8	41.9	37	8	BZ377667	SALK_0987
736	8.8	41.9	29	5	BQ595553	BQ595553	810	8.8	41.9	37	8	BZ377667	SALK_0987
737	8.8	41.9	29	8	AQ025252	AQ025252	811	8.8	41.9	37	8	BZ377667	SALK_0987
738	8.8	41.9	29	8	AZ775915	AZ775915	812	8.8	41.9	37	8	BZ377667	SALK_0987
739	8.8	41.9	29	8	BH906395	BH906395	813	8.8	41.9	37	8	BZ377667	SALK_0987
740	8.8	41.9	29	8	BZ380586	BZ380586	814	8.8	41.9	37	8	BZ377667	SALK_0987
741	8.8	41.9	29	8	BZ380648	BZ380648	815	8.8	41.9	37	8	BZ377667	SALK_0987
742	8.8	41.9	29	8	BZ380770	BZ380770	816	8.8	41.9	37	8	BZ377667	SALK_0987
743	8.8	41.9	29	8	BZ384011	BZ384011	817	8.8	41.9	37	8	BZ377667	SALK_0987
744	8.8	41.9	29	8	BZ765533	BZ765533	818	8.8	41.9	37	8	BZ377667	SALK_0987
745	8.8	41.9	30	9	AX289793	AX289793	819	8.8	41.9	37	8	BZ377667	SALK_0987
746	8.8	41.9	31	1	AA781776	AA781776	820	8.8	41.9	37	8	BZ377667	SALK_0987
747	8.8	41.9	31	1	AA107884	AA107884	821	8.8	41.9	37	8	BZ377667	SALK_0987
748	8.8	41.9	31	1	AA590433	AA590433	822	8.8	41.9	37	8	BZ377667	SALK_0987
749	8.8	41.9	31	4	BG432088	BG432088	823	8.8	41.9	37	8	BZ377667	SALK_0987
750	8.8	41.9	31	7	CO782526	CO782526	824	8.8	41.9	37	8	BZ377667	SALK_0987
751	8.8	41.9	31	8	AZ318049	AZ318049	825	8.8	41.9	37	8	BZ377667	SALK_0987
752	8.8	41.9	31	8	AZ318049	AZ318049	826	8.8	41.9	37	8	BZ377667	SALK_0987
753	8.8	41.9	31	8	BZ381518	BZ381518	827	8.8	41.9	37	8	BZ377667	SALK_0987
754	8.8	41.9	31	9	BZ383871	BZ383871	827	8.8	41.9	37	8	BZ377667	SALK_0987

828	8.8	41.9	37	8	B2381631	B2381631	SALK_1170	901	8.8	41.9	45	8	BH908303	BH908303	SALK_0471
829	8.8	41.9	37	8	B2381688	B2381688	SALK_1171	c 902	8.8	41.9	45	8	CC178546	CC178546	NPX482 Ba
830	8.8	41.9	37	8	B2381722	B2381722	SALK_1171	c 903	8.8	41.9	45	9	AL764750	AL764750	Arabidops
831	8.8	41.9	37	8	B2381723	B2381723	SALK_1171	904	8.8	41.9	46	1	AV834157	AV834157	AV834157
832	8.8	41.9	37	8	B2381736	B2381736	SALK_1171	905	8.8	41.9	46	1	AA616469	AA616469	vn66d10.1
833	8.8	41.9	37	8	B2383575	B2383575	SALK_1341	906	8.8	41.9	45	8	BH861568	BH861568	SALK_0818
834	8.8	41.9	37	8	B2383596	B2383596	SALK_1341	907	8.8	41.9	46	8	BZ287326	BZ287326	SALK_0206
835	8.8	41.9	37	8	B2383623	B2383623	SALK_1341	908	8.8	41.9	46	8	BZ383801	BZ383801	SALK_1345
836	8.8	41.9	37	8	B2383627	B2383627	SALK_1341	909	8.8	41.9	46	9	AL7622642	AL7622642	Drosophil
837	8.8	41.9	37	8	B2383631	B2383631	SALK_1342	910	8.8	41.9	46	9	AL758842	AL758842	Arabidops
838	8.8	41.9	37	8	B2383632	B2383632	SALK_1342	911	8.8	41.9	47	6	CF329526	CF329526	NACL--04-
839	8.8	41.9	37	8	B2383659	B2383659	SALK_1342	912	8.8	41.9	47	8	AZ856490	AZ856490	2M0160K22
840	8.8	41.9	37	8	B2383661	B2383661	SALK_1342	913	8.8	41.9	47	8	CC039002	CC039002	3591_1_99
841	8.8	41.9	37	8	B2383666	B2383666	SALK_1342	914	8.8	41.9	48	1	AI749566	AI749566	at30f01.x
842	8.8	41.9	37	8	B2383686	B2383686	SALK_1342	c 915	8.8	41.9	48	7	D19123	D19123	MUSGS01337
843	8.8	41.9	37	8	B2383686	B2383686	SALK_1342	916	8.8	41.9	48	8	AZ458771	AZ458771	1M0263H10
844	8.8	41.9	37	8	B2383862	B2383862	SALK_1346	917	8.8	41.9	48	8	AZ503560	AZ503560	1M0343821
845	8.8	41.9	37	8	B2766033	B2766033	SALK_1365	c 918	8.8	41.9	48	8	CC179090	CC179090	SALK_0582
846	8.8	41.9	37	8	BH857421	BH857421	SALK_0748	c 919	8.8	41.9	48	9	EX122790	EX122790	Danio_per
847	8.8	41.9	38	8	BH857421	BH857421	SALK_0748	920	8.8	41.9	48	9	CG778060	CG778060	1123025E0
c 848	8.8	41.9	38	8	BZ380646	BZ380646	SALK_1154	c 921	8.8	41.9	48	9	CG918667	CG918667	01S0556-0
c 849	8.8	41.9	38	8	BZ768853	BZ768853	SALK_1408	c 922	8.8	41.9	48	9	CL528747	CL528747	ASV7F07.f
c 850	8.8	41.9	38	9	AL942413	AL942413	Arabidops	c 923	8.8	41.9	49	1	AA657082	AA657082	vs23c09.1
c 851	8.8	41.9	38	9	BX287148	BX287148	Arabidops	c 924	8.8	41.9	49	1	AA948394	AA948394	on52b09.s
c 852	8.8	41.9	39	8	AG217395	AG217395	Drosophil	c 925	8.8	41.9	49	1	AI004508	AI004508	ot66g10.s
c 853	8.8	41.9	39	8	AZ595333	AZ595333	1M0407F23	c 926	8.8	41.9	49	1	AI359268	AI359268	gy27c06.x
c 854	8.8	41.9	39	8	AZ773859	AZ773859	2M0001110	c 927	8.8	41.9	49	1	AI444171	AI444171	fb43b07.y
c 855	8.8	41.9	40	1	AG261161	AG261161	Lotus cor	c 928	8.8	41.9	49	1	AI638467	AI638467	tt07d10.x
c 856	8.8	41.9	40	1	AI219362	AI219362	qg14e08.x	c 929	8.8	41.9	49	1	AI738824	AI738824	wi39d04.x
c 857	8.8	41.9	40	6	CF305521	CF305521	CLD1--01-	c 930	8.8	41.9	49	4	BI525053	BI525053	602325110
c 858	8.8	41.9	40	6	BZ723776	BZ723776	1M0583011	c 931	8.8	41.9	49	6	CB337845	CB337845	laa29h07.
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c 863	8.8	41.9	41	1	AU266348	AU266348		c 936	8.8	41.9	49	8	CC045158	CC045158	3591_1_17
c 864	8.8	41.9	41	7	CO732377	CO732377	SILL01B01	c 937	8.8	41.9	49	8	CC060297	CC060297	EY04028-5
c 865	8.8	41.9	41	7	H89001	H89001	Yw26b07.r1	c 938	8.8	41.9	49	9	AJ599619	AJ599619	Arabidops
c 866	8.8	41.9	41	7	TI7567	TI7567	mps v288.Th	c 939	8.8	41.9	49	9	CG718294	CG718294	1119052D0
c 867	8.8	41.9	41	9	AJ600758	AJ600758	Arabidops	c 940	8.8	41.9	49	9	CL213029	CL213029	G030H04.G
c 868	8.8	41.9	41	9	AL756926	AL756926	Arabidops	c 941	8.8	41.9	50	1	AA116917	AA116917	mq25g06.x
c 869	8.8	41.9	41	9	DME547050	DME547050		c 942	8.8	41.9	50	1	AU102357	AU102357	AU102357
c 870	8.8	41.9	41	9	CF799936	CF799936	01S0783-0	c 943	8.8	41.9	50	1	AU102880	AU102880	AU102880
c 871	8.8	41.9	41	9	CC884734	CC884734	SALK_1350	c 944	8.8	41.9	50	1	AU102957	AU102957	AU102957
c 872	8.8	41.9	41	9	AB081895	AB081895	Drosophil	c 945	8.8	41.9	50	1	AU103632	AU103632	AU103632
c 873	8.8	41.9	42	7	H07866	H07866	y186b08.s1	c 946	8.8	41.9	50	1	AU103632	AU103632	AU103632
c 874	8.8	41.9	42	8	BH000535	BH000535	2M0288B05	c 947	8.8	41.9	50	1	AU103633	AU103633	AU103633
c 875	8.8	41.9	42	8	BH799740	BH799740	1008109H1	c 948	8.8	41.9	50	1	AU103997	AU103997	AU103997
c 876	8.8	41.9	42	9	AL763435	AL763435	Arabidops	c 949	8.8	41.9	50	1	AU104135	AU104135	AU104135
c 877	8.8	41.9	42	9	DME545209	DME545209		c 950	8.8	41.9	50	1	AU104175	AU104175	AU104175
c 878	8.8	41.9	43	1	AA948203	AA948203	op99h09.s	c 951	8.8	41.9	50	1	AU104448	AU104448	AU104448
c 879	8.8	41.9	43	1	AA976713	AA976713	qo6d06.s	c 952	8.8	41.9	50	1	AU104885	AU104885	AU104885
c 880	8.8	41.9	43	1	AA976713	AA976713	qo6d06.s	c 953	8.8	41.9	50	1	AU104953	AU104953	AU104953
c 881	8.8	41.9	43	1	AI115342	AI115342	uh84a06.r	c 954	8.8	41.9	50	1	AU105325	AU105325	AU105325
c 882	8.8	41.9	43	1	AJ666206	AJ666206	6J666206	c 955	8.8	41.9	50	1	AU105434	AU105434	AU105434
c 883	8.8	41.9	43	4	B1333375	B1333375	6J2996772	c 956	8.8	41.9	50	1	AU105452	AU105452	AU105452
c 884	8.8	41.9	43	5	BX551512	BX551512	EX551512	c 957	8.8	41.9	50	1	AU105954	AU105954	AU105954
c 885	8.8	41.9	43	6	CF321300	CF321300	HD--12-I0	c 958	8.8	41.9	50	1	AU106291	AU106291	AU106291
c 886	8.8	41.9	43	7	W38487	W38487	zb19b07.r1	c 959	8.8	41.9	50	1	AU107257	AU107257	AU107257
c 887	8.8	41.9	43	8	BH643347	BH643347	1008057B0	c 960	8.8	41.9	50	1	AU107258	AU107258	AU107258
c 888	8.8	41.9	43	8	BH892893	BH892893	Arabidops	c 961	8.8	41.9	50	1	AU107260	AU107260	AU107260
c 889	8.8	41.9	44	6	CF315888	CF315888	HD--04-F1	c 962	8.8	41.9	50	1	AU107261	AU107261	AU107261
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c 891	8.8	41.9	44	8	BH905113	BH905113	SALK_1056	c 964	8.8	41.9	50	1	AU107636	AU107636	AU107636
c 892	8.8	41.9	44	8	BZ384007	BZ384007	SALK_1349	c 965	8.8	41.9	50	1	AU107648	AU107648	AU107648
c 893	8.8	41.9	44	8	BZ384717	BZ384717	SALK_1359	c 966	8.8	41.9	50	1	AU107652	AU107652	AU107652
c 894	8.8	41.9	44	8	CC455081	CC455081	SALK_0476	c 967	8.8	41.9	50	1	AU107653	AU107653	AU107653
c 895	8.8	41.9	44	9	CC795527	CC795527	SALK_0814	c 968	8.8	41.9	50	1	AU107654	AU107654	AU107654
c 896	8.8	41.9	45	8	AZ345886	AZ345886	1M0080P17	c 969	8.8	41.9	50	1	AU107892	AU107892	AU107892
c 897	8.8	41.9	45	8	AZ605963	AZ605963	1M0427A12	c 970	8.8	41.9	50	1	AU108020	AU108020	AU108020
c 898	8.8	41.9	45	8	BH638406	BH638406	1008022D0	c 971	8.8	41.9	50	1	AU108057	AU108057	AU108057
c 899	8.8	41.9	45	8	BH759240	BH759240	KG00542-3	c 972	8.8	41.9	50	1	AV836264	AV836264	AV836264
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992 8.6 41.0 22 8 AZ824852
993 8.6 41.0 23 9 TA184F06Q
994 8.6 41.0 23 9 TA270501Q
995 8.6 41.0 24 4 BM396768
996 8.6 41.0 24 9 AJ587571
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1000 8.6 41.0 25 9 AJ588696 Arabidops

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ALIGNMENTS

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RESULT 1
TA199C08P
LOCUS TA199C08P 32 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 199c08, forward sequence,
genomic survey sequence.
ACCESSION AL475986
VERSION AL475986.1 GI:11842726
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 32)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.B., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
source
location/Qualifiers
1..32
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
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/clone="199c08"

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Query Match 60.0%; Score 12.6; DB 9; Length 32;
Best Local Similarity 78.9%; Pred. No. 3.3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTTAATGACC 20
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DB 7 CGCGTACGGTCTTAATGACC 25
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RESULT 2
AW004201/c
LOCUS AW004201 50 bp mRNA linear EST 08-SEP-1999
DEFINITION 701550260 A. thaliana, Columbia Col-0, inflorescence-2 Arabidopsis
thaliana cDNA clone 701550260, mRNA sequence.
ACCESSION AW004201
VERSION AW004201.1 GI:5851230
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 50)
AUTHORS Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D.,
Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D.,
Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C.,
Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S.,
Nobrega, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
Hanson, D.

```

TITLE Arabidopsis thaliana Gene Expression MicroArray

```

JOURNAL Unpublished (1999)
COMMENT Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte
Pharmaceuticals, Inc., 4633 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-2733
Fax: 314-427-3324
Email: service@genomesystems.com.

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FEATURES source

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1..50
/organism="Arabidopsis thaliana"
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/dev_stage="4 - 7 weeks"
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/notes="Vector: pSPORF; Site 1: NotI; Site 2: SalI; cDNA
library was derived from untreated inflorescence tissue
from Arabidopsis thaliana, Columbia Col-0, at 4 - 7
weeks. Plants were grown in 1:1:1 peat
moss/vermiculite/perlite soil at 22 deg. C +/- 3 deg. C
under constant light, and watered with fertilizer. cDNA
synthesis was initiated using a NotI-oligo(dT) primer.
Double-stranded cDNA was blunted, ligated to SalI
adaptors, digested with NotI, size-selected, and cloned
into the NotI and SalI sites of the pSPORT vector."

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ORIGIN

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Query Match 58.1%; Score 12.2; DB 1; Length 50;
Best Local Similarity 82.4%; Pred. No. 5.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CGCGTACGGTCTTAATGCA 18
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DB 47 CGCGTACGGTATATTGA 31
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RESULT 3
CF338319

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LOCUS CF338319 33 bp mRNA linear EST 18-AUG-2003
 DEFINITION RC11--01-F04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa (japonica cultivar-group) cDNA clone RCL1--01-F04,
 mRNA sequence.
 ACCESSION CF338319
 VERSION CF338319.1 GI:33825024
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
 FEATURES
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 Best Local Similarity 75.0%; Pred. No. 7.3e+04;
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 Qy 1 TCGGTACGGTCTAATGACC 20
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 Db 8 TCAAGTAGTGTCTAATTACC 27
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 LOCUS BQ592384 36 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012681-024-020-N04-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-020-N04 5-PRIME, mRNA sequence.
 ACCESSION BQ592384
 VERSION BQ592384.1 GI:26121967
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 36)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189

12472698
 CONTACT: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weissnaem@mpiz-koeln.mpg.de
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 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SstI-NotI, primer sites and
 orientation:
 SP6-SstI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"
 ORIGIN
 Query Match 55.2%; Score 11.6; DB 5; Length 36;
 Best Local Similarity 77.8%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 CGCGTACGGTCTAATGAC 19
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 Db 5 CGCGTACGATTATTATAC 22
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 RESULT 5
 BH903257
 LOCUS BH903257 43 bp DNA linear GSS 04-SEP-2002
 DEFINITION SALK_102332.18 30-x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_102332.18.30.x, genomic
 survey sequence.
 ACCESSION BH903257
 VERSION BH903257.1 GI:22714417
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGnAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.

JOURNAL
MEDLINE
PUBMED
COMMENT

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. .50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="KAT06186"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACCG 21
Db 22 TCCCTATGGTCTCATGTCTAG 2

RESULT 9
AUI06626/c
LOCUS
DEFINITION
AUI06626 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT11544, mRNA sequence.

ACCESSION
AUI06626
VERSION
AUI06626.1 GI:13556147
KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL
MEDLINE
PUBMED
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1. .50
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="KAT11544"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 54.3%; Score 11.4; DB 1; Length 50;
Best Local Similarity 71.4%; Pred. No. 1.6e+05;
Matches 15; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCGGTACGGTCTAATGACCG 21
Db 30 TCCCTATGGTCTCATGTCTG 10

RESULT 10
BH615074/c
LOCUS

DEFINITION
BH615074 31 bp DNA linear GSS 28-JAN-2002
KG02618-Sprime Drosophila melanogaster P(SUPor-P) P element
insertion lines Drosophila melanogaster genomic Sequence recovered
from 5' end of P element, genomic survey sequence.

ACCESSION
BH615074
VERSION
BH615074.1 GI:18379762
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)

ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS
Lewis, R., Hoskins, R., Liao, G., Mozdzen, N., Tsang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.

TITLE
JOURNAL
COMMENT
The Berkeley Drosophila Genome Project
Unpublished (2001)

Contact: Gerald Rubin

Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947

Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 24 in the 31 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.

Class: transposon-tagged.

Location/Qualifiers

source

1. .31
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P(SUPor-P) P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P(SUPor-P) P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 31;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TACGGTCTAATGACCG 21
Db 17 TACGGCCCATGACCG 2

RESULT 11
CL303319/c
LOCUS

DEFINITION
CL303319 43 bp mRNA linear GSS 30-JUN-2004
W130C02 GGTG Gene Trap Library GV03C04 Mus musculus cDNA clone
W130C02, mRNA sequence.

ACCESSION
CL303319
VERSION
CL303319.2 GI:49489549
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)

REFERENCE
AUTHORS
Hansen, J., Flores, T., van Sloun, P., Fuchtbauer, E.M., Vauti, P., Arnold, H.H., Schmitgen, F., Wurst, W., Von Melchner, H. and Ruiz, P.

TITLE
A large-scale, gene-driven mutagenesis approach for the functional analysis of the mouse genome

JOURNAL
MEDLINE
Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)

PUBMED
22810117

COMMENT
On Jun 30, 2004 this sequence version replaced gi:42744159.
Contact: GGC
German Genetrap Consortium (GGTC)
Email: info@genetrap.de
pTibetago gene trap. Sequence tag generated by 5'RACE. Additional sequence information can be found at:
'http://genetrap.gsf.de/project/web_new/database/result_clones.html?clone_id=W130C02'. ES cell line harboring insertion mutation of target gene is available at:
'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm'
1' Inhouse Sequence Identifier: 08816
Class: Gene Trap.

FEATURES
source
1..43
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Sv"
/db_xref="taxon:10090"
/clone="W130C02"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="ES cells 129S2 (formerly 129/SvPas)"
/clone_lib="GGTC Gene Trap Library GV03C04"
/note="Vector: pTibetago"

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 43;
Best Local Similarity 72.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 CGTACGGTCTAATGACCG 21
||||| ||| ||| |||

DB 38 CGTACGTTNNTAAACCG 21

RESULT 12
BX287629

LOCUS
Arabidopsis thaliana T-DNA flanking sequence GK-403C11-017864,
genomic survey sequence.

DEFINITION
BX287629.1 GI:28886625

ACCESSION
BX287629

VERSION
BX287629.1

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.

AUTHORS
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

TITLE
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
MEDLINE
22755829

PUBMED
12874060

REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

AUTHORS
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

TITLE
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL
MEDLINE
23117147

14756321

REFERENCE
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weisshaar, B.

TITLE
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL
MEDLINE
Biotechniques 35 (6), 1164-1168 (2003)

PUBMED
14682050

REFERENCE
4 (bases 1 to 45)

AUTHORS
Rosso, M.G., Li, Y., Strizhov, N. and Weisshaar, B.

TITLE
Direct Submission

JOURNAL
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T12C14. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source

1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-403C11-017864"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 45;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCGCGTACGGTCTAAT 16
||||| ||| ||| |||

DB 23 TCGGTACGTCTACT 38

RESULT 13
BX650703

LOCUS
Arabidopsis thaliana T-DNA flanking sequence GK-551H04-022301,
genomic survey sequence.

DEFINITION
BX650703.1 GI:37607091

ACCESSION
BX650703

VERSION
BX650703.1

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.

AUTHORS
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

TITLE
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
MEDLINE
22755829

PUBMED
12874060

REFERENCE
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

AUTHORS
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weishaar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 45)
Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuchtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At3g53580.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

Location/Qualifiers

1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-551H04-022301"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN

Query Match 53.3%; Score 11.2; DB 9; Length 45;
Best Local Similarity 81.2%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGCGTACGCTCTAATG 17

Db 13 CGCATAGTGTCTAATG 28

RESULT 14

AZ583945
LOCUS
DEFINITION
clone UUGC1M0388107 F, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AZ583945.1 GI:11704336

GSS
Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)

REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, I.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0388 row: 1 column: 07

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 46.

Location/Qualifiers

1..46

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0388107"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 53.3%; Score 11.2; DB 8; Length 46;

Best Local Similarity 81.2%; Pred. No. 2.1e+05;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TACGCTCTAATGACCG 21

Db 4 TAGGACTAATGACAG 19

RESULT 15

CG774856/c
LOCUS
DEFINITION
1123021C02.1BLx1 1123 - RescueMu Grid L Zea mays genomic, genomic
survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

CG774856
CG774856.1 GI:38031309

GSS.
Zea mays

ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 49)

REFERENCE
AUTHORS
Walbot, V.

TITLE
JOURNAL
COMMENT

Maize genomic sequences found using engineered RescueMu transposon

Unpublished (2001)

Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1123021 row: 16
Class: transposon-tagged.
Location/Qualifiers
1. .49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: Leaf; Vector: RescueMu (engineered from pluescript backbone); Site1: BamHI; Site2: BglII; RescueMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.znadb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

FEATURES
source
1. .49
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1123 - RescueMu Grid L"
/note="Organ: Leaf; Vector: RescueMu (engineered from pluescript backbone); Site1: BamHI; Site2: BglII; RescueMu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.znadb.iastate.edu' and follow the links for 'RescueMu.' Grid L was grown in Molokai in 2001. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 53.3%; Score 11.2; DB 9; Length 49;
Best Local Similarity 81.2%; Pred. NO. 2.1e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 GCGTACGGTCTAATGA 18
||||| ||||| |||||
Db 36 GCGTATGGTCGAATAA 21

RESULT 16
AL754718 42 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-055D02-012479,
genomic survey sequence.
AL754718.1 GI:21487216
VERSION GSS.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
3
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 42)
Li.Y., Rosso,M.G., Strizhov,N. and Weishaar,B.
Direct Submission
Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion close to or within gene At1g78560.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1. .42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strains="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="GK-055D02-012479"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match 52.4%; Score 11; DB 9; Length 42;
Best Local Similarity 73.7%; Pred. NO. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 TCGCGTACGGTCTAATGAC 19
||||| ||||| |||||
Db 11 TCGATTGCTATCTAATGAC 29

RESULT 17
AL939959 47 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-243C02-014389,
genomic survey sequence.
AL939959.1 GI:24396408
VERSION GSS.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li.Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
22755829
12874060
2
Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
23117147
14756321
3
Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
JOURNAL
COMMENT

Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA
 mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 14682050
 4 (bases 1 to 47)
 Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
 Direct Submission
 Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 K14B15. Details on the protocols used for generation of the
 sequence are described in References 1-3. The sequences are
 generated at the MPI for Plant Breeding Research in the context of
 the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
 program designated 'GABI'. Information on line availability can be
 found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source
 1. .47
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="GK-243C02-014389"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 52.4%; Score 11; DB 9; Length 47;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CGCTACGGTCTAATGACC 20
 ||||| ||||| ||||| |||||
Db 5 CGCTGCGAGTTTAAACACC 23

RESULT 18
LOCUS BH895527 48 bp DNA linear GSS 14-AUG-2002
DEFINITION 3526_1_34_1_F09_2EL_x1 3526 - RescueMu Grid K Zea mays genomic,
 genomic survey sequence.
ACCESSION BH895527
VERSION BH895527
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526_1_34_1 row: 3
 Class: transposon-tagged.

FEATURES
source

1. .48
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="3526 - RescueMu Grid K"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site 'www.zmdb.iastate.edu' and follow the links for
 'RescueMu'. Grid K was grown at Molokai, Hawaii in Winter
 2000-2001. DNA was extracted from leaf punches, double
 digested using BamHI and BglII, and ligated to form
 circular plasmids. DH10B cells were transformed and then
 screened on LB plates with ampicillin."

ORIGIN

Query Match 52.4%; Score 11; DB 8; Length 48;
Best Local Similarity 73.7%; Pred. No. 2.7e+05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CGCTACGGTCTAATGACCG 21
 ||||| ||||| ||||| |||||
Db 2 CGGACCATCTAGTGCCCG 20

RESULT 19

LOCUS BI223057 32 bp mRNA linear EST 11-JUL-2001
DEFINITION 602942007F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5105088 5',
 mRNA sequence.

ACCESSION BI223057
VERSION BI223057.1 GI:14676501
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11253 row: n column: 01
 High quality sequence stop: 32.

FEATURES
source

1. .32
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5105088"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."

ORIGIN

Query Match 51.4%; Score 10.8; DB 4; Length 32;
 Best Local Similarity 85.7%; Pred. No. 3.6e+05;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAA 15
 |||||
 Db 4 CGCGTACGGTGCAA 17
 |||||

RESULT 20

BH810122
 LOCUS SALK_040987 Arabidopsis thaliana DNA linear GSS 02-MAY-2002
 DEFINITION thaliana genomic clone SALK_040987, genomic survey sequence.

ACCESSION BH810122

VERSION BH810122.1 GI:20387940

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 36)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
 Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
 Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

FEATURES

source

Location/Qualifiers
 1..36

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_040987"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines" each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

KEYWORDS

SOURCE

ORGANISM

GSS.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 36)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers
 1..36

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_041377"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines" each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 51.4%; Score 10.8; DB 8; Length 36;

Best Local Similarity 85.7%; Pred. No. 3.6e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TACGGTCTAATGAC 19
 |||||

Db 9 TACGGTATAATAAC 22
 |||||

RESULT 22

CR360542/c

LOCUS CR360542/1

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-821B07-025531,

genomic survey sequence.

ACCESSION CR360542

VERSION CR360542.1 GI:45543464

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1

Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.

GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis

thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE

2

Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and

Weishaar,B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for


```

FEATURES
  source
    Location/Qualifiers
      1..45
        /organism="Pan troglodytes"
        /mol_type="genomic DNA"
        /db_xref="taxon:9598"
        /clone="RP43-068014.TJ"
        /sex="male"
        /cell_type="lymphocytes"
        /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN
  Query Match
  Best Local Similarity 51.4%; Score 10.8; DB 9; Length 45;
  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 2 CGCGTACGGTCTAA 15
  Db 2 CGCATACGGTATTA 15
  RESULT 25
  AUI02564/c
  LOCUS
  DEFINITION
    AUI02564 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
    HEP07440, mRNA sequence.
  ACCESSION
  VERSION
  KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 50)
  Hata,H., Oca,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
  Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
  EMBO Rep. 2 (5), 388-393 (2001)
  21270072
  11375929
  CONTACT: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: ysuzuki@ims.u-tokyo.ac.jp
  Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
  Sugano,S. Construction and characterization of a full
  length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
  149-156 (1997).
FEATURES
  source
    Location/Qualifiers
      1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HEP07440"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match
  Best Local Similarity 51.4%; Score 10.8; DB 1; Length 50;
  Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 5 GTACCGTCTAATGA 18
  Db 15 GCACCGTCTAATGA 2
  RESULT 26
  BZ358744
  LOCUS
  DEFINITION
    SALK_133243.27.05.x Arabidopsis thaliana TDNA insertion lines
    Arabidopsis thaliana genomic clone SALK_133243.27.05.x, genomic

```

```

survey sequence.
BZ358744
VERSION
BZ358744.1 GI:24951173
GSS
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 32)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers
  1..32
    /organism="Arabidopsis thaliana"
    /mol_type="genomic DNA"
    /ecotype="Col-0"
    /db_xref="taxon:3702"
    /clone="SALK_133243.27.05.x"
    /clone_lib="Arabidopsis thaliana TDNA insertion lines"
    /note="PCR was performed on Arabidopsis thaliana lines
    each of which contains one or more TDNA insertion
    elements. The resultant fragment for each line was
    directly sequenced to determine the genomic sequence at
    the site of insertion. Details of the protocols used can
    be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
  Query Match
  Best Local Similarity 50.5%; Score 10.6; DB 8; Length 32;
  Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  QY 4 CGTACGGTCTAATGACC 20
  Db 12 CGTACGGACATGAGC 28
  RESULT 27
  A2492641/c
  LOCUS
  DEFINITION
    A2492641
    IM0326D24R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
    clone UUGCLM0326D24 R, genomic survey sequence.
  ACCESSION
  VERSION
  KEYWORDS
  SOURCE
  ORGANISM
    Mus musculus (house mouse)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 38)
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center

```


directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

```

ORIGIN
Query Match      50.5%; Score 10.6; DB 8; Length 43;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGCGTACGGTCTAATGA 18
|||||
Db 25 CGCGTACGGTCTAATGA 41
|||||

RESULT 30
AA441847/c
LOCUS
DEFINITION
ZW6204.1 Soares total_fetus_ND2HF8_9w Homo sapiens cDNA clone
IMAGE:774630 5' similar to TR:G558458 G558458 ACIDIC 82 KDA
PROTEIN. i, mRNA sequence.
ACCESSION
AA441847
VERSION
AA441847.1 GI:2153731
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 46)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:774630"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total_fetus_ND2HF8_9w"
/notes="Vector: pTT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match      50.5%; Score 10.6; DB 1; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GTACGGTCTAATGACCG 21
|||||

```

```

Db 43 GTCAGGTGTAATGACGG 27

RESULT 31
AZ769367
LOCUS
DEFINITION
1M0569021R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0569021 R, genomic survey sequence.
ACCESSION
AZ769367
VERSION
AZ769367.1 GI:12889428
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0569 row: 0 column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
FEATURES
source
1..46
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0569021"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      50.5%; Score 10.6; DB 8; Length 46;
Best Local Similarity 76.5%; Pred. No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TCGGTACGGTCTAATG 17
|||||

```


Db
RESULT 32
BZ379971
LOCUS 46 bp DNA linear GSS 26-NOV-2002
DEFINITION SALK_114399.18.50.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_114399.18.50.x, genomic
survey sequence.
ACCESSION BZ379971
VERSION BZ379971.1 GI:25472355
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 46)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g03070.
CLASS: TDNA tagged.
FEATURES Location/Qualifiers
source 1..46
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_114399.18.50.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html."

ORIGIN
Query Match 50.5%; Score 10.6; DB 8; Length 46;
Best Local Similarity 76.5%; Pred No. 4.6e+05;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCGCGTACGGTCTAATG 17
||||| ||| |||
23 TCGCGTAAGGTAATATG 39

Db
RESULT 33
AL753413/c
LOCUS 46 bp DNA linear GSS 01-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-049H07-013871,
genomic survey sequence.
ACCESSION AL753413
VERSION AL753413.1 GI:21485911
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1

AUTHORS	Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE	GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE	22755823
PUBMED	12874060
REFERENCE	2
AUTHORS	Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.
TITLE	An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL	Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE	23117147
PUBMED	14756321
REFERENCE	3
AUTHORS	Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.
TITLE	High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL	BioTechniques 35 (6), 1164-1168 (2003)
PUBMED	14682050
REFERENCE	4 (bases 1 to 46)
AUTHORS	Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.
TITLE	Direct Submission
JOURNAL	Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone F26G5. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .
FEATURES	Location/Qualifiers 1. .46 /organism="Arabidopsis thaliana" /mol_type="Genomic DNA" /strain="Columbia 0" /db_xref="taxon:3702" /clone="GK-049H07-013871" /clone_lib="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN	
Query Match	50.5%; Score 10.6; DB 9; Length 46;
Best Local Similarity	76.5%; Pred. No. 4.6e+05;
Matches	13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy	2 CGCGTACGGTCTAATGA 18
Db	40 CGAGTACGTTTAATGA 24
RESULT 34	
H50401/c	
LOCUS	H50401 49 bp mRNA linear EST 18-SEP-1995
DEFINITION	yo29h01.r1 Soares adult brain Nb25HB55Y Homo sapiens cDNA clone IMAGE:179377 5' similar to SP:A45072 A45072 TYPE L K+ CHANNEL, KV3.1 - HUMAN i, mRNA sequence.
ACCESSION	H50401
VERSION	H50401.1 GI:990242
KEYWORDS	EST.
ORGANISM	Homo sapiens (human)
SOURCE	Homo sapiens

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT
84112, USA
Tel: 801 585 5066
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0036 row: K column: 16
Seq primer: CACACGGAACACCTATGACC
Class: plasmid ends
High quality sequence stop: 30:
Location/Qualifiers
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0036K16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-rafted with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 30;
Best Local Similarity 70.0%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TC CGGTACGGTCTAATGACC 20
|||||
DB 1 TCATCTCGGTCCGATGACC 20
|||||

RESULT 37
AZ381857/c

LOCUS
AZ381857 30 bp DNA linear GSS 02-OCT-2000

DEFINITION
IM0138A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0138A10 R, genomic survey sequence.

ACCESSION
A2381857

VERSION
A2381857.1 GI:10495557

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokess, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaabs-i@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES

source

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1. .37
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1301547"
/tissue type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP GCBI"
```

/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

```
Query Match 49.5%; Score 10.4; DB 1; Length 37;
Best Local Similarity 70.0%; Pred. No. 6.1e+05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

QY 2 CGCGTACGCTTAATGACCG 21

```
|||||
Db 33 CGCGCAGCGTCATCGGAGCG 14
```

RESULT 39

BZ377768

LOCUS

DEFINITION SALK_106163.28.55.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_106163.28.55.n, genomic survey sequence.

ACCESSION

BZ377768

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of At2g25610.

Class: TDNA tagged.

FEATURES

source

```
1. .37
/organism="Arabidopsis thaliana"
```

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_106163.28.55.n"

/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

```
Query Match 49.5%; Score 10.4; DB 8; Length 37;
Best Local Similarity 91.7%; Pred. No. 6.1e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 7 ACGGCTTAATGA 18

```
|||||
Db 13 ACGGCTTAATGA 24
```

RESULT 40

BZ383634

LOCUS

DEFINITION BZ383634 37 bp DNA linear GSS 26-NOV-2002 SALK_134205.28.00.n Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_134205.28.00.n, genomic survey sequence.

ACCESSION

BZ383634

VERSION

GSS.

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 37)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within 300 bases of the 5' end of

At2g25610.

Class: TDNA tagged.

Location/Qualifiers

1. .37

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_134205.28.00.n"

/note="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 37;
Best Local Similarity 91.7%; Pred. NO. 6.1e+05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 7 ACGCTCTAATGA 18
Db 13 ACGCTCTAATGA 24

Search completed: November 23, 2004, 22:21:54
Job time : 1040.82 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 594.247 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33

Sequence: 1 cgggtactaccggtccgcagaccactatggc 33

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4526729 seqs, 23644849745.residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	31	93.9	31	6	AX802289	Sequence 5	AX802289 Sequence 5
C 2	30.4	92.1	36	6	A52660	Sequence 12	A52660 Sequence 12
C 3	27.4	83.0	29	6	A68291	A method	A68291 Sequence 12
4	22	66.7	34	6	BD181364		BD181364 A method
5	22	66.7	34	6	AX523944		AX523944 Sequence
6	22	66.7	34	6	AX524842		AX524842 Sequence
7	22	66.7	41	6	BD171248		BD171248 Method of
C 8	21	63.6	41	6	E25774		E25774 Method for
9	20.4	61.8	26	6	AR411540		AR411540 Sequence
10	20.4	61.8	26	6	BD000266		BD000266 Oligonucle
11	20.4	61.8	28	6	AR094968		AR094968 Sequence
C 12	20.4	61.8	28	6	BD183050		BD183050 Nucleic a
C 13	20.4	61.8	36	6	A70977		A70977 Sequence 31
C 14	20.4	61.8	36	6	BD244766		BD244766 Isolation
C 15	20.4	61.8	36	6	AR255272		AR255272 Sequence
C 16	20	60.6	32	6	AX147026		AX147026 Sequence
C 17	20	60.6	37	6	E25770		E25770 Method for
C 18	20	60.6	38	6	I17519		I17519 Sequence, 9
C 19	20	60.6	38	6	I17520		I17520 Sequence 10

93	15.2	46.1	38	6	AR391943	Sequence	166	14.4	43.6	36	6	AX061258	Sequence
94	15.2	46.1	38	6	AR391945	Sequence	c 167	14.4	43.6	41	6	AR109120	Sequence
95	15.2	46.1	38	6	AX076510	Sequence	c 168	14.4	43.6	41	6	AR200775	Sequence
96	15.2	46.1	38	6	AX076512	Sequence	c 169	14.2	43.0	21	6	AX134096	Sequence
97	15.2	46.1	38	6	AX076644	Sequence	c 170	14.2	43.0	21	6	AX189705	Sequence
98	15.2	46.1	38	6	AX076646	Sequence	c 171	14.2	43.0	21	6	AX189705	Sequence
99	15.2	46.1	38	6	AX076648	Sequence	c 172	14.2	43.0	30	6	AR491621	Sequence
100	15.2	46.1	38	6	AX076650	Sequence	c 173	14.2	43.0	30	6	BD074883	Group A s
101	15.2	46.1	40	6	E01694	DNA encodin	c 174	14.2	43.0	33	6	AX323171	Sequence
102	15.2	46.1	46	6	CQ54922	Sequence	c 175	14.2	43.0	36	9	HSTCARB25	Sequence
103	15	45.5	15	6	AR033238	Sequence	c 176	14.2	43.0	36	9	HSTCARB45	Sequence
104	15	45.5	15	6	AR113060	Sequence	c 177	14	42.4	20	6	E08281	Sequence
105	15	45.5	15	6	BD206416	Enzymatic	c 178	14	42.4	25	6	BD222531	Methods f
106	15	45.5	15	6	BD206971	Enzymatic	c 179	14	42.4	25	6	BD222532	Methods f
107	15	45.5	15	6	E17467	Sequence 4	c 180	14	42.4	25	6	BD222533	Methods f
108	15	45.5	18	6	BD142099	A method	c 181	14	42.4	25	6	BD222534	Methods f
109	15	45.5	18	6	BD142136	A method	c 182	14	42.4	26	6	AR428913	Sequence
110	15	45.5	18	6	BD171237	Method of	c 183	14	42.4	26	6	AX696021	Sequence
111	15	45.5	21	6	A68285	Sequence 6	c 184	14	42.4	26	6	AX720385	Sequence
112	15	45.5	25	6	E44264	E44264 Oligo-DNA s	c 185	14	42.4	26	6	AX720389	Sequence
113	15	45.5	26	6	AR488116	Sequence	c 186	14	42.4	26	6	AX814300	Sequence
114	15	45.5	26	6	AX472309	Sequence	c 187	14	42.4	26	6	AX814303	Sequence
115	15	45.5	37	6	AR050591	Sequence	c 188	14	42.4	37	6	AR351559	Sequence
116	15	45.5	50	6	E44268	E44268 Oligo-DNA s	c 189	14	42.4	38	6	AR286735	Sequence
117	14.8	44.8	18	6	A68282	Sequence 3	c 190	14	42.4	38	6	AR398725	Sequence
118	14.8	44.8	19	6	A64951	Sequence 5	c 191	14	42.4	42	6	A68288	Sequence 9
119	14.8	44.8	21	6	AR166996	Sequence	c 192	14	42.4	42	6	AX003364	Sequence
120	14.8	44.8	21	6	AR210651	Sequence	c 193	14	42.4	47	6	AR237984	Sequence
121	14.8	44.8	23	6	AX098132	Sequence	c 194	13.8	41.8	20	6	AR167034	Sequence
122	14.8	44.8	25	6	AR089655	Sequence	c 195	13.8	41.8	20	6	AR210689	Sequence
123	14.8	44.8	25	6	E09662	Primer for	c 196	13.8	41.8	23	6	AX805796	Sequence
124	14.8	44.8	25	6	I93330	Sequence 4	c 197	13.8	41.8	25	6	CQ626245	Sequence
125	14.8	44.8	25	6	AR308955	Sequence	c 198	13.8	41.8	25	6	AR467308	Sequence
126	14.8	44.8	25	6	AR317086	Sequence	c 199	13.8	41.8	28	6	AX404625	Sequence
127	14.8	44.8	25	6	AX555526	Sequence	c 200	13.8	41.8	31	6	AX248737	Sequence
128	14.8	44.8	25	6	BD095878	Sequence	c 201	13.8	41.8	34	6	AR126133	Sequence
129	14.8	44.8	26	6	I46685	I46685 Sequence 66	c 202	13.8	41.8	36	6	CQ784496	Sequence
130	14.8	44.8	28	6	AR094969	Sequence	c 203	13.8	41.8	37	6	AR122589	Sequence
131	14.8	44.8	28	6	AR094995	Sequence	c 204	13.8	41.8	40	6	A99066	Sequence 74
132	14.8	44.8	32	6	AX746459	Sequence	c 205	13.8	41.8	40	6	BD235443	Translati
133	14.8	44.8	32	6	AX763805	Sequence	c 206	13.8	41.8	40	6	AR195381	Sequence
134	14.8	44.8	33	6	AR004393	Sequence	c 207	13.8	41.8	40	6	AX001472	Sequence
135	14.8	44.8	33	6	AR064955	Sequence	c 208	13.8	41.8	42	6	E06011	A part of s
136	14.8	44.8	33	6	AR097185	Sequence	c 209	13.8	41.8	43	6	AX554432	Sequence
137	14.8	44.8	33	6	AR130683	Sequence	c 210	13.8	41.8	45	9	S80711	gamma delta
138	14.8	44.8	33	6	AR131570	Sequence	c 211	13.8	41.8	48	6	BD081886	Method fo
139	14.8	44.8	33	6	AR172032	Sequence	c 212	13.8	41.8	50	6	CQ003759	Sequence
140	14.8	44.8	33	6	BD189449	Sequence	c 213	13.6	41.2	38	6	AX220482	Sequence
141	14.8	44.8	33	6	BD189296	Sequence	c 214	13.6	41.2	38	6	AX223143	Sequence
142	14.8	44.8	33	6	BD189443	Sequence	c 215	13.6	41.2	48	6	AR307709	Sequence
143	14.8	44.8	33	6	I82868	I82868 Sequence 47	c 216	13.6	41.2	48	6	BD076359	Ligand ho
144	14.8	44.8	33	6	AR199504	Sequence	c 217	13.6	41.2	48	10	AB001358	Mus muscu
145	14.8	44.8	33	6	AR200975	Sequence	c 218	13.6	41.2	50	6	AX199460	Sequence
146	14.8	44.8	33	6	AR488734	Sequence	c 219	13.4	40.6	23	6	CQ840432	Sequence
147	14.8	44.8	33	6	AX419726	Sequence	c 220	13.4	40.6	27	6	BD091003	Assay emp
148	14.8	44.8	33	6	BD084988	Target-de	c 221	13.4	40.6	33	6	BD238547	Expressio
149	14.8	44.8	46	6	I49767	I49767 Sequence 12	c 222	13.4	40.6	39	6	I09580	Sequence 15
150	14.8	44.8	50	6	AX397950	Sequence	c 223	13.4	40.6	47	6	AR290168	Sequence
151	14.8	44.8	50	6	AX397958	Sequence	c 224	13.4	40.6	48	6	AX181923	Sequence
152	14.4	43.6	18	6	AX469411	Sequence	c 225	13.4	40.6	48	6	BD077303	Method an
153	14.4	43.6	18	6	AX109100	Sequence	c 226	13.4	40.6	50	6	CQ008965	Sequence
154	14.4	43.6	18	6	BD001051	Method an	c 227	13.4	40.6	50	6	CQ008987	Sequence
155	14.4	43.6	18	6	BD001480	Method an	c 228	13.2	40.0	24	6	AR474765	Sequence
156	14.4	43.6	22	6	AR124658	Sequence	c 229	13.2	40.0	26	6	AR090276	Sequence
157	14.4	43.6	22	6	AR242411	Sequence	c 230	13.2	40.0	26	6	AR197311	Sequence
158	14.4	43.6	22	6	AX540622	Sequence	c 231	13.2	40.0	26	6	AR259465	Sequence
159	14.4	43.6	25	6	E58847	Method for	c 232	13.2	40.0	29	6	A32376	Synthetic 1
160	14.4	43.6	26	6	AR411539	Sequence	c 233	13.2	40.0	29	6	AX712192	Sequence
161	14.4	43.6	26	6	BD000265	Oligonucl	c 234	13.2	40.0	32	6	AX180384	Sequence
162	14.4	43.6	35	6	BD175039	Method fo	c 235	13.2	40.0	33	6	AX839492	Sequence
163	14.4	43.6	36	6	AX061253	Sequence	c 236	13.2	40.0	41	6	AX515871	Sequence
164	14.4	43.6	36	6	AX061254	Sequence	c 237	13.2	40.0	41	6	AX521128	Sequence
165	14.4	43.6	36	6	AX061257	Sequence	c 238	13.2	40.0	45	6	A69002	Sequence 26

239	13.2	40.0	45	6	AR139228	AR139228 Sequence	C 312	13.	39.4	50	6	E50439	E50439 Method for
240	13.2	40.0	45	6	AR309884	AR309884 Sequence	C 313	13.	39.4	50	6	AR302197	AR302197 Sequence
C 241	13.2	40.0	45	9	HSELH1B	X72117 H.sapiens (C 314	13.4	39.4	50	6	AR349554	AR349554 Sequence
C 242	13.2	40.0	45	9	HSELH1B	X72118 H.sapiens (C 315	13	39.4	50	6	AR349555	AR349555 Sequence
C 243	13.2	40.0	47	6	AR291379	AR291379 Sequence	C 316	13	39.4	50	6	AX161828	AX161828 Sequence
C 244	13	39.4	14	6	AX067858	AX067858 Sequence	C 317	13	39.4	50	6	AX322179	AX322179 Sequence
C 245	13	39.4	15	6	AR033329	AR033329 Sequence	C 318	13	39.4	50	6	BD000119	BD000119 Nucleic a
C 246	13	39.4	15	6	AR113061	AR113061 Sequence	C 319	13	39.4	50	6	BD004784	BD004784 Method fo
C 247	13	39.4	15	6	BD206415	BD206415 Enzymatic	C 320	13	39.4	50	6	BD006778	BD006778 Method fo
C 248	13	39.4	15	6	BD206417	BD206417 Enzymatic	C 321	13	39.4	50	6	BD091995	BD091995 Potentiati
C 249	13	39.4	15	6	BD206972	BD206972 Enzymatic	C 322	13	39.4	50	6	AF057517	AF057517 Homo sapi
C 250	13	39.4	15	6	BD208267	BD208267 Enzymatic	C 323	13	39.4	50	9	F2020249	F2020249 Homo sapi
C 251	13	39.4	15	6	IS7468	IS7468 Sequence 5	C 324	12.8	38.8	16	6	AR285635	AR285635 Sequence
C 252	13	39.4	18	6	AR0959	AR0959 Sequence 13	C 325	12.8	38.8	16	6	AR397626	AR397626 Sequence
253	13	39.4	20	6	AR167032	AR167032 Sequence	C 326	12.8	38.8	20	6	BD196029	BD196029 Antisense
254	13	39.4	20	6	AR1210687	AR1210687 Sequence	C 327	12.8	38.8	20	6	AR382820	AR382820 Sequence
255	13	39.4	24	6	AR173112	AR173112 Sequence	C 328	12.8	38.8	21	6	E25775	E25775 Method for
256	13	39.4	24	6	BD139591	BD139591 Arginine	C 329	12.8	38.8	21	6	AX739982	AX739982 Sequence
C 257	13	39.4	25	6	CQ626241	CQ626241 Sequence	C 330	12.8	38.8	24	6	AX2575	AX2575 Sequence 13
C 258	13	39.4	25	6	CQ626242	CQ626242 Sequence	C 331	12.8	38.8	25	6	AX615728	AX615728 Sequence
C 259	13	39.4	25	6	CQ626243	CQ626243 Sequence	C 332	12.8	38.8	25	6	AX615729	AX615729 Sequence
C 260	13	39.4	25	6	CQ626244	CQ626244 Sequence	C 333	12.8	38.8	26	6	I46580	I46580 Sequence 55
C 261	13	39.4	25	6	CQ626246	CQ626246 Sequence	C 334	12.8	38.8	26	6	AX708898	AX708898 Sequence
C 262	13	39.4	25	6	CQ626247	CQ626247 Sequence	C 335	12.8	38.8	26	6	AX708902	AX708902 Sequence
C 263	13	39.4	25	6	CQ626248	CQ626248 Sequence	C 336	12.8	38.8	27	6	AR228696	AR228696 Sequence
C 264	13	39.4	25	6	CQ626249	CQ626249 Sequence	C 337	12.8	38.8	27	6	AR228700	AR228700 Sequence
C 265	13	39.4	25	6	E44263	E44263 Oligo-DNA s	C 338	12.8	38.8	29	6	E13337	E13337 Probe. 4/19
C 266	13	39.4	25	6	AR467304	AR467304 Sequence	C 339	12.8	38.8	30	6	BD175843	BD175843 Glutamina
C 267	13	39.4	25	6	AR467305	AR467305 Sequence	C 340	12.8	38.8	30	6	E04700	E04700 Synthetic n
C 268	13	39.4	25	6	AR467306	AR467306 Sequence	C 341	12.8	38.8	30	6	AR302472	AR302472 Sequence
C 269	13	39.4	25	6	AR467307	AR467307 Sequence	C 342	12.8	38.8	31	6	AR207931	AR207931 Sequence
C 270	13	39.4	25	6	AR467309	AR467309 Sequence	C 343	12.8	38.8	31	6	AR383217	AR383217 Sequence
C 271	13	39.4	25	6	AR467310	AR467310 Sequence	C 344	12.8	38.8	32	6	I38810	I38810 Sequence 48
C 272	13	39.4	25	6	AR467311	AR467311 Sequence	C 345	12.8	38.8	32	6	BD012896	BD012896 Gene codi
C 273	13	39.4	25	6	AR467312	AR467312 Sequence	C 346	12.8	38.8	37	6	AR112772	AR112772 Sequence
C 274	13	39.4	26	6	I83632	I83632 Sequence 6	C 347	12.8	38.8	37	6	AR374165	AR374165 Sequence
275	13	39.4	29	6	BD177926	BD177926 Sequence	C 348	12.8	38.8	38	6	AX260002	AX260002 Sequence
276	13	39.4	29	6	AR351574	AR351574 Sequence	C 349	12.8	38.8	39	6	AR103921	AR103921 Sequence
277	13	39.4	29	6	AX492884	AX492884 Sequence	C 350	12.8	38.8	39	6	AR401400	AR401400 Sequence
C 278	13	39.4	31	6	AR003412	AR003412 Sequence	C 351	12.8	38.8	39	6	AR474276	AR474276 Sequence
C 279	13	39.4	31	6	AR003418	AR003418 Sequence	C 352	12.8	38.8	40	6	AR043925	AR043925 Sequence
C 280	13	39.4	31	6	I21201	I21201 Sequence 47	C 353	12.8	38.8	40	6	BD000714	BD000714 Drug comp
C 281	13	39.4	31	6	I21207	I21207 Sequence 53	C 354	12.8	38.8	40	6	BD000716	BD000716 Inhibitor
C 282	13	39.4	31	6	I74468	I74468 Sequence 47	C 355	12.8	38.8	41	6	A61793	A61793 Sequence 16
C 283	13	39.4	31	6	I74474	I74474 Sequence 53	C 356	12.8	38.8	41	6	AR109121	AR109121 Sequence
284	13	39.4	32	6	BD211604	BD211604 Canine an	C 357	12.8	38.8	41	6	AR200776	AR200776 Sequence
285	13	39.4	32	6	AR241582	AR241582 Sequence	C 358	12.8	38.8	44	6	AR002174	AR002174 Sequence
286	13	39.4	32	6	AR254538	AR254538 Sequence	C 359	12.8	38.8	45	6	A23129	A23129 Gene fragme
C 287	13	39.4	37	6	AX930625	AX930625 Sequence	C 360	12.8	38.8	48	6	AR179422	AR179422 Sequence
C 288	13	39.4	38	6	BD177912	BD177912 Sequence	C 361	12.8	38.8	48	6	BD191685	BD191685 Enzymatic
C 289	13	39.4	38	6	AR286543	AR286543 Sequence	C 362	12.8	38.8	48	6	AX927790	AX927790 Sequence
C 290	13	39.4	38	6	AR286788	AR286788 Sequence	C 363	12.8	38.8	48	8	AJ718213	AJ718213 Nicotiana
C 291	13	39.4	38	6	AR351560	AR351560 Sequence	C 364	12.8	38.8	48	11	AL845045	AL845045 Arabidops
C 292	13	39.4	38	6	AR398533	AR398533 Sequence	C 365	12.6	38.2	20	6	AR272094	AR272094 Sequence
C 293	13	39.4	38	6	AR398778	AR398778 Sequence	C 366	12.6	38.2	20	6	AR489988	AR489988 Sequence
C 294	13	39.4	38	6	AX220269	AX220269 Sequence	C 367	12.6	38.2	20	6	AX175400	AX175400 Sequence
C 295	13	39.4	38	6	AX223176	AX223176 Sequence	C 368	12.6	38.2	22	6	I58643	I58643 Sequence 11
C 296	13	39.4	38	6	AX492870	AX492870 Sequence	C 369	12.6	38.2	23	6	AX172363	AX172363 Sequence
297	13	39.4	38	6	BD141414	BD141414 Protein d	C 370	12.6	38.2	23	6	AX183979	AX183979 Sequence
298	13	39.4	40	6	BD185266	BD185266 Method fo	C 371	12.6	38.2	24	6	BD233483	BD233483 Novel hum
299	13	39.4	40	6	CQ795377	CQ795377 Sequence	C 372	12.6	38.2	25	6	CQ626239	CQ626239 Sequence
C 300	13	39.4	40	6	CQ795383	CQ795383 Sequence	C 373	12.6	38.2	25	6	CQ626240	CQ626240 Sequence
301	13	39.4	40	6	E16986	E16986 Sense prime	C 374	12.6	38.2	25	6	AR467302	AR467302 Sequence
302	13	39.4	41	6	AX514328	AX514328 Sequence	C 375	12.6	38.2	25	6	AR467303	AR467303 Sequence
303	13	39.4	41	6	AX519881	AX519881 Sequence	C 376	12.6	38.2	26	6	AR373108	AR373108 Sequence
304	13	39.4	42	6	AR184222	AR184222 Sequence	C 377	12.6	38.2	26	6	AX098337	AX098337 Sequence
305	13	39.4	42	6	AR184343	AR184343 Sequence	C 378	12.6	38.2	27	6	AX371712	AX371712 Sequence
306	13	39.4	42	6	AX127931	AX127931 Sequence	C 379	12.6	38.2	27	10	MMBR177	MMBR177 M.musculus
C 307	13	39.4	45	6	AX175313	AX175313 Sequence	C 380	12.6	38.2	28	6	AR090298	AR090298 Sequence
C 308	13	39.4	46	6	AX930620	AX930620 Sequence	C 381	12.6	38.2	28	6	BD273400	BD273400 Compositi
C 309	13	39.4	47	6	AR291704	AR291704 Sequence	C 382	12.6	38.2	28	6	AR197333	AR197333 Sequence
C 310	13	39.4	47	6	AX323099	AX323099 Sequence	C 383	12.6	38.2	28	6	AR259487	AR259487 Sequence
C 311	13	39.4	50	6	E44267	E44267 Oligo-DNA s	C 384	12.6	38.2	30	6	AX482519	AX482519 Sequence

C 385	12.6	38.2	32	6	CQ827782	Sequence	C 458	12.4	37.6	33	6	AR151927	Sequence
C 386	12.6	38.2	32	6	CQ827783	Sequence	C 459	12.4	37.6	33	6	AR226328	Sequence
C 387	12.6	38.2	34	6	AR285932	Sequence	C 460	12.4	37.6	36	4	PICAMPO	M60002 S.scrofa SI
C 388	12.6	38.2	35	6	AR062177	Sequence	C 461	12.4	37.6	37	6	AX581815	Sequence
C 389	12.6	38.2	35	6	AR135155	Sequence	C 462	12.4	37.6	37	6	AX582035	Sequence
C 390	12.6	38.2	35	6	AR397922	Sequence	C 463	12.4	37.6	37	6	AX582063	Sequence
C 391	12.6	38.2	36	6	A64974	Sequence 4	C 464	12.4	37.6	38	6	CQ759371	Sequence
C 392	12.6	38.2	36	6	CQ809461	Sequence	C 465	12.4	37.6	38	6	AR286548	Sequence
C 393	12.6	38.2	36	6	AR285933	Sequence	C 466	12.4	37.6	38	6	AR286567	Sequence
C 394	12.6	38.2	36	6	AR478920	Sequence	C 467	12.4	37.6	38	6	AR286583	Sequence
C 395	12.6	38.2	37	6	AR397923	Sequence	C 468	12.4	37.6	38	6	AR286608	Sequence
C 396	12.6	38.2	37	6	AX357426	Sequence	C 469	12.4	37.6	38	6	AR286635	Sequence
C 397	12.6	38.2	37	6	AX551183	Sequence	C 470	12.4	37.6	38	6	AR286635	Sequence
C 398	12.6	38.2	37	6	AX551183	Sequence	C 471	12.4	37.6	38	6	AR286635	Sequence
C 399	12.6	38.2	37	6	AX581921	Sequence	C 472	12.4	37.6	38	6	AR286635	Sequence
C 400	12.6	38.2	37	6	AX770380	Sequence	C 473	12.4	37.6	38	6	AR286635	Sequence
C 401	12.6	38.2	37	6	AX805518	Sequence	C 474	12.4	37.6	38	6	AR286635	Sequence
C 402	12.6	38.2	38	6	CQ785742	Sequence	C 475	12.4	37.6	38	6	AR286635	Sequence
C 403	12.6	38.2	38	6	AR286920	Sequence	C 476	12.4	37.6	38	6	AR286635	Sequence
C 404	12.6	38.2	38	6	AR287036	Sequence	C 477	12.4	37.6	38	6	AR286635	Sequence
C 405	12.6	38.2	38	6	AR287102	Sequence	C 478	12.4	37.6	38	6	AR286635	Sequence
C 406	12.6	38.2	38	6	AR398910	Sequence	C 479	12.4	37.6	38	6	AR286635	Sequence
C 407	12.6	38.2	38	6	AR399026	Sequence	C 480	12.4	37.6	38	6	AR286635	Sequence
C 408	12.6	38.2	38	6	AR399092	Sequence	C 481	12.4	37.6	38	6	AR286635	Sequence
C 409	12.6	38.2	38	6	AX840442	Sequence	C 482	12.4	37.6	38	6	AR286635	Sequence
C 410	12.6	38.2	39	6	AX554035	Sequence	C 483	12.4	37.6	38	6	AR286635	Sequence
C 411	12.6	38.2	39	6	AX554036	Sequence	C 484	12.4	37.6	38	6	AR286635	Sequence
C 412	12.6	38.2	39	6	AX664363	Sequence	C 485	12.4	37.6	38	6	AR286635	Sequence
C 413	12.6	38.2	39	6	AX720241	Sequence	C 486	12.4	37.6	38	6	AR286635	Sequence
C 414	12.6	38.2	42	6	BD233647	Sequence	C 487	12.4	37.6	38	6	AR286635	Sequence
C 415	12.6	38.2	42	6	E06010	Sequence	C 488	12.4	37.6	38	6	AR286635	Sequence
C 416	12.6	38.2	42	6	AR476058	Sequence	C 489	12.4	37.6	38	6	AR286635	Sequence
C 417	12.6	38.2	45	6	AX405397	Sequence	C 490	12.4	37.6	38	6	AR286635	Sequence
C 418	12.6	38.2	47	6	CQ654175	Sequence	C 491	12.4	37.6	38	6	AR286635	Sequence
C 419	12.6	38.2	47	6	CQ771101	Sequence	C 492	12.4	37.6	38	6	AR286635	Sequence
C 420	12.6	38.2	47	6	CQ779466	Sequence	C 493	12.4	37.6	38	6	AR286635	Sequence
C 421	12.6	38.2	47	6	AR291823	Sequence	C 494	12.4	37.6	38	6	AR286635	Sequence
C 422	12.6	38.2	47	6	AX357428	Sequence	C 495	12.4	37.6	38	6	AR286635	Sequence
C 423	12.6	38.2	47	6	AX551185	Sequence	C 496	12.4	37.6	38	6	AR286635	Sequence
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C 425	12.6	38.2	47	6	AX770382	Sequence	C 498	12.4	37.6	38	6	AR286635	Sequence
C 426	12.6	38.2	49	6	AX772607	Sequence	C 499	12.4	37.6	38	6	AR286635	Sequence
C 427	12.6	38.2	50	6	AX14174	Sequence	C 500	12.4	37.6	38	6	AR286635	Sequence
C 428	12.6	38.2	50	6	AX14176	Sequence	C 501	12.4	37.6	38	6	AR286635	Sequence
C 429	12.6	38.2	50	6	AX14178	Sequence	C 502	12.4	37.6	38	6	AR286635	Sequence
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C 431	12.6	38.2	50	6	AX159306	Sequence	C 504	12.4	37.6	38	6	AR286635	Sequence
C 432	12.4	37.6	16	6	AR285634	Sequence	C 505	12.4	37.6	38	6	AR286635	Sequence
C 433	12.4	37.6	16	6	AR397625	Sequence	C 506	12.4	37.6	38	6	AR286635	Sequence
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C 437	12.4	37.6	26	6	AR490873	Sequence	C 510	12.4	37.6	38	6	AR286635	Sequence
C 438	12.4	37.6	27	6	AR160071	Sequence	C 511	12.4	37.6	38	6	AR286635	Sequence
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C 440	12.4	37.6	27	6	BD217917	Sequence	C 513	12.4	37.6	38	6	AR286635	Sequence
C 441	12.4	37.6	27	6	AR266434	Sequence	C 514	12.4	37.6	38	6	AR286635	Sequence
C 442	12.4	37.6	27	6	AR349292	Sequence	C 515	12.4	37.6	38	6	AR286635	Sequence
C 443	12.4	37.6	28	6	AR451728	Sequence	C 516	12.4	37.6	38	6	AR286635	Sequence
C 444	12.4	37.6	28	6	AR090964	Sequence	C 517	12.4	37.6	38	6	AR286635	Sequence
C 445	12.4	37.6	28	6	AR197999	Sequence	C 518	12.4	37.6	38	6	AR286635	Sequence
C 446	12.4	37.6	28	6	AR260153	Sequence	C 519	12.4	37.6	38	6	AR286635	Sequence
C 447	12.4	37.6	30	6	AS1854	Sequence	C 520	12.4	37.6	38	6	AR286635	Sequence
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C 449	12.4	37.6	30	6	AR085827	Sequence	C 522	12.4	37.6	38	6	AR286635	Sequence
C 450	12.4	37.6	30	6	AX598073	Sequence	C 523	12.4	37.6	38	6	AR286635	Sequence
C 451	12.4	37.6	32	6	I18656	Sequence 8	C 524	12.4	37.6	38	6	AR286635	Sequence
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C 453	12.4	37.6	32	6	AX099693	Sequence	C 526	12.4	37.6	38	6	AR286635	Sequence
C 454	12.4	37.6	32	6	AX367135	Sequence	C 527	12.4	37.6	38	6	AR286635	Sequence
C 455	12.4	37.6	33	6	AR068945	Sequence	C 528	12.4	37.6	38	6	AR286635	Sequence
C 456	12.4	37.6	33	6	AR141801	Sequence	C 529	12.4	37.6	38	6	AR286635	Sequence
C 457	12.4	37.6	33	6	AR143318	Sequence	C 530	12.4	37.6	38	6	AR286635	Sequence
C 458	12.4	37.6	33	6	AR151927	Sequence	C 458	12.4	37.6	33	6	AR151927	Sequence
C 459	12.4	37.6	33	6	AR226328	Sequence	C 459	12.4	37.6	33	6	AR226328	Sequence
C 460	12.4	37.6	36	4	PICAMPO	M60002 S.scrofa SI	C 460	12.4	37.6	36	4	PICAMPO	M60002 S.scrofa SI
C 461	12.4	37.6	37	6	AX581815	Sequence	C 461	12.4	37.6	37	6	AX581815	Sequence
C 462	12.4	37.6	37	6	AX582035	Sequence	C 462	12.4	37.6	37	6	AX582035	Sequence
C 463	12.4	37.6	37	6	AX582063	Sequence	C 463	12.4	37.6	37	6	AX582063	Sequence
C 464	12.4	37.6	38	6	CQ759371	Sequence	C 464	12.4	37.6	38	6	CQ759371	Sequence
C 465	12.4	37.6	38	6	AR286548	Sequence	C 465	12.4	37.6	38	6	AR286548	Sequence
C 466	12.4	37.6	38	6	AR286567	Sequence	C 466	12.4	37.6	38	6	AR286567	Sequence
C 467	12.4	37.6	38	6	AR286583	Sequence	C 467	12.4	37.6	38	6	AR286583	Sequence
C 468	12.4	37.6	38	6	AR286608	Sequence	C 468	12.4	37.6	38	6	AR286608	Sequence
C 469	12.4	37.6	38	6	AR286635	Sequence	C 469	12.4	37.6	38	6	AR286635	Sequence
C 470	12.4	37.6	38	6	AR286635	Sequence	C 470	12.4	37.6	38	6	AR286635	Sequence
C 471	12.4	37.6	38	6	AR286635	Sequence	C 471	12.4	37.6	38	6	AR286635	Sequence
C 472	12.4	37.6	38	6	AR286635	Sequence	C 472	12.4	37.6	38	6	AR286635	Sequence
C 473	12.4	37.6	38	6	AR286635	Sequence	C 473	12.4	37.6	38	6	AR286635	Sequence
C 474	12.4	37.6	38	6	AR286635	Sequence	C 474	12.4	37.6	38	6	AR286635	Sequence
C 475	12.4	37.6	38	6	AR286635	Sequence	C 475	12.4	37.6	38	6	AR286635	Sequence
C 476	12.4	37.6	38	6	AR286635	Sequence	C 476	12.4	37.6	38	6	AR286635	Sequence
C 477	12.4	37.6	38	6	AR286635	Sequence	C 477	12.4	37.6	38	6	AR286635	Sequence
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C 486	12.4	37.6	38	6	AR286635	Sequence	C 486	12.4	37.6	38	6	AR286	

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532	12.2	37.0	24	6	A62564	A62564 Sequence 2	c 605	12.2	37.0	38	6	AR125846	AR125846 Sequence
533	12.2	37.0	24	6	A62573	A62573 Sequence 11	c 606	12.2	37.0	38	6	AR125846	AR125846 Sequence
c 534	12.2	37.0	24	6	AX446291	AX446291 Sequence	607	12.2	37.0	38	6	BD063148	BD063148 Human G-p
c 535	12.2	37.0	25	6	A67701	A67701 Sequence 31	608	12.2	37.0	39	6	AR027114	AR027114 Sequence
536	12.2	37.0	25	6	C0629861	C0629861 Sequence	c 609	12.2	37.0	39	6	HSZ78049	Z78049 H. sapiens T
537	12.2	37.0	25	6	C0629862	C0629862 Sequence	c 610	12.2	37.0	40	6	AR053630	AR053630 Sequence
538	12.2	37.0	25	6	AR361078	AR361078 Sequence	611	12.2	37.0	40	6	AR240057	AR240057 Sequence
539	12.2	37.0	25	6	AR470924	AR470924 Sequence	c 612	12.2	37.0	40	6	AR258565	AR258565 Sequence
540	12.2	37.0	25	6	AR470925	AR470925 Sequence	613	12.2	37.0	40	6	AR279859	AR279859 Sequence
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c 542	12.2	37.0	25	6	AX615727	AX615727 Sequence	c 615	12.2	37.0	42	6	AX201868	AX201868 Sequence
c 543	12.2	37.0	25	6	AX649745	AX649745 Sequence	616	12.2	37.0	42	11	CR378503	CR378503 Arabidops
544	12.2	37.0	25	6	AX782792	AX782792 Sequence	617	12.2	37.0	45	6	AX612160	AX612160 Sequence
545	12.2	37.0	26	6	AR090455	AR090455 Sequence	618	12.2	37.0	45	6	AX612161	AX612161 Sequence
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c 548	12.2	37.0	26	6	AX115295	AX115295 Sequence	621	12.2	37.0	47	6	AR288784	AR288784 Sequence
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c 552	12.2	37.0	27	6	BD267965	BD267965 Inhibitor	c 625	12.2	37.0	48	6	EL1489	EL1489 PCR primer
c 553	12.2	37.0	27	6	BD270868	BD270868 Inhibitor	c 626	12.2	37.0	48	6	AX777210	AX777210 Sequence
c 554	12.2	37.0	27	6	BD272019	BD272019 Inhibitor	c 627	12.2	37.0	49	6	AX404131	AX404131 Sequence
c 555	12.2	37.0	27	6	BD272038	BD272038 Inhibitor	c 628	12.2	37.0	50	6	CQ002897	CQ002897 Sequence
c 556	12.2	37.0	27	6	BD274576	BD274576 Inhibitor	c 629	12.2	37.0	50	6	CQ003417	CQ003417 Sequence
c 557	12.2	37.0	27	6	BD274595	BD274595 Inhibitor	c 630	12.2	37.0	50	6	CQ004558	CQ004558 Sequence
c 558	12.2	37.0	27	6	AR181811	AR181811 Sequence	631	12.2	37.0	50	6	CQ005922	CQ005922 Sequence
c 559	12.2	37.0	27	6	AR195277	AR195277 Sequence	632	12.2	37.0	50	6	AX159730	AX159730 Sequence
c 560	12.2	37.0	27	6	AR199993	AR199993 Sequence	c 633	12.2	37.0	50	6	AX952063	AX952063 Sequence
c 561	12.2	37.0	27	6	AR201346	AR201346 Sequence	c 634	12.2	37.0	50	6	AX952657	AX952657 Sequence
c 562	12.2	37.0	27	6	AR201365	AR201365 Sequence	c 635	12.2	36.4	12	6	AX170909	AX170909 Sequence
c 563	12.2	37.0	27	6	AR216089	AR216089 Sequence	c 636	12.2	36.4	12	6	BD001050	BD001050 Method an
c 564	12.2	37.0	27	6	AR224798	AR224798 Sequence	c 637	12.2	36.4	12	6	BD001479	BD001479 Method an
c 565	12.2	37.0	27	6	AR317257	AR317257 Sequence	c 638	12.2	36.4	20	6	AR131567	AR131567 Sequence
c 566	12.2	37.0	27	6	AR337532	AR337532 Sequence	c 639	12.2	36.4	20	6	AR199501	AR199501 Sequence
c 567	12.2	37.0	27	6	AR366756	AR366756 Sequence	c 640	12.2	36.4	20	6	AR200972	AR200972 Sequence
c 568	12.2	37.0	27	6	AR368671	AR368671 Sequence	641	12.2	36.4	20	6	AR379351	AR379351 Sequence
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c 571	12.2	37.0	27	6	BD075044	BD075044 Method fo	644	12.2	36.4	20	6	AX497092	AX497092 Sequence
c 572	12.2	37.0	28	6	AR160054	AR160054 Sequence	645	12.2	36.4	20	6	BD016612	BD016612 Genes and
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c 574	12.2	37.0	28	6	AR090290	AR090290 Sequence	c 647	12.2	36.4	21	6	I46602	I46602 Sequence 58
575	12.2	37.0	29	6	BD174673	BD174673 Transcrip	c 648	12.2	36.4	21	6	AX298146	AX298146 Sequence
c 576	12.2	37.0	29	6	BD198147	BD198147 Method an	c 649	12.2	36.4	23	6	BD133326	BD133326 Method fo
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c 578	12.2	37.0	29	6	AR197325	AR197325 Sequence	651	12.2	36.4	24	6	AI5591	AI5591 Oligonucleo
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c 580	12.2	37.0	29	6	BD006858	BD006858 Method fo	c 653	12.2	36.4	24	6	ES0442	ES0442 Method for
c 581	12.2	37.0	30	6	AR125708	AR125708 Sequence	654	12.2	36.4	24	6	AR182273	AR182273 Sequence
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c 589	12.2	37.0	32	6	AR308126	AR308126 Sequence	c 662	12.2	36.4	25	6	AR240245	AR240245 Sequence
c 590	12.2	37.0	33	6	E36464	E36464 DNA polymer	c 663	12.2	36.4	25	6	AR467313	AR467313 Sequence
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596	12.2	37.0	36	6	BD084652	BD084652 Human com	669	12.2	36.4	25	6	AX782524	AX782524 Sequence
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598	12.2	37.0	37	6	I69358	I69358 Sequence 5	671	12.2	36.4	27	6	A09177	A09177 reverse com
599	12.2	37.0	37	6	AR205505	AR205505 Sequence	c 672	12.2	36.4	27	6	A09177	A09177 Nucleotide
600	12.2	37.0	37	6	AX076520	AX076520 Sequence	673	12.2	36.4	27	6	A09513	A09513 Mutagenic p
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602	12.2	37.0	37	6	AX513009	AX513009 Sequence	c 675	12.2	36.4	27	6	AX380913	AX380913 Sequence
603	12.2	37.0	38	6	AR034798	AR034798 Sequence	c 676	12.2	36.4	27	10	MM1121	X94880 M.musculus

677	12	36.4	28	6	BD225867	BD225867 Promoter	c 750	12	36.4	39	6	CQ821263	CQ821263 Sequence
c 678	12	36.4	28	6	E48749	E48749 Process for	751	12	36.4	39	6	AR366594	AR366594 Sequence
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c 693	12	36.4	33	6	AR302217	AR302217 Sequence	c 766	12	36.4	41	6	BD170575	BD170575 Novel pro
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c 701	12	36.4	35	6	E09146	E09146 Synthetic D	c 774	12	36.4	43	6	AX590458	AX590458 Sequence
c 702	12	36.4	35	6	AR397826	AR397826 Sequence	c 775	12	36.4	43	6	A65369	A65369 Sequence
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c 704	12	36.4	36	6	AR285836	AR285836 Sequence	c 777	12	36.4	47	6	AR284660	AR284660 Sequence
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c 708	12	36.4	37	6	CQ771098	CQ771098 Sequence	c 781	12	36.4	48	9	HSA224222	HSA224222 Homo sapi
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c 710	12	36.4	37	6	CQ779463	CQ779463 Sequence	c 783	12	36.4	50	6	A11298	A11298 Nucleotide
711	12	36.4	37	6	CQ779464	CQ779464 Sequence	c 784	12	36.4	50	6	CQ006922	CQ006922 Sequence
c 712	12	36.4	37	6	AR397827	AR397827 Sequence	c 785	12	36.4	50	6	CQ008164	CQ008164 Sequence
c 713	12	36.4	37	6	AX357425	AX357425 Sequence	c 786	12	36.4	50	6	AR443593	AR443593 Sequence
c 714	12	36.4	37	6	AX551182	AX551182 Sequence	c 787	12	36.4	50	9	HSHLX1A3	HSHLX1A3
c 715	12	36.4	37	6	AX551182	AX551182 Sequence	c 788	12	36.4	50	9	S85460	S85460 immunoglobu
c 716	12	36.4	37	6	AX581958	AX581958 Sequence	c 789	11.8	35.8	15	6	AR037377	AR037377 Sequence
c 717	12	36.4	37	6	AX770379	AX770379 Sequence	c 790	11.8	35.8	15	6	AR043858	AR043858 Sequence
c 718	12	36.4	37	6	AX805517	AX805517 Sequence	c 791	11.8	35.8	15	6	I47009	I47009 Sequence
c 719	12	36.4	38	6	AR156777	AR156777 Sequence	c 792	11.8	35.8	15	6	I47657	I47657 Sequence
c 720	12	36.4	38	6	AR286565	AR286565 Sequence	c 793	11.8	35.8	15	6	I63158	I63158 Sequence
c 721	12	36.4	38	6	AR286616	AR286616 Sequence	c 794	11.8	35.8	15	6	I81415	I81415 Sequence
c 722	12	36.4	38	6	AR286961	AR286961 Sequence	c 795	11.8	35.8	15	6	I93806	I93806 Sequence
c 723	12	36.4	38	6	AR286990	AR286990 Sequence	c 796	11.8	35.8	16	6	AR057413	AR057413 Sequence
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c 727	12	36.4	38	6	AR336250	AR336250 Sequence	c 800	11.8	35.8	17	6	A44456	A44456 Sequence
c 728	12	36.4	38	6	AR365595	AR365595 Sequence	c 801	11.8	35.8	17	6	AR062073	AR062073 Sequence
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c 735	12	36.4	38	6	AX222466	AX222466 Sequence	c 808	11.8	35.8	17	6	AX265803	AX265803 Sequence
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c 738	12	36.4	38	6	AX273532	AX273532 Sequence	c 811	11.8	35.8	18	6	A70960	A70960 Sequence
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c 740	12	36.4	38	6	AX273918	AX273918 Sequence	c 813	11.8	35.8	19	6	AX250627	AX250627 Sequence
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c 742	12	36.4	38	6	AX425312	AX425312 Sequence	c 815	11.8	35.8	20	6	A32034	A32034 primer DNA
c 743	12	36.4	38	6	AX425318	AX425318 Sequence	c 816	11.8	35.8	20	6	AR016183	AR016183 Sequence
c 744	12	36.4	38	6	AX425355	AX425355 Sequence	c 817	11.8	35.8	20	6	AR019181	AR019181 Sequence
c 745	12	36.4	38	6	AX425362	AX425362 Sequence	c 818	11.8	35.8	20	6	AR037376	AR037376 Sequence
c 746	12	36.4	38	6	AX425471	AX425471 Sequence	c 819	11.8	35.8	20	6	AR043857	AR043857 Sequence
c 747	12	36.4	39	6	AR156776	AR156776 Sequence	c 820	11.8	35.8	20	6	AR060259	AR060259 Sequence
c 748	12	36.4	39	6	CQ821260	CQ821260 Sequence	c 821	11.8	35.8	20	6	BD195412	BD195412 Male info
c 749	12	36.4	39	6	CQ821261	CQ821261 Sequence	c 822	11.8	35.8	20	6	E08714	E08714 Probe for d

C 823	11.8	35.8	20	6	I47008	I47008 Sequence 21	C 896	11.8	35.8	37	6	AX048271	AX048271 Sequence
C 824	11.8	35.8	20	6	I47656	I47656 Sequence 21	C 897	11.8	35.8	37	6	AX921633	AX921633 Sequence
C 825	11.8	35.8	20	6	I63157	I63157 Sequence 21	C 898	11.8	35.8	37	6	BD057643	BD057643 Fusion pr
C 826	11.8	35.8	20	6	I81414	I81414 Sequence 21	C 899	11.8	35.8	38	6	BD081473	BD081473 Soluble s
C 827	11.8	35.8	20	6	I93805	I93805 Sequence 21	C 900	11.8	35.8	38	6	A65595	A65595 Sequence 53
C 828	11.8	35.8	20	6	AR195026	AR195026 Sequence	C 901	11.8	35.8	38	6	AR443276	AR443276 Sequence
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C 830	11.8	35.8	20	6	AR350259	AR350259 Sequence	C 903	11.8	35.8	39	6	AX463645	AX463645 Sequence
C 831	11.8	35.8	20	6	AR352442	AR352442 Sequence	C 904	11.8	35.8	39	6	AX463653	AX463653 Sequence
C 832	11.8	35.8	20	6	AX004543	AX004543 Sequence	C 905	11.8	35.8	40	6	AX538556	AX538556 Sequence
C 833	11.8	35.8	20	6	AX135671	AX135671 Sequence	C 906	11.8	35.8	41	6	AR213224	AR213224 Sequence
C 834	11.8	35.8	20	6	AX349217	AX349217 Sequence	C 907	11.8	35.8	41	6	AR213226	AR213226 Sequence
C 835	11.8	35.8	20	6	AX349218	AX349218 Sequence	C 908	11.8	35.8	41	6	AR213228	AR213228 Sequence
C 836	11.8	35.8	20	6	AX816169	AX816169 Sequence	C 909	11.8	35.8	41	6	AR213236	AR213236 Sequence
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C 838	11.8	35.8	21	6	CQ818175	CQ818175 Sequence	C 911	11.8	35.8	41	6	BD009292	BD009292 Mutant pe
C 839	11.8	35.8	21	6	E15261	E15261 Primer. 7/1	C 912	11.8	35.8	41	6	BD009294	BD009294 Mutant pe
C 840	11.8	35.8	21	6	AX751611	AX751611 Sequence	C 913	11.8	35.8	41	6	BD009302	BD009302 Mutant pe
C 841	11.8	35.8	22	6	AR489468	AR489468 Sequence	C 914	11.8	35.8	42	6	AR159935	AR159935 Sequence
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C 845	11.8	35.8	24	6	AX289482	AX289482 Sequence	C 918	11.8	35.8	42	6	AX127930	AX127930 Sequence
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C 848	11.8	35.8	25	6	BD227222	BD227222 Human dea	C 921	11.8	35.8	47	6	AR238992	AR238992 Sequence
C 849	11.8	35.8	25	6	I47010	I47010 Sequence 23	C 922	11.8	35.8	47	6	AR240159	AR240159 Sequence
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C 851	11.8	35.8	25	6	I63159	I63159 Sequence 23	C 924	11.8	35.8	47	6	AR289588	AR289588 Sequence
C 852	11.8	35.8	25	6	I81416	I81416 Sequence 23	C 925	11.8	35.8	47	6	AR289679	AR289679 Sequence
C 853	11.8	35.8	25	6	I93807	I93807 Sequence 23	C 926	11.8	35.8	47	6	AR290813	AR290813 Sequence
C 854	11.8	35.8	25	6	AX010744	AX010744 Sequence	C 927	11.8	35.8	47	6	AX278794	AX278794 Sequence
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C 859	11.8	35.8	26	6	I59962	I59962 Sequence 17	C 932	11.8	35.8	48	9	HSU14084	U14084 Human T cel
C 860	11.8	35.8	26	6	I86043	I86043 Sequence 17	C 933	11.8	35.8	49	6	BD022496	BD022496 Multi-fun
C 861	11.8	35.8	26	6	AR182633	AR182633 Sequence	C 934	11.8	35.8	49	6	BD170228	BD170228 Process f
C 862	11.8	35.8	27	6	BD206505	BD206505 Enzymatic	C 935	11.8	35.8	50	6	A49265	A49265 Sequence 31
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C 869	11.8	35.8	29	6	AR068555	AR068555 Sequence	C 942	11.8	35.8	50	6	I42277	I42277 Sequence 90
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C 871	11.8	35.8	29	6	BD227320	BD227320 Secreted	C 944	11.8	35.8	50	6	AX960344	AX960344 Sequence
C 872	11.8	35.8	29	6	BD250919	BD250919 A plant d	C 945	11.8	35.8	50	6	BD014222	BD014222 Probe for
C 873	11.8	35.8	30	6	A42937	A42937 Sequence 7	C 946	11.8	35.8	50	6	BD070624	BD070624 Complemen
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C 876	11.8	35.8	31	6	AX249214	AX249214 Sequence	C 949	11.8	35.8	50	10	MMU41917	U41917 Mus musculu
C 877	11.8	35.8	31	6	BD002741	BD002741 Gene comp	C 950	11.6	35.2	18	6	A63383	A63383 Sequence 4
C 878	11.8	35.8	33	6	A20241	A20241 Mutagenic o	C 951	11.6	35.2	18	6	CQ755488	CQ755488 Sequence
C 879	11.8	35.8	33	6	I43794	I43794 Sequence 13	C 952	11.6	35.2	18	6	AR215491	AR215491 Sequence
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C 881	11.8	35.8	34	6	AX003062	AX003062 Sequence	C 954	11.6	35.2	18	6	AX958845	AX958845 Sequence
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C 884	11.8	35.8	34	6	BD167734	BD167734 High effi	C 957	11.6	35.2	20	6	AR163928	AR163928 Sequence
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C 888	11.8	35.8	35	6	AX087983	AX087983 Sequence	C 961	11.6	35.2	20	6	AR304435	AR304435 Sequence
C 889	11.8	35.8	36	3	DME544033	AJ544033 Drosophil	C 962	11.6	35.2	20	6	AX750548	AX750548 Sequence
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C 894	11.8	35.8	37	6	AR213585	AR213585 Sequence	C 967	11.6	35.2	21	6	AX146145	AX146145 Sequence
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973 11.6 35.2 23 6 A97878 Sequence
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975 11.6 35.2 23 6 E14076 Primer. 7/1
976 11.6 35.2 23 6 AR254871 Sequence
977 11.6 35.2 23 6 AR303868 Sequence
978 11.6 35.2 23 6 AR476280 Sequence
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985 11.6 35.2 24 6 AR337850 Sequence
986 11.6 35.2 24 6 AR439869 Sequence
987 11.6 35.2 25 6 CQ626238 Sequence
988 11.6 35.2 25 6 I05385 Sequence 6
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990 11.6 35.2 25 6 AX491318 Sequence
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993 11.6 35.2 26 6 E39415 Novel phys1
994 11.6 35.2 26 6 AX431505 Sequence
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996 11.6 35.2 26 6 BD173732 Use of ga
997 11.6 35.2 27 6 AR000197 Sequence
998 11.6 35.2 27 6 E41699 Process for
999 11.6 35.2 27 6 AX927898 Sequence
c1000 11.6 35.2 27 10 MM1131 X94883 M.musculus

ALIGNMENTS

RESULT 1
AX802289 31 bp DNA linear PAT 24-NOV-2003
LOCUS
DEFINITION Sequence 1 from Patent WO03057910.
ACCESSION AX802289
VERSION AX802289.1 GI:38501180
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Pinsl-Ober,J., Wenzig,P., Weindel,K., Bartl,K., Schoenbrunner,R.,
TITLE Malhotra,K., O'Donnell,P. and Kyger,E.
JOURNAL Use of silica material in an amplification reaction
COMMENT Patent: WO 03057910-A 1 17-JUL-2003;
FEATURES Roche Diagnostics GmbH (DE)
source Location/Qualifiers
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/organism="synthetic construct"
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/note="HCV specific probe"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31

RESULT 2
AS2660/c 36 bp DNA linear PAT 12-DEC-1997
LOCUS
DEFINITION Sequence 5 from Patent WO9624662.
ACCESSION AS2660
VERSION AS2660.1 GI:2851824
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Ravagnan,G., Battaglia,M., Carloni,G., Ponsetto,A. and Iacovacci,S.
TITLE PROCESS TO 'IN VITRO' PROPAGATE THE HEPATITIS C VIRUS (HCV) IN NON
JOURNAL LYMPHOBLASTOID ANIMAL CELL CULTURES AND PRODUCTS THEREOF
COMMENT Patent: WO 9624662-A 5 15-AUG-1996;
FEATURES CONSIGLIO NAZIONALE RICERCA (IT)
Other publication AU 1822195 960827.
source Location/Qualifiers
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/organism="unidentified"
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ORIGIN
Query Match 92.1%; Score 30.4; DB 6; Length 36;
Best Local Similarity 96.9%; Pred. No. 0.34;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 32 CGGTGTACTACCGTTCGCGAGACCACCTATG 1

RESULT 3
A68291/c 29 bp DNA linear PAT 06-MAY-1999
LOCUS
DEFINITION Sequence 12 from Patent WO9746716.
ACCESSION A68291
VERSION A68291.1 GI:4759412
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bosio,P., Strumia,C. and Clemenza,F.
TITLE METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS
JOURNAL Patent: WO 9746716-A 12 11-DEC-1997;
COMMENT WABCO B V (NL)
FEATURES Other publication IT RM960404 19971209.
source Location/Qualifiers
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/db_xref="taxon:32644"

ORIGIN
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Best Local Similarity 96.6%; Pred. No. 5.2;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TGTACTACCGTTCGCGAGACCACCTATG 32
Db 29 TGTACTACCGTTCGCGAGACCACCTATG 1

RESULT 4
BD181364 34 bp DNA linear PAT 15-MAY-2003
LOCUS
DEFINITION A method for determination of a nucleic acid using a control.
ACCESSION BD181364
VERSION BD181364.1 GI:30792282
KEYWORDS JP 2002335981-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34) artificial sequences.
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Jaeger, S.
 A method for determination of a nucleic acid using a control
 Patent: JP 2002335981-A 3 26-NOV-2002;
 F. HOFFMANN LA ROCHE AG
 OS Artificial Sequence
 PN JP 2002335981-A/3
 PD 26-NOV-2002
 PF 04-MAR-2002 JP 2002057515
 PR 02-MAR-2001 EP 01105172.9
 PI STEPHAN JAEGER
 PC C12N15/09, C12Q1/68, G01N33/50, G01N33/53, G01N33/566, G01N33/58,
 C12N15/00
 CC Description of Artificial Sequence: ST650 HCV specific probe
 sequence
 CC n represents abasic linker ((2-amino-cyclohexyl-)propan-1,3-
 diol)
 FH Key Location/Qualifiers
 FT N_region (15).
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
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 Best Local Similarity 97.1%; Pred. No. 6.8e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CGGTGTACTACCG-TTCGCGAGACCACTATGGC 33
 DB 1 CGGTGTACTACCGTTCGCGAGACCACTATGGC 34
 RESULT 5
 AX523944
 LOCUS Sequence 3 from Patent EP1236804. 34 bp DNA linear PAT 21-NOV-2002
 DEFINITION
 ACCESSION AX523944
 VERSION AX523944.1 GI:25168875
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Jaeger, S.
 TITLE A method for determination of a nucleic acid using a control
 JOURNAL Patent: EP 1236804-A 3 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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 source Location/Qualifiers
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
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 /note="n represents abasic linker
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 Query Match 66.7%; Score 22; DB 6; Length 34;
 Best Local Similarity 97.1%; Pred. No. 6.8e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CGGTGTACTACCG-TTCGCGAGACCACTATGGC 33
 DB 1 CGGTGTACTACCGTTCGCGAGACCACTATGGC 34
 RESULT 6
 AX524842
 LOCUS Sequence 3 from Patent EP1236805. 34 bp DNA linear PAT 21-NOV-2002
 DEFINITION

AX524842
 VERSION AX524842.1 GI:25169936
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Jaeger, S.
 TITLE A method for the determination of a nucleic acid using a control
 JOURNAL Patent: EP 1236805-A 3 04-SEP-2002;
 Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
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 source Location/Qualifiers
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 /note="n represents abasic linker
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 ORIGIN
 Query Match 66.7%; Score 22; DB 6; Length 34;
 Best Local Similarity 97.1%; Pred. No. 6.8e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CGGTGTACTACCG-TTCGCGAGACCACTATGGC 33
 DB 1 CGGTGTACTACCGTTCGCGAGACCACTATGGC 34
 RESULT 7
 BD171248
 LOCUS Method of detecting pathogenic microorganism. 41 bp DNA linear PAT 17-JAN-2003
 DEFINITION
 ACCESSION BD171248
 VERSION BD171248.1 GI:27877060
 KEYWORDS WO 02052043-A/40.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 41)
 AUTHORS Shimada, M., Hino, F. and Kato, I.
 TITLE Method of detecting pathogenic microorganism
 JOURNAL Patent: WO 02052043-A 40 04-JUL-2002;
 TAKARA SHUZO CO LTD, MASAMITSU SHIMADA, FUMITSUGU HINO, IKUNOSHIN KATO
 COMMENT OS Artificial Sequence
 PN WO 02052043-A/40
 PD 04-JUL-2002
 PF 26-DEC-2001 WO 2001JP011422
 PR 26-DEC-2000 JP 00P 396222, 26-DEC-2000 JP 00P 396321 PR
 29-JUN-2001 JP 01P 199552, 13-SEP-2001 JP 01P 278920 PI
 MASAMITSU SHIMADA, FUMITSUGU HINO, IKUNOSHIN KATO PC
 C12Q1/68, C12N15/09
 CC Primer area to amplify a portion of HCV.
 FH Key Location/Qualifiers
 FT source 1..41
 /organism="Artificial Sequence".
 source Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 ORIGIN
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 Best Local Similarity 97.1%; Pred. No. 6.6e+02;
 Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 CGGTGTACTACCG-TTCGCGAGACCACTATGGC 33
 DB 5 CGGTGTACTACCGTTCGCGAGACCACTATGGC 38


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RESULT 8
E25774/c
LOCUS          E25774          41 bp    DNA          linear          PAT 18-JUN-2001
DEFINITION    Method for assaying HCV gene by real time detection PCR method and
               primer and probe to be used therein.
ACCESSION     E25774
VERSION       JP 1999103899-A/5.
KEYWORDS      unclassified
SOURCE        unclassified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 41)
AUTHORS       Michinori,O., Ryuji,K. and Aki,A.
TITLE         Method for assaying HCV gene by real time detection PCR method and
               primer and probe to be used therein
JOURNAL       Patent: JP 1999103899-A 5 20-APR-1999;
COMMENT       TOKYO MET GOV RINSHO IGAKU SOGO KENKYUSHO, SRL INC
OS            Unidentified
PN            JP 1999103899-A/5
PD            20-APR-1999
PE            30-SEP-1997 JP 1997283042
PF            PR
PI            MICHINORI OBARA, RYUJI KAWAGUCHI, AKI ABE
PC            C12Q1/70.C12N15/09.G01N21/78.G01N33/58.C12N15/00 CC
FH            Key
FT            Location/Qualifiers
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               Location/Qualifiers
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Query Match      63.6%; Score 21; DB 6; Length 41;
Best Local Similarity 97.0%; Pred. No. 1.6e+03;
Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGGTGTACTCACC-GTTCGCGAGACCACCTATGG 32
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Db 33 CGGTGTACTCACC-GTTCGCGAGACCACCTATGG 1
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RESULT 9
AR411540
LOCUS          AR411540          26 bp    DNA          linear          PAT 18-DEC-2003
DEFINITION    Sequence 4 from patent US 6638714.
ACCESSION     AR411540
VERSION       AR411540.1 GI:40163884
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 26)
AUTHORS       Linnen,J.M. and Gorman,K.M.
TITLE         Oligonucleotide primers for efficient detection of hepatitis C
               virus (HCV) and methods of use thereof
JOURNAL       Patent: US 6638714-A 4 28-OCT-2003;
FEATURES      source
               Location/Qualifiers
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               /organism="unknown"
               /mol_type="genomic DNA"
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Query Match      61.8%; Score 20.4; DB 6; Length 26;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACCTATGGC 33
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Db 1 CCGTTCGCGAGACCACCTATGGC 22
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RESULT 10
BD000266
LOCUS          BD000266          26 bp    DNA          linear          PAT 31-JAN-2002
DEFINITION    Oligonucleotide primers for efficient detection of hepatitis C
               virus (HCV) and methods of use thereof.
ACCESSION     BD000266
VERSION       BD000266.1 GI:18623345
KEYWORDS      JP 2000279200-A/4.
SOURCE        synthetic construct
ORGANISM      synthetic construct
               artificial sequences.
               1 (bases 1 to 26)
REFERENCE     1 (bases 1 to 26)
AUTHORS       Lynnen,J.M. and Gorman,K.M.
TITLE         Oligonucleotide primers for efficient detection of hepatitis C
               virus (HCV) and methods of use thereof
JOURNAL       Patent: JP 2000279200-A 4 10-OCT-2000;
COMMENT       ORTHO CLINICAL DIAGNOSTICS INC
OS            Artificial Sequence
PN            JP 2000279200-A/4
PD            10-OCT-2000
PE            PD
PF            03-FEB-2000 JP 2000032656
PR            03-FEB-1999 US 60/118497
PI            JEFFREY M LYNEN, KEVIN M GORMAN
PC            C12Q1/68.C12N15/09/(C12N15/09.C12R1:92).C12N15/00.(C12N15/00.
               C12R1:92).
FH            Key
FT            Location/Qualifiers
FEATURES      source
               Location/Qualifiers
               1..26
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               /mol_type="genomic DNA"
               /db_xref="taxon:32630"
ORIGIN
Query Match      61.8%; Score 20.4; DB 6; Length 26;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACCTATGGC 33
    |||||
Db 1 CCGTTCGCGAGACCACCTATGGC 22
    |||||

RESULT 11
AR094968
LOCUS          AR094968          28 bp    DNA          linear          PAT 08-SEP-2000
DEFINITION    Sequence 6 from patent US 6001990.
ACCESSION     AR094968
VERSION       AR094968.1 GI:10022389
KEYWORDS      Unknown.
SOURCE        Unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 28)
AUTHORS       Wands,J.R., Wakita,T. and Moradpour,D.
TITLE         Antisense inhibition of hepatitis C virus
               Patent: US 6001990-A 6 14-DEC-1999;
JOURNAL       Location/Qualifiers
FEATURES      source
               Location/Qualifiers
               1..28
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               /mol_type="unassigned DNA"
ORIGIN
Query Match      61.8%; Score 20.4; DB 6; Length 28;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACCTATGGC 33
    |||||
Db 4 CCGTTCGCGAGACCACCTATGGC 25
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RESULT 12
BD183050/c
LOCUS
DEFINITION Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same.
ACCESSION BD183050
VERSION BD183050.1 GI:31875250
KEYWORDS JP 2002345467-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 28)
AUTHORS Mukaide,M., Tsunoda,K. and Hikiji,K.
TITLE Nucleic acids for grouping hepatitis C virus and method for group
ing hepatitis C virus using the same
JOURNAL Patent: JP 2002345467-A 22 03-DEC-2002;
SRL INC
COMMENT OS Artificial Sequence
PN JP 2002345467-A/22
PD 03-DEC-2002
PF 17-APR-2001 JP 2001118810
PI MASAKAZU MUKAIDE,KOICHI TSUNODA,KAZUMASA HIKIJI PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC Nucleic Acid
used as signal-amplifying probe which hybridizes CC
with a
CC region in HCV 5'-UTR region
FH Key Location/Qualifiers
FT source 1..28
FT /organism='Artificial Sequence'.
FEATURES
source
1..28
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 28;
Best Local Similarity 95.5%; Pred. No. 3e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCGTTCGCGACCACTATGGC 33
Db 26 CCGTTCGCGACCACTATGGC 5
RESULT 13
A70977/c
LOCUS
DEFINITION Sequence 31 from Patent W09813522.
ACCESSION A70977
VERSION A70977.1 GI:4774962
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 36)
AUTHORS Uhlen,M. and Lundeberg,J.
TITLE THE USE OF MODULAR OLIGONUCLEOTIDES AS PROBES OR PRIMERS IN NUCLEIC
ACID BASED ASSAY
JOURNAL Patent: WO 9813522-A 31 02-APR-1998;
DZIEGLEWSKA HANNA EVA (GB)
FEATURES
source
1..36
/organism='Hepatitis C virus'
/mol_type='unassigned DNA'
/db_xref='taxon:11103'
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6
RESULT 14
BD244766/c
LOCUS
DEFINITION Isolation method of primer extension products by modular
oligonucleotide.
ACCESSION BD244766
VERSION BD244766.1 GI:33054536
KEYWORDS JP 2002525076-A/45.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 36)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Isolation method of primer extension products by modular
oligonucleotide.
JOURNAL Patent: JP 2002525076-A 45 13-AUG-2002;
DYNAL AS
COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002525076-A/45
PD 13-AUG-2002
PF 15-SEP-1999 JP 2000570369
PR 15-SEP-1998 US 09/153242,16-SEP-1998 GB 9820185.8 PI
JOAKIM LUNDEBERG, MATHIAS UHLEN
PC C12N15/09,C12Q1/68,C12N15/00
CC Isolation method of primer extension products by modular CC
oligonucleotide
FH Key Location/Qualifiers
FT source 1..36
FT /organism='Hepatitis virus (hepatitis C FT
virus)'.
FEATURES
source
1..36
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
ORIGIN
Query Match 61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.9e+03;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6
RESULT 15
AR255272/c
LOCUS
DEFINITION Sequence 39 from patent US 6482592.
ACCESSION AR255272
VERSION AR255272.1 GI:27304321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Lundeberg,J. and Uhlen,M.
TITLE Methods and kits for isolating primer extension products using
modular oligonucleotides
JOURNAL Patent: US 6482592-A 39 19-NOV-2002;
FEATURES
source
1..36
Location/Qualifiers
/organism='unknown'
/mol_type='genomic DNA'
ORIGIN

Query Match	61.8%; Score 20.4; DB 6; Length 36;
Best Local Similarity	95.5%; Pred. No. 2.9e+03;
Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	12 CGGTTCCGCAGACCACTATGGC 33 Db 27 CGGTTCCGCAGACCACTATGGC 6
RESULT 16	
AXI47026	AXI47026 32 bp DNA linear PAT 08-JUN-2001
LOCUS	Sequence 20 from Patent WO0137291.
DEFINITION	AXI47026
ACCESSION	AXI47026.1 GI:14346297
VERSION	
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1 Weindel,K., Riedling,M. and Geiger,A. Magnetic glass particles, method for their preparation and uses thereof
AUTHORS	Patent: WO 0137291-A 20 25-MAY-2001;
TITLE	Roche Diagnostics GmbH (DE)
JOURNAL	Location/Qualifiers
FEATURES	source
misc_feature	1..32 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Synthetic oligonucleotide probe (HCV)"
misc_feature	15 /note="N represents a pentamethine-di-indocarbocyanine via a alkyphosphatidyl-linker (Pharmacia Biotech Cys-N-ethyl-phosphoramidite)"
modified_base	31 /note="derivatisation with a 3'-terminal phosphate group"
ORIGIN	/mod_base=OTHER
Query Match	60.6%; Score 20; DB 6; Length 32;
Best Local Similarity	96.9%; Pred. No. 4.2e+03;
Matches	31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1 CGGTGTACTCACCG-TTCGCGAGACCATTATG 31 Db 1 CGGTGTACTCACCGTTCGCGAGACCATTATG 32
RESULT 17	
E25770/c	E25770 37 bp DNA linear PAT 18-JUN-2001
LOCUS	Method for assaying HCV gene by real time detection PCR method and primer and probe to be used therein.
DEFINITION	E25770
ACCESSION	E25770.1 GI:13024958
VERSION	
KEYWORDS	unidentified
SOURCE	unclassified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 37) Michinori,O., Ryuji,K. and Aki,A. Method for assaying HCV gene by real time detection PCR method and primer and probe to be used therein
AUTHORS	Patent: JP 1999103899-A 1 20-APR-1999;
TITLE	TOKYO MET GOV RINSHO IGAKU SOGO KENKYUSHO, SRL INC
JOURNAL	OS Unidentified
COMMENT	

PN	JP 1999103899-A/1
PD	20-APR-1999
PF	30-SEP-1997 JP 1997283042
PR	
PI	MICHINORI OBARA,RYUJI KAWAGUCHI,AKI ABE
PC	C12Q1/70,C12N15/09,G01N21/78,G01N33/58,C12N15/00 CC
FH	Key Location/Qualifiers
FT	source 1..37
FT	/organism='Unidentified'.
FEATURES	Location/Qualifiers
source	1..37
	/organism='unidentified'
	/mol_type='genomic DNA'
	/db_xref="taxon:32644"
ORIGIN	
Query Match	60.6%; Score 20; DB 6; Length 37;
Best Local Similarity	100.0%; Pred. No. 4.1e+03;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	14 GTTCCGACGACCACTATGGC 33 Db 37 GTTCCGACGACCACTATGGC 18
RESULT 18	
I17519/c	I17519 38 bp DNA linear PAT 07-OCT-1996
LOCUS	Sequence 9 from patent US 5491063.
DEFINITION	I17519
ACCESSION	I17519.1 GI:1597874
VERSION	
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 38) Fisher,M.E. and Watson,R.M. Methods for in-solution quenching of fluorescently labeled oligonucleotide probes
AUTHORS	Patent: US 5491063-A 9 13-FEB-1996;
TITLE	Journal Location/Qualifiers
JOURNAL	source 1..38
FEATURES	/organism="unknown"
	/mol_type="unassigned DNA"
ORIGIN	
Query Match	60.6%; Score 20; DB 6; Length 38;
Best Local Similarity	96.9%; Pred. No. 4.1e+03;
Matches	31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1 CGGTGTACTCACCG-GTTCCGCGACCACTATG 31 Db 32 CGGTGTACTCACCGTTCGCGACCACTATG 1
RESULT 19	
I17520/c	I17520 38 bp DNA linear PAT 07-OCT-1996
LOCUS	Sequence 10 from patent US 5491063.
DEFINITION	I17520
ACCESSION	I17520.1 GI:1597875
VERSION	
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 38) Fisher,M.E. and Watson,R.M. Methods for in-solution quenching of fluorescently labeled oligonucleotide probes
AUTHORS	Patent: US 5491063-A 10 13-FEB-1996;
TITLE	Journal Location/Qualifiers
JOURNAL	source 1..38
FEATURES	/organism="unknown"

ORIGIN /mol_type="unassigned DNA"

Query Match 60.6%; Score 20; DB 6; Length 38;
Best Local Similarity 96.9%; Pred. No. 4.1e+03;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTACC-GTTCGCGAGACCCTATGG 31
|||||
Db 32 CGGTGTACTACCGGTTCCGCGAGACCCTATG 1
|||||

RESULT 20
LOCUS AR080402 30 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 3 from patent US 5968775.
ACCESSION AR080402
VERSION AR080402.1 GI:10007137
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
AUTHORS Houghton,M., Steimer,K.S. and Weiner,A.J.
TITLE Hepatitis C virus infected cell systems
JOURNAL Patent: US 5968775-A 3 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CCGTTCGCGAGACCCTATGG 1
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RESULT 21
LOCUS AR118787 30 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 217 from patent US 6150087.
ACCESSION AR118787
VERSION AR118787.1 GI:14100697
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
AUTHORS Chien,D.Y.
TITLE NANBV diagnostics and vaccines
JOURNAL Patent: US 6150087-A 217 21-NOV-2000;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CCGTTCGCGAGACCCTATGG 1
|

RESULT 22
LOCUS E51970 30 bp DNA linear PAT 18-JUN-2001

DEFINITION Diagnostic for NANBV.
ACCESSION E51970
VERSION E51970.1 GI:13019297
KEYWORDS JP 2000039434-A/13.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Michael,H., Quilim,C. and George,K.
TITLE Diagnostic for NANBV
JOURNAL Patent: JP 2000039434-A 13 08-FEB-2000;
COMMENT CHIRON CORP
OS Unidentified
PN JP 2000039434-A/13
PD 08-FEB-2000
PR 03-JUN-1999 JP 1999157192
PR 17-MAR-1989 US 325.338, 20-APR-1989 US 341.334, PR
18-MAY-1989 US 355.002
PI MICHAEL HOUGHTON,QUI-LIM CHOO,GEORGE KUO
PC GOIN33/569,C07K14/18,G01N33/576//C12N15/09,C12P21/02, PC
(C12P21/02,C12R1:19),
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1..30
/organism='Unidentified'.

FEATURES
source 1..30
Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CCGTTCGCGAGACCCTATGG 1
|

RESULT 23
LOCUS I70136 30 bp DNA linear PAT 02-APR-1998
DEFINITION Sequence 3 from patent US 5679342.
ACCESSION I70136
VERSION I70136.1 GI:3006271
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
AUTHORS Houghton,M., Steimer,K.S. and Weiner,A.J.
TITLE Hepatitis C virus infected cell systems
JOURNAL Patent: US 5679342-A 3 21-OCT-1997;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCCTATGG 32
|
Db 21 CCGTTCGCGAGACCCTATGG 1
|

RESULT 24

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BD004842/c
LOCUS          BD004842          30 bp      DNA          linear      PAT 31-JAN-2002
DEFINITION    Method for manufacturing amplicons, detecting method thereby.
ACCESSION     BD004842
VERSION       BD004842.1 GI:18632803
KEYWORDS      JP 2001046080-A/5.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 30)
AUTHORS       Matsuzaki,S.
TITLE         Method for manufacturing amplicons, detecting method thereby
JOURNAL       MIZUHO MEDY CO LTD
COMMENT       OS Artificial Sequence
PN            JP 2001046080-A/5
PD            20-FEB-2001
PF            15-MAR-2000 JP 2000071790
PR            SEIICHIRO MATSUZAKI
PC            C12N15/09,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
PFH           Key Location/Qualifiers
FT            1..30
              /organism='Artificial Sequence'.
FEATURES      source
              1..30
              /organism='synthetic construct'
              /mol_type='genomic DNA'
              /db_xref='taxon:32630'
ORIGIN
Query Match          58.8%; Score 19.4; DB 6; Length 30;
Best Local Similarity 95.2%; Pred. No. 7.3e+03;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGTTCCGCAGACCACTATGG 32
Db 21 CGTTCCGCAGACCACTATGG 1

RESULT 25
E07367/c
LOCUS          E07367          22 bp      DNA          linear      PAT 29-SEP-1997
DEFINITION    PCR primer for gaining hepatitis C virus gene 5'noncoding region.
ACCESSION     E07367
VERSION       E07367.1 GI:2175506
KEYWORDS      JP 1994121700-A/5.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 22)
AUTHORS       Yagasaki,M. and Nunomura,K.
TITLE         METHOD FOR DETECTING HEPATITIS C VIRUS GENE
JOURNAL       Patent: JP 1994121700-A 5 06-MAY-1994;
              CHUGAI PHARMACEUT CO LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1994121700-A/5
              PD 06-MAY-1994
              PF 13-OCT-1992 JP 1992274273
              PI YAGASAKI MITSUO, NUNOMURA KIYOTADA
              PC C12Q1/68,C12Q1/68,C12N15/10,C12N15/51,C12Q1/70; CC
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key Location/Qualifiers
              FT source
              FT            1..22
              /organism='Artificial sequences'.
FEATURES      source
              1..22
              /organism='unidentified'
              /mol_type='genomic DNA'
              /db_xref='taxon:32644'
ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4

RESULT 27
AX250662/c
LOCUS          AX250662          24 bp      DNA          linear      PAT 05-OCT-2001
DEFINITION    Sequence 58 from Patent WO0168921.
ACCESSION     AX250662
VERSION       AX250662.1 GI:15984406
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              /organism='Artificial sequences'.
REFERENCE     1
AUTHORS       Koshinsky,H., Zwick,M.S. and Mccue,K.F.
TITLE         Compositions and methods for simultaneous detection of multiple
              biological entities
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/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4

RESULT 26
E07369/c
LOCUS          E07369          22 bp      DNA          linear      PAT 29-SEP-1997
DEFINITION    PCR primer for gaining hepatitis C virus gene 5'noncoding region.
ACCESSION     E07369
VERSION       E07369.1 GI:2175508
KEYWORDS      JP 1994121700-A/7.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1 (bases 1 to 22)
AUTHORS       Yagasaki,M. and Nunomura,K.
TITLE         METHOD FOR DETECTING HEPATITIS C VIRUS GENE
JOURNAL       Patent: JP 1994121700-A 7 06-MAY-1994;
              CHUGAI PHARMACEUT CO LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1994121700-A/7
              PD 06-MAY-1994
              PF 13-OCT-1992 JP 1992274273
              PI YAGASAKI MITSUO, NUNOMURA KIYOTADA
              PC C12Q1/68,C12Q1/68,C12N15/10,C12N15/51,C12Q1/70; CC
              CC topology: Linear;
              CC hypothetical: No;
              CC anti-sense: No;
              FH Key Location/Qualifiers
              FT source
              FT            1..22
              /organism='Artificial sequences'.
FEATURES      source
              1..22
              /organism='unidentified'
              /mol_type='genomic DNA'
              /db_xref='taxon:32644'
ORIGIN
Query Match          57.6%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
Db 22 TTCCGCAGACCACTATGGC 4

RESULT 27
AX250662/c
LOCUS          AX250662          24 bp      DNA          linear      PAT 05-OCT-2001
DEFINITION    Sequence 58 from Patent WO0168921.
ACCESSION     AX250662
VERSION       AX250662.1 GI:15984406
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              /organism='Artificial sequences'.
REFERENCE     1
AUTHORS       Koshinsky,H., Zwick,M.S. and Mccue,K.F.
TITLE         Compositions and methods for simultaneous detection of multiple
              biological entities
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RESULT 32
BD000246/c

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LOCUS       BD000246                25 bp    DNA    linear    PAT 31-JAN-2002
DEFINITION  Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof.
ACCESSION   BD000246
VERSION     BD000246.1  GI:18623325
KEYWORDS    JP 2000279198-A/1.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1  (bases 1 to 25)
AUTHORS     Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE       Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof
JOURNAL     Patent: JP 2000279198-A 1 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     PN JP 2000279198-A/1
            PD 10-OCT-2000
            PF 02-FEB-2000 JP 2000030237
            PR 03-FEB-1999 US 60/118498
            PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
            C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
            C12R1:92)
FH          Key      Location/Qualifiers
FT          source   1..25
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
FEATURES             source
ORIGIN
Query Match      57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15  TTCCGCAGACCACTATGGC 33
        |||||
        25  TTCCGCAGACCACTATGGC 7

RESULT 33
LOCUS     BD000255/c
DEFINITION Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof.
ACCESSION   BD000255
VERSION     BD000255.1  GI:18623334
KEYWORDS    JP 2000279198-A/10.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1  (bases 1 to 25)
AUTHORS     Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE       Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof
JOURNAL     Patent: JP 2000279198-A 10 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     PN JP 2000279198-A/10
            PD 10-OCT-2000
            PF 02-FEB-2000 JP 2000030237
            PR 03-FEB-1999 US 60/118498
            PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
            C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
            C12R1:92)
FH          Key      Location/Qualifiers
FT          source   1..25
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
FEATURES             source
ORIGIN
Query Match      57.6%; Score 19; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof.
ACCESSION   BD000255
VERSION     BD000255.1  GI:18623334
KEYWORDS    JP 2000279198-A/10.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1  (bases 1 to 25)
AUTHORS     Gorman,K.M., Paterson,D.R., Lynen,J.M. and Son,K.
TITLE       Oligonucleotide primers for efficient multiplex detection of
             hepatitis C virus (HCV) and human immunodeficiency virus (HIV) and
             methods of use thereof
JOURNAL     Patent: JP 2000279198-A 10 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     PN JP 2000279198-A/10
            PD 10-OCT-2000
            PF 02-FEB-2000 JP 2000030237
            PR 03-FEB-1999 US 60/118498
            PI KEVIN M GORMAN, DAVID R PATERSON, JEFFREY M LYNEN, KEMIN SON PC
            C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00, PC
            C12R1:92)
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FEATURES             source
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RESULT 35
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DEFINITION Sequence 6 from Patent EP0714988.
ACCESSION   A49280
VERSION     A49280.1  GI:2302803
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unidentified

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FH          Key      Location/Qualifiers
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Query Match      57.6%; Score 19; DB 6; Length 25;
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DEFINITION Oligonucleotide primers for efficient detection of hepatitis C
             virus (HCV) and methods of use thereof.
ACCESSION   BD000264
VERSION     BD000264.1  GI:18623343
KEYWORDS    JP 2000279200-A/2.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1  (bases 1 to 25)
AUTHORS     Lynen,J.M. and Gorman,K.M.
TITLE       Oligonucleotide primers for efficient detection of hepatitis C
             virus (HCV) and methods of use thereof
JOURNAL     Patent: JP 2000279200-A 2 10-OCT-2000;
            ORTHO CLINICAL DIAGNOSTICS INC
COMMENT     PN JP 2000279200-A/2
            PD 10-OCT-2000
            PF 03-FEB-2000 JP 2000032656
            PR 03-FEB-1999 US 60/118497
            PI JEFFREY M LYNEN, KEVIN M GORMAN
            PC C12Q1/68, C12N15/09// (C12N15/09, C12R1:92), C12N15/00, (C12N15/00,
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS     A49280
DEFINITION Sequence 6 from Patent EP0714988.
ACCESSION   A49280
VERSION     A49280.1  GI:2302803
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unidentified

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unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.D., Haemmerle,T.D., Himmelspach,M.D., Kohl,J.D. and
Dorner,F.F.
TITLE Method for quantifying nucleic acids
JOURNAL Patent: EP 0714988-A 6 05-JUN-1996;
IMMUNO AG (AT)
COMMENT Other publication JP 8107798 960430
Other publication CA 2159044 960327
Other publication AT 401062 960625
Other publication AT 183194 951015.
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AR301416/C
LOCUS AR301416 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 125 from patent US 6538126.
ACCESSION AR301416
VERSION AR301416.1 GI:31689200
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Cho,J.M., Lee,Y.B., Park,Y.W., Lim,K.J., Choi,D.Y., So,H.S.,
Kim,C.H., Kim,S.T. and Yang,J.Y.
TITLE Hepatitis C diagnostics and vaccines
JOURNAL Patent: US 6538126-A 125 25-MAR-2003;
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RESULT 39
AX004406
LOCUS AX004406 20 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 9 from Patent WO9918198.
ACCESSION AX004406
VERSION AX004406.1 GI:9927871
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Grandi,G. and Abrignani,S.
TITLE Hepatitis c receptor protein cd81
JOURNAL Patent: WO 9918198-A 9 15-APR-1999;
CHIRON S P A (IT); GRANDI GUIDO (IT)
FEATURES
source
Location/Qualifiers
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/db_xref="taxon:32630"
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Query Match 55.8%; Score 18.4; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e+04;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.D., Haemmerle,T.D., Himmelspach,M.D., Kohl,J.D. and
Dorner,F.F.
TITLE Method for quantifying nucleic acids
JOURNAL Patent: EP 0714988-A 6 05-JUN-1996;
IMMUNO AG (AT)
COMMENT Other publication JP 8107798 960430
Other publication CA 2159044 960327
Other publication AT 401062 960625
Other publication AT 183194 951015.
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Best Local Similarity 95.0%; Pred. No. 1.9e+04;
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RESULT 36
A64953
LOCUS A64953 20 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 7 from Patent WO9732040.
ACCESSION A64953
VERSION A64953.1 GI:4530922
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1
AUTHORS Stirling,D. and Ludlam,C.A.
TITLE NUCLEIC ACID SEQUENCE DETECTION
JOURNAL Patent: WO 9732040-A 7 04-SEP-1997;
ROYAL INFIRMARY OF EDINBURGH N (GB)
COMMENT Other publication AU 1889797 19970916.
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AR020188
LOCUS AR020188 20 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 6 from patent US 5789153.
ACCESSION AR020188
VERSION AR020188.1 GI:3974803
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Falkner,F.-G., Haemmerle,T., Himmelspach,M., Kohl,J. and Dorner,F.
TITLE Method of quantitating nucleic acid

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OM nucleic - nucleic search, using sw model

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Title: US-10-087-631B-3

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3992700

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	30.4	92.1	36	2	AAT39735 Hepatitis
C 5	27.4	83.0	29	2	AAV15324 Hepatitis
6	22	66.7	41	6	AAI40116 Pathogeni
C 7	21	63.6	41	2	AAI37635 HCV detec
8	20.4	61.8	26	3	AAI29447 Hepatitis
9	20.4	61.8	28	2	AAI05216 Hepatitis
10	20.4	61.8	28	3	AAI05216 Hepatitis
C 11	20.4	61.8	28	10	ADCS4071 HCV 5'UTR
C 12	20.4	61.8	36	3	AAI29447 Hepatitis
C 13	20	60.6	21	2	AAV35207 Hepatitis
C 14	20	60.6	22	2	AAI01497 Hepatitis
C 15	20	60.6	24	12	ADP87801 TEX on mi
C 16	20	60.6	25	8	ABZ75892 HCV RT-PC
C 17	20	60.6	25	12	ADH79952 Hepatitis
18	20	60.6	26	12	ADP87799 TEX on mi
19	20	60.6	32	4	AH25418 Detection
C 20	20	60.6	37	2	AAI37631 HCV detec
C 21	20	60.6	38	2	AAT12490 Labelled

C 22	19.4	58.8	30	2	AAQ21851	Aac21851 HCV probe
C 23	19.4	58.8	30	2	AAT94722	Aat94722 Hepatitis
C 24	19.4	58.8	30	2	AAZ27492	Aaz27492 Probe for
C 25	19.4	58.8	30	3	AAA75276	AAa75276 Probe use
C 26	19.4	58.8	30	12	ADN35930	Adn35930 HCV cDNA
C 27	19.4	58.8	31	3	AAZ99214	Aaz99214 Primer fo
C 28	19	57.6	19	10	ADD67939	Adf67939 Hepatitis
C 29	19	57.6	19	10	ADFS1488	Adfs1488 Hepatitis
C 30	19	57.6	19	10	ADFS1492	Adfs1492 Hepatitis
C 31	19	57.6	19	10	ADFS2184	Adfs2184 Hepatitis
C 32	19	57.6	19	10	ADFS2188	Adfs2188 Hepatitis
C 33	19	57.6	19	10	ABX10611	Abx10611 Light Cyc
C 34	19	57.6	20	2	AAQ65023	Aaq65023 Antisense
C 35	19	57.6	20	3	AAZ88590	Aaz88590 Hepatitis
C 36	19	57.6	22	2	AAQ67619	Aaq67619 Primer fo
C 37	19	57.6	24	4	AAI19054	Aai19054 Hepatitis
C 38	19	57.6	25	3	AAA96551	Aaa96551 Forward P
C 39	19	57.6	25	3	AAA96560	Aaa96560 Forward P
C 40	19	57.6	25	3	AAA74620	Aaa74620 HCV-speci
C 41	19	57.6	25	8	ABV76863	Abv76863 Nucleotid
C 42	18.4	55.8	20	2	AAQ33387	Aaq33387 Hepatitis
C 43	18.4	55.8	20	2	AAT28894	Aat28894 Hepatitis
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C 53	18.4	55.8	26	12	ADH22647	Adh22647 Hepatitis
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C 56	18	54.5	18	6	ABQ78214	Abq78214 Antisense
C 57	18	54.5	18	10	ADFS1491	Adfs1491 Hepatitis
C 58	18	54.5	19	10	ADFS1490	Adfs1490 Hepatitis
C 59	18	54.5	19	10	ADFS2187	Adfs2187 Hepatitis
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C 61	18	54.5	21	6	ABA02494	Abao2494 Hepatitis
C 62	18	54.5	21	6	ABA01125	Abao1125 HCV prime
C 63	18	54.5	46	8	ACC79265	Acc79265 Hepatitis
C 64	18	54.5	46	8	ADFS2182	Adfs2182 Hepatitis
C 65	17.4	52.7	19	10	ADFS1486	Adfs1486 Hepatitis
C 66	17.4	52.7	20	2	AAQ58412	Aaq58412 Antisense
C 67	17.4	52.7	20	10	ACC69191	Acc69191 HCV inter
C 68	17.4	52.7	23	10	ADFS2811	Adfs2811 Hepatitis
C 69	17.4	52.7	26	2	AAQ65019	Aaq65019 Antisense
C 70	17.4	52.7	26	2	AAQ64952	Aaq64952 Antisense
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C 72	17	51.5	17	8	ACD56834	Acd56834 HCV DNaz
C 73	17	51.5	17	8	ACD65841	Acd65841 HCV minus
C 74	17	51.5	17	12	ADI82784	Adi82784 HCV DNaz
C 75	17	51.5	17	12	ADI82784	Adi82784 HCV DNaz
C 76	17	51.5	17	10	ADFS2179	Adfs2179 Hepatitis
C 77	17	51.5	19	10	ADFS2179	Adfs2179 Hepatitis
C 78	17	51.5	19	10	ADFS1483	Adfs1483 Hepatitis
C 79	17	51.5	20	2	AAQ64953	Aaq64953 Antisense
C 80	17	51.5	20	10	ACF04427	Acf04427 Hepatitis
C 81	17	51.5	21	2	AAI08539	Aai08539 Primer, H
C 82	17	51.5	22	5	AAH46508	Aah46508 Hepatitis
C 83	17	51.5	24	2	AAQ64954	Aaq64954 Antisense
C 84	17	51.5	24	6	ABL46270	Abi46270 Hepatitis
C 85	17	51.5	27	2	AAQ64955	Aaq64955 Antisense
C 86	17	51.5	30	2	AAQ64950	Aaq64950 Antisense
C 87	17	51.5	50	3	AAA52575	Aaa52575 HCV RNA P
C 88	16.4	49.7	19	10	ADFS1485	Adfs1485 Hepatitis
C 89	16.4	49.7	19	10	ADFS2181	Adfs2181 Hepatitis
C 90	16.4	49.7	20	2	AAI01502	Aai01502 Hepatitis
C 91	16.4	49.7	20	2	AAV15325	Aav15325 Hepatitis
C 92	16	48.5	16	2	AAT90592	Aat90592 Hepatitis
C 93	16	48.5	16	3	AAAI3409	Aai3409 Hepatitis
C 94	16	48.5	16	8	ABX74328	Abx74328 Hepatitis

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c 97	16	48.5	19	10	ADFS1484	Adfs1484 Hepatitis	c 170	15	45.5	19	10	ADFS2183	Adfs2183 Hepatitis
c 98	16	48.5	19	10	ADFS2180	Adfs2180 Hepatitis	c 171	15	45.5	21	2	AAV15318	AAV15318 Hepatitis
c 99	16	48.5	24	2	AAV11280	AAV11280 Hepatitis	c 172	15	45.5	21	12	ADJ57847	Adj57847 Primer #1
c 100	16	48.5	24	10	ADJ5637	Adj5637 Oligonucle	c 173	15	45.5	21	12	ADJ57755	Adj57755 Primer #1
c 101	16	48.5	24	10	ADD55641	Add55641 Oligonucle	c 174	15	45.5	21	12	ADL46122	Adl46122 Hepatitis
102	16	48.5	33	2	AAQ31153	AAQ31153 Probe 122	c 175	15	45.5	25	3	AAAS2570	AAAS2570 Oligonucle
103	16	48.5	33	2	AAQ46459	AAQ46459 Hepatitis	c 176	15	45.5	26	6	ABK88590	Abk88590 Hepatitis
104	16	48.5	33	2	AAV07856	AAV07856 HCV-33.4	c 177	15	45.5	31	10	AAAL57066	AAAL57066 Flavivirus
105	16	48.5	33	2	AAV83084	AAV83084 Capture p	c 178	15	45.5	34	10	ADB98999	Adb98999 Xmt8 PCR
106	16	48.5	39	5	AAAC8352	AAAC8352 ICAM-1 PC	c 179	15	45.5	34	10	ADBE2586	Adbe2586 Primer of
107	16	48.5	39	6	ABA97126	ABA97126 Human t1c	c 180	15	45.5	37	2	AAV66472	AAV66472 Primer MO
108	16	48.5	39	9	ACQ27630	Acq27630 Human t1c	c 181	15	45.5	45	10	ADC38532	Adc38532 Template
109	15.8	47.9	21	2	AAQ30154	AAQ30154 NANB hepa	c 182	15	45.5	50	3	AAAS2574	AAAS2574 HCV RNA p
110	15.8	47.9	21	2	AAQ31812	AAQ31812 Antisense	c 183	14.8	44.8	18	2	AAV15315	AAV15315 Hepatitis
111	15.8	47.9	21	2	AAQ30783	AAQ30783 Hepatitis	c 184	14.8	44.8	19	2	AAAT86456	AAAT86456 PCR prime
112	15.8	47.9	21	2	AAQ50783	AAQ50783 Hepatitis	c 185	14.8	44.8	19	8	ADL51014	Adl51014 Hepatitis
113	15.8	47.9	21	10	ADF52922	Adf52922 Hepatitis	c 186	14.8	44.8	19	10	ADFS2167	Adfs2167 Hepatitis
114	15.8	47.9	21	10	ADF52979	Adf52979 Hepatitis	c 187	14.8	44.8	19	10	ADFS1463	Adfs1463 Hepatitis
c 115	15.4	46.7	17	8	ACD56835	Accl56835 HCV DNazzy	c 188	14.8	44.8	19	10	ADFS1471	Adfs1471 Hepatitis
c 116	15.4	46.7	17	12	ADI82785	Adi82785 HCV DNazzy	c 189	14.8	44.8	19	10	ADFS2159	Adfs2159 Hepatitis
c 117	15.4	46.7	18	2	AAV70475	AAV70475 Non-bridg	c 190	14.8	44.8	21	2	AAQ58376	AAQ58376 Antisense
c 118	15.4	46.7	18	6	ABL46085	AbL46085 Non-bridg	c 191	14.8	44.8	21	3	AAAT72992	AAAT72992 Hepatitis
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c 120	15.4	46.7	19	10	ADFS2185	Adfs2185 Hepatitis	c 193	14.8	44.8	21	9	ADAL13856	Adal13856 Short int
c 121	15.4	46.7	19	10	ADFS1489	Adfs1489 Hepatitis	c 194	14.8	44.8	21	9	ADAL13855	Adal13855 Short int
c 122	15.4	46.7	23	10	ADFS2967	Adfs2967 Hepatitis	c 195	14.8	44.8	21	9	ADAL13816	Adal13816 Short int
c 123	15.4	46.7	23	10	ADFS2910	Adfs2910 Hepatitis	c 196	14.8	44.8	21	9	ADAL13863	Adal13863 Short int
c 124	15.4	46.7	24	2	AAV11273	AAV11273 Hepatitis	c 197	14.8	44.8	21	10	ADFS2833	Adfs2833 Hepatitis
c 125	15.4	46.7	25	8	ABV76987	Abv76987 Control p	c 198	14.8	44.8	21	10	ADFS2858	Adfs2858 Hepatitis
c 126	15.4	46.7	35	2	AAQ75822	AAQ75822 Sense pri	c 199	14.8	44.8	21	10	ADFS2840	Adfs2840 Hepatitis
c 127	15.4	46.7	44	12	ADN00279	Adn00279 RT-PCR pr	c 200	14.8	44.8	21	10	ADFS2859	Adfs2859 Hepatitis
c 128	15.2	46.1	33	2	AAV12106	AAV12106 Human B7	c 201	14.8	44.8	21	10	ADFS2866	Adfs2866 Hepatitis
c 129	15.2	46.1	38	2	AAV04401	AAV04401 Primer us	c 202	14.8	44.8	23	6	ABN79966	Abn79966 Hepatitis
c 130	15.2	46.1	38	2	AAV04403	AAV04403 Primer us	c 203	14.8	44.8	23	10	ADFS2805	Adfs2805 Hepatitis
c 131	15.2	46.1	38	2	AAV04405	AAV04405 Primer us	c 204	14.8	44.8	23	10	ADFS2807	Adfs2807 Hepatitis
c 132	15.2	46.1	38	2	AAV04344	AAV04344 Primer us	c 205	14.8	44.8	24	2	AAQ98287	AAQ98287 Hepatitis
c 133	15.2	46.1	38	2	AAV04346	AAV04346 Primer us	c 206	14.8	44.8	25	2	AAQ98279	AAQ98279 Hepatitis
c 134	15.2	46.1	38	2	AAV04407	AAV04407 Primer us	c 207	14.8	44.8	25	2	AAQ98274	AAQ98274 Hepatitis
c 135	15.2	46.1	38	5	AAFS7863	AAFS7863 Murine OP	c 208	14.8	44.8	25	2	AAV76723	AAV76723 Stacker o
c 136	15.2	46.1	38	5	AAFS7747	AAFS7747 Murine OP	c 209	14.8	44.8	25	2	AAV53936	AAV53936 Nucleotid
c 137	15.2	46.1	38	5	AAFS7745	AAFS7745 Murine OP	c 210	14.8	44.8	25	6	ADFS2939	Adfs2939 FEN-1 rel
c 138	15.2	46.1	38	5	AAFS7865	AAFS7865 Murine OP	c 211	14.8	44.8	28	2	AAAT05243	AAAT05243 Hepatitis
c 139	15.2	46.1	38	5	AAFS7867	AAFS7867 Murine OP	c 212	14.8	44.8	28	2	AAAT05217	AAAT05217 Hepatitis
c 140	15.2	46.1	38	5	AAFS7861	AAFS7861 Murine OP	c 213	14.8	44.8	28	3	AAZ57783	AAZ57783 Hepatitis
c 141	15.2	46.1	38	12	ADM28848	Adm28848 Mouse OP	c 214	14.8	44.8	28	3	AAZ57752	AAZ57752 Hepatitis
c 142	15.2	46.1	38	12	ADM28854	Adm28854 Mouse OP	c 215	14.8	44.8	29	2	AAV60679	AAV60679 Primer #1
c 143	15.2	46.1	38	12	ADM28716	Adm28716 Mouse OP	c 216	14.8	44.8	30	2	AAQ71841	AAQ71841 DNA probe
c 144	15.2	46.1	38	12	ADM28714	Adm28714 Mouse OP	c 217	14.8	44.8	31	8	ABZ81787	Abz81787 HCV 5' UT
c 145	15.2	46.1	38	12	ADM28850	Adm28850 Mouse OP	c 218	14.8	44.8	32	10	ADC79170	Adc79170 Human CD8
c 146	15.2	46.1	38	12	ADM28852	Adm28852 Mouse OP	c 219	14.8	44.8	33	2	AAQ31154	AAQ31154 Probe 123
c 147	15.2	46.1	40	1	AAH81426	AAH81426 Plasmid p	c 220	14.8	44.8	33	2	AAQ46460	AAQ46460 Hepatitis
c 148	15.2	46.1	46	6	ABN72439	Abn72439 Streptoco	c 221	14.8	44.8	33	2	AAV07857	AAV07857 HCV-33.5
c 149	15	45.5	15	2	AAQ64951	AAQ64951 Antisense	c 222	14.8	44.8	33	2	AAV07857	AAV07857 HCV-33.5
c 150	15	45.5	15	2	AAQ64941	AAQ64941 Hepatitis	c 223	14.8	44.8	33	2	AAV83085	AAV83085 Oligonucle
c 151	15	45.5	15	3	AAZ61838	AAZ61838 HCV 5' no	c 224	14.8	44.8	33	6	ABL46096	AbL46096 Capture p
c 152	15	45.5	15	3	AAZ62393	AAZ62393 Substrate	c 225	14.8	44.8	33	12	ADK82286	Adk82286 Nucleic a
c 153	15	45.5	15	6	ABX011779	Abx011779 Hepatitis	c 226	14.8	44.8	50	10	ADD31951	Add31951 BBP-BIX a
c 154	15	45.5	15	6	ABX01817	Abx01817 Hepatitis	c 227	14.6	44.2	30	8	ABX90079	Abx90079 S. aureus
c 155	15	45.5	15	6	ABX03367	Abx03367 Hepatitis	c 228	14.6	44.2	30	10	ADD25368	Add25368 Oligonucle
c 156	15	45.5	15	6	ABX00224	Abx00224 Hepatitis	c 229	14.6	44.2	33	2	AAQ66336	AAQ66336 Primer fo
c 157	15	45.5	15	6	ABX01780	Abx01780 Hepatitis	c 230	14.6	44.2	34	5	AAAD16133	AAAD16133 Human VEG
c 158	15	45.5	15	6	ABX01781	Abx01781 Hepatitis	c 231	14.6	44.2	34	12	ADO50775	Ado50775 Human VEG
c 159	15	45.5	15	8	ACD66277	Accl66277 Anti-HCV	c 232	14.6	44.2	40	2	AAAT61664	AAAT61664 Antibody
c 160	15	45.5	15	8	ACD65920	Accl65920 Anti-HCV	c 233	14.6	44.2	41	11	ADP75582	Adp75582 Human ADA
c 161	15	45.5	15	12	ADI87519	Adi87519 Anti-HCV	c 234	14.4	43.6	17	8	ACD56838	Accl56838 HCV DNazzy
c 162	15	45.5	15	12	ADP87835	Adp87835 TEX on mi	c 235	14.4	43.6	17	8	ACD65840	Accl65840 HCV minus
c 163	15	45.5	15	12	ADP87835	Adp87835 TEX on mi	c 236	14.4	43.6	17	12	ADI87278	Adi87278 HCV DNazzy
c 164	15	45.5	17	8	ACD56833	Accl56833 HCV DNazzy	c 237	14.4	43.6	17	12	ADI82788	Adi82788 HCV DNazzy
c 165	15	45.5	17	12	ADI82783	Adi82783 HCV DNazzy	c 238	14.4	43.6	18	2	AAQ52819	AAQ52819 HCV targe
c 166	15	45.5	18	6	AAAL40105	AAAL40105 Pathogeni	c 239	14.4	43.6	18	2	ABLS57845	AbL57845 Hepatitis
c 167	15	45.5	18	6	ABN80473	Abn80473 DNA-RNA h	c 240	14.4	43.6	19	10	ADFS2163	Adfs2163 Hepatitis

C 241	14.4	43.6	19	10	ADP52164	Adf52164 Hepatitis	C 314	14	42.4	26	8	ACC43166	Acc43166 Probe use
C 242	14.4	43.6	19	10	ADP52171	Adf52171 Hepatitis	C 315	14	42.4	26	9	ACF36232	ACF36232 HCV 5' IR
C 243	14.4	43.6	19	10	ADP51468	Adf51468 Hepatitis	C 316	14	42.4	26	10	ACF36229	ACF36229 HCV 5' IR
C 244	14.4	43.6	19	10	ADP51467	Adf51467 Hepatitis	C 317	14	42.4	26	10	ACF36282	ACF36282 HCV 5' IR
C 245	14.4	43.6	19	10	ADP51475	Adf51475 Hepatitis	C 318	14	42.4	26	10	ABZ76309	ABZ76309 HCV RNA 5
C 246	14.4	43.6	22	2	AAZ25789	Aaz25789 Hepatitis	C 319	14	42.4	27	2	AAQ64949	AAQ64949 Antisense
C 247	14.4	43.6	22	2	AAZ25835	Aaz25835 Upstream	C 320	14	42.4	27	2	AAQ64654	AAQ64654 Antibody
C 248	14.4	43.6	22	3	AAAG5005	AAa65005 Hepatitis	C 321	14	42.4	37	6	ACN31721	ACN31721 WNV minus
C 249	14.4	43.6	22	3	AAAG62977	AAa62977 Upstream	C 322	14	42.4	37	6	ACN19491	ACN19491 WNV Zinzy
C 250	14.4	43.6	22	3	AAAG63599	AAa63599 PCR prime	C 323	14	42.4	37	6	ACN31718	ACN31718 WNV minus
C 251	14.4	43.6	22	4	AAAS14802	AAa14802 Hepatitis	C 324	14	42.4	37	6	ACN30808	ACN30808 WNV minus
C 252	14.4	43.6	22	4	AAAS14802	AAa14802 Hepatitis	C 325	14	42.4	37	11	ADL75647	ADL75647 Human PTG
C 253	14.4	43.6	22	6	AAKS0239	AAk50239 Hepatitis	C 326	14	42.4	39	2	AAAT87242	AAAT87242 IL-4 2'NH
C 254	14.4	43.6	22	9	ABX16142	ABx16142 HCV PCR p	C 327	14	42.4	42	2	AAAV15321	AAV15321 Hepatitis
C 255	14.4	43.6	22	9	ACD26344	ACd26344 Hepatitis	C 328	14	42.4	42	2	AAAG60959	AAg60959 Hepatitis
C 256	14.4	43.6	22	10	ADE76486	AdE76486 PCR prime	C 329	14	42.4	46	6	ABA90113	ABa90113 Oestrogen
C 257	14.4	43.6	25	2	AAQ98278	AAq98278 Hepatitis	C 330	14	42.4	46	6	ABA90125	ABa90125 Oestrogen
C 258	14.4	43.6	25	4	AAAF58267	AAf58267 Hepatitis	C 331	14	42.4	46	6	ABA90115	ABa90115 Oestrogen
C 259	14.4	43.6	25	9	AAIC194261	AAi194261 Human mic	C 332	14	42.4	46	6	ABA90139	ABa90139 Oestrogen
C 260	14.4	43.6	26	3	AAAF64666	AAa64666 Human TRA	C 333	14	42.4	46	6	ABA90104	ABa90104 Oestrogen
C 261	14.4	43.6	29	3	AAAC64666	AAc64666 Human DNA	C 334	14	42.4	46	6	ABA90137	ABa90137 Oestrogen
C 262	14.4	43.6	32	12	ADO05664	AdO05664 HCV RNA f	C 335	14	42.4	46	6	ABQ87822	ABq87822 Human ESR
C 263	14.4	43.6	33	8	ABZ57541	ABz57541 5-phospha	C 336	14	42.4	46	6	ABQ87848	ABq87848 Human ESR
C 264	14.4	43.6	35	8	ACC79269	ACc79269 Hepatitis	C 337	14	42.4	46	6	ABQ87846	ABq87846 Human ESR
C 265	14.4	43.6	36	4	AAAF28373	AAf28373 Clostridi	C 338	14	42.4	46	6	ABQ87824	ABq87824 Human ESR
C 266	14.4	43.6	36	4	AAAF28377	AAf28377 Clostridi	C 339	14	42.4	46	6	ABQ87834	ABq87834 Human ESR
C 267	14.4	43.6	36	4	AAAF28374	AAf28374 Clostridi	C 340	14	42.4	46	6	ABQ87813	ABq87813 Human ESR
C 268	14.4	43.6	36	4	AAAF28378	AAf28378 Clostridi	C 341	14	42.4	46	8	ABX33870	ABx33870 Human ESR
C 269	14.4	43.6	41	3	AAAT26640	AAa26640 Human HPC	C 342	14	42.4	46	8	ABX33884	ABx33884 Human ESR
C 270	14.4	43.6	45	12	ADM88395	Adm88395 Gene expr	C 343	14	42.4	46	8	ABX33849	ABx33849 Human ESR
C 271	14.4	43.6	50	6	ABZ03830	ABz03830 Human leu	C 344	14	42.4	46	8	ABX33860	ABx33860 Human ESR
C 272	14.4	43.6	50	6	ABZ06043	ABz06043 Human leu	C 345	14	42.4	46	8	ABX33882	ABx33882 Human ESR
C 273	14.2	43.0	21	4	AAAG1579	AAa1579 PCR prime	C 346	14	42.4	46	8	ABX33858	ABx33858 Human ESR
C 274	14.2	43.0	25	8	ABX90046	ABx90046 S. aureus	C 347	14	42.4	47	3	AAAC81264	AAc81264 Human/mou
C 275	14.2	43.0	25	10	ADD25342	AdD25342 Oligonuc	C 348	14	42.4	49	12	ADP03533	ADp03533 PCR prime
C 276	14.2	43.0	30	2	AAAX30306	Aax30306 Streptoco	C 349	13.8	41.8	19	10	ADP51464	ADf51464 Hepatitis
C 277	14.2	43.0	33	6	ABAO5833	ABa05833 A thalian	C 350	13.8	41.8	19	10	ADP52160	ADf52160 Hepatitis
C 278	14.2	43.0	34	12	ADM97814	Adm97814 Glucocort	C 351	13.8	41.8	20	2	AAQ58413	AAq58413 Antisense
C 279	14.2	43.0	45	1	AAAN80951	Aan80951 Long prob	C 352	13.8	41.8	21	9	ADAI3807	ADa13807 Short int
C 280	14.2	43.0	45	2	AAQ62683	AAq62683 Enkephali	C 353	13.8	41.8	21	9	ADAI3814	ADa13814 Short int
C 281	14.2	43.0	45	2	AAQ62680	AAq62680 Enkephali	C 354	13.8	41.8	21	9	ADAI3862	ADa13862 Short int
C 282	14.2	43.0	50	3	ADCL17102	Adc17102 Human sin	C 355	13.8	41.8	21	10	ADP52838	ADf52838 Hepatitis
C 283	14	42.4	15	6	ABX017402	ABx01742 Hepatitis	C 356	13.8	41.8	21	10	ADP52831	ADf52831 Hepatitis
C 284	14	42.4	15	8	ACD65936	ACd65936 Anti-HCV	C 357	13.8	41.8	21	10	ADP52865	ADf52865 Hepatitis
C 285	14	42.4	15	8	ACD66048	ACd66048 Anti-HCV	C 358	13.8	41.8	23	2	AAQ80471	AAq80471 Subtilase
C 286	14	42.4	15	8	ACD66050	ACd66050 Anti-HCV	C 359	13.8	41.8	24	2	AAQ63500	AAq63500 NANBH pr
C 287	14	42.4	15	8	ACD66276	ACd66276 Anti-HCV	C 360	13.8	41.8	25	6	ABN10993	ABn10993 Human GDM
C 288	14	42.4	15	8	ACD66272	ACd66272 Anti-HCV	C 361	13.8	41.8	25	9	ACI07693	ACi07693 Human mic
C 289	14	42.4	15	12	ADI87535	Adi87535 Anti-HCV	C 362	13.8	41.8	25	9	ACK17452	ACK17452 Human mic
C 290	14	42.4	15	12	ADI87582	Adi87582 Anti-HCV	C 363	13.8	41.8	25	9	ACK17453	ACK17453 Human mic
C 291	14	42.4	15	12	ADI87584	Adi87584 Anti-HCV	C 364	13.8	41.8	28	6	AAZ05960	AAz05960 Corynebac
C 292	14	42.4	15	12	ADI87701	Adi87701 Anti-HCV	C 365	13.8	41.8	34	2	AAZ06813	AAz06813 Maize elo
C 293	14	42.4	15	12	ADI87705	Adi87705 Anti-HCV	C 366	13.8	41.8	36	12	ADL24398	ADL24398 Multiple
C 294	14	42.4	17	8	ACD65837	ACd65837 HCV minus	C 367	13.8	41.8	37	2	AAQ50969	AAq50969 Wild-type
C 295	14	42.4	17	8	ACD56839	ACd56839 HCV DNazy	C 368	13.8	41.8	39	12	ADP87792	ADp87792 HCV cDNA
C 296	14	42.4	17	12	ADI82789	Adi82789 HCV DNazy	C 369	13.8	41.8	40	2	AAZ08605	AAz08605 Assembly
C 297	14	42.4	17	12	ADI87275	Adi87275 HCV DNazy	C 370	13.8	41.8	40	2	AAZ01615	AAz01615 Helix-tur
C 298	14	42.4	18	12	ADP87834	ADp87834 TEX on mi	C 371	13.8	41.8	40	3	AAZ61346	AAz61346 PCR prime
C 299	14	42.4	19	10	ADP52190	ADf52190 Hepatitis	C 372	13.8	41.8	43	6	AAAL41123	AAa141123 pRL5CAT H
C 300	14	42.4	19	10	ADP51494	ADf51494 Hepatitis	C 373	13.8	41.8	45	6	ABK33723	ABk33723 S. pneumo
C 301	14	42.4	19	10	ADP51442	ADf51442 Hepatitis	C 374	13.8	41.8	45	6	ABK33722	ABk33722 S. pneumo
C 302	14	42.4	19	10	ADP51465	ADf51465 Hepatitis	C 375	13.8	41.8	50	4	AAAL29191	AAa129191 Human SNP
C 303	14	42.4	19	10	ADP52161	ADf52161 Hepatitis	C 376	13.8	41.8	50	6	ABZ03836	ABz03836 Human leu
C 304	14	42.4	19	10	ADP52138	ADf52138 Hepatitis	C 377	13.8	41.8	50	6	ABZ03337	ABz03337 Human leu
C 305	14	42.4	20	2	AAQ75230	AAq75230 Antisense	C 378	13.8	41.8	50	10	ADG33597	ADg33597 Human DNA
C 306	14	42.4	20	2	AAAT11283	AAa11283 Hepatitis	C 379	13.8	41.8	50	10	ADG33416	ADg33416 Human DNA
C 307	14	42.4	25	3	AAZ60850	AAz60850 Oligonuc	C 380	13.6	41.2	25	9	ACI64479	ACi64479 Human mic
C 308	14	42.4	25	3	AAZ60849	AAz60849 Oligonuc	C 381	13.6	41.2	31	8	ACD43736	ACd43736 Human gen
C 309	14	42.4	25	3	AAZ60851	AAz60851 Oligonuc	C 382	13.6	41.2	37	6	ACN31108	ACn31108 WNV minus
C 310	14	42.4	25	3	AAZ60848	AAz60848 Oligonuc	C 383	13.6	41.2	37	11	ADL73583	ADl73583 Human PKR
C 311	14	42.4	25	9	ACK15326	ACK15326 Human mic	C 384	13.6	41.2	38	4	ABK05924	ABk05924 Human NOG
C 312	14	42.4	25	9	ACK09419	ACK09419 Human mic	C 385	13.6	41.2	38	4	ABK08585	ABk08585 Human CD2
C 313	14	42.4	26	8	ACC48584	Acc48584 Hepatitis	C 386	13.6	41.2	41	6	ABZ50544	ABz50544 Human car

387	13.6	41.2	41	6	ABZ45285	Human car	Abz45285	Human car	13	39.4	15	3	AAZ63689	Substrate
388	13.6	41.2	47	3	Aaz68762	Human map	Aaz68762	Human map	13	39.4	15	3	AAZ61839	HCV 5', no
389	13.6	41.2	48	3	Aax36361	Primer fo	Aax36361	Primer fo	13	39.4	15	3	AAZ62394	Substrate
390	13.6	41.2	48	6	ABZ65550	Human TIE	ABZ65550	Human TIE	13	39.4	15	3	AAX61837	HCV 5', no
391	13.6	41.2	50	4	Aah89609	Human gly	Aah89609	Human gly	13	39.4	15	6	ABX01782	Hepatitis
392	13.6	41.2	50	6	ABZ03706	Human leu	ABZ03706	Human leu	13	39.4	15	6	ABX03379	Hepatitis
393	13.6	41.2	50	6	ADD41458	Synthetic	ADD41458	Synthetic	13	39.4	15	6	ABX03368	Hepatitis
394	13.4	40.6	15	6	ABX01775	Hepatitis	ABX01775	Hepatitis	13	39.4	15	6	ABX00225	Hepatitis
395	13.4	40.6	15	8	ACD66255	Anti-HCV	ACD66255	Anti-HCV	13	39.4	17	8	ABX00223	Hepatitis
396	13.4	40.6	15	12	AD187684	Anti-HCV	AD187684	Anti-HCV	13	39.4	17	8	ACD65843	HCV minus
397	13.4	40.6	15	12	ADP87836	TEX on mi	ADP87836	TEX on mi	13	39.4	17	8	ACD5836	HCV minus
398	13.4	40.6	18	12	ADP87780	Hepatitis	ADP87780	Hepatitis	13	39.4	17	12	AD187274	HCV DNaz
399	13.4	40.6	19	10	ADF51479	Hepatitis	ADF51479	Hepatitis	13	39.4	17	12	AD187281	HCV DNaz
400	13.4	40.6	19	10	ADF52175	Hepatitis	ADF52175	Hepatitis	13	39.4	18	3	AAV28797	HCV isola
401	13.4	40.6	23	12	ADP82853	Probe use	ADP82853	Probe use	13	39.4	18	3	AAV28797	HCV isola
402	13.4	40.6	25	9	ACK00350	Human mic	ACK00350	Human mic	13	39.4	18	3	AAA29449	Hepatitis
403	13.4	40.6	25	9	ACI29544	Human mic	ACI29544	Human mic	13	39.4	19	10	ADP51474	Hepatitis
404	13.4	40.6	25	9	ACI99891	Human mic	ACI99891	Human mic	13	39.4	19	10	ADP52170	Hepatitis
405	13.4	40.6	26	8	ACD17036	Sample pr	ACD17036	Sample pr	13	39.4	19	10	ADF51482	Hepatitis
406	13.4	40.6	27	2	AAX58190	Primer fo	Aax58190	Primer fo	13	39.4	20	2	ADF52178	Hepatitis
407	13.4	40.6	30	8	ACC42739	Geldanam	ACC42739	Geldanam	13	39.4	21	12	ADP03553	RT-PCR pr
408	13.4	40.6	30	10	AD61815	Streptomy	AD61815	Streptomy	13	39.4	24	3	AAA90945	Mutagenic
409	13.4	40.6	33	3	AAX38686	DNA encod	Aax38686	DNA encod	13	39.4	24	6	AD22588	PCR prime
410	13.4	40.6	33	10	ADK71260	Drug-tole	ADK71260	Drug-tole	13	39.4	24	10	AD66184	PCR prime
411	13.4	40.6	38	2	AAV31367	Trichoder	Aav31367	Trichoder	13	39.4	24	12	ADJ51126	Human CDN
412	13.4	40.6	39	3	AAQ95766	Hepatitis	Aaq95766	Hepatitis	13	39.4	25	3	AAA52569	Oligonucl
413	13.4	40.6	40	2	AAQ88332	Maize alp	Aaq88332	Maize alp	13	39.4	25	6	ABN10996	Human GDM
414	13.4	40.6	40	3	AAQ69959	TGF-beta-	Aaq69959	TGF-beta-	13	39.4	25	6	ABN10994	Human GDM
415	13.4	40.6	46	12	ADU94558	Oligonucl	ADU94558	Oligonucl	13	39.4	25	6	ABN10992	Human GDM
416	13.4	40.6	47	3	AAZ67556	Human map	Aaz67556	Human map	13	39.4	25	6	ABN10991	Human GDM
417	13.4	40.6	48	2	AAZ00287	HEV speci	Aaz00287	HEV speci	13	39.4	25	6	ABN10995	Human GDM
418	13.4	40.6	50	4	AAL34419	Human SNP	Aal34419	Human SNP	13	39.4	25	6	ABN10994	Human GDM
419	13.4	40.6	50	4	AAL34397	Human SNP	Aal34397	Human SNP	13	39.4	25	6	ABN10990	Human GDM
420	13.2	40.0	20	3	AAQ59882	Oligonucl	Aaq59882	Oligonucl	13	39.4	25	6	ABN10990	Human GDM
421	13.2	40.0	24	2	AAV65882	Stacker o	Aav65882	Stacker o	13	39.4	25	9	ACI89303	Human mic
422	13.2	40.0	24	9	ADAG6093	DNAP-rela	Ada66093	DNAP-rela	13	39.4	25	9	ACK07452	Human mic
423	13.2	40.0	25	9	ACI31794	Human mic	ACI31794	Human mic	13	39.4	25	9	ACI88877	Human mic
424	13.2	40.0	25	9	ACI68851	Human mic	ACI68851	Human mic	13	39.4	25	9	ACI57751	Human mic
425	13.2	40.0	25	9	ACK04538	Human mic	ACK04538	Human mic	13	39.4	26	2	AAQ51830	Human mic
426	13.2	40.0	25	9	ACI95287	Human mic	ACI95287	Human mic	13	39.4	26	2	ABQ570880	Hepatitis
427	13.2	40.0	25	9	ACI69798	Human mic	ACI69798	Human mic	13	39.4	29	6	ABQ70880	Hepatitis
428	13.2	40.0	25	9	ACI78988	Human mic	ACI78988	Human mic	13	39.4	30	12	ADG18952	Hepatitis
429	13.2	40.0	26	8	ABZ66308	Human gen	Abz66308	Human gen	13	39.4	30	12	ADG18954	Hepatitis
430	13.2	40.0	29	8	ABZ81899	Primer AA	Abz81899	Primer AA	13	39.4	31	2	AAQ78581	Vector am
431	13.2	40.0	31	11	ADM55506	DNazyme t	Adm55506	DNazyme t	13	39.4	31	2	AAQ78587	Vector am
432	13.2	40.0	32	5	AAC86131	Llewellyn	Aac86131	Llewellyn	13	39.4	31	2	AAT80876	Vector am
433	13.2	40.0	33	5	AAC86145	Forward p	Aac86145	Forward p	13	39.4	32	2	AAQ37755	VMM-Ndel
434	13.2	40.0	33	6	ABL61584	Human glu	AbL61584	Human glu	13	39.4	32	2	AAQ37755	VMM-Ndel
435	13.2	40.0	36	3	AAZ88354	Bispecifi	Aaz88354	Bispecifi	13	39.4	32	3	AAZ55592	Canine IL
436	13.2	40.0	40	9	ACD27914	E'/bacter	ACd27914	E'/bacter	13	39.4	32	3	AAZ55592	Canine IL
437	13.2	40.0	41	6	ABL96052	Brassica	AbL96052	Brassica	13	39.4	35	8	AC45333	Escherich
438	13.2	40.0	41	10	ABQ83785	Human mul	Abq83785	Human mul	13	39.4	35	8	AC45333	Escherich
439	13.2	40.0	42	2	AAX83839	Antibody	Aax83839	Antibody	13	39.4	37	6	ACN30889	WNV minus
440	13.2	40.0	45	2	AAV49402	Primer AB	Aav49402	Primer AB	13	39.4	37	6	ACN31892	WNV minus
441	13.2	40.0	50	6	ABZ07910	Human leu	Abz07910	Human leu	13	39.4	37	6	ACN31892	WNV minus
442	13.2	40.0	13	8	ACD65935	Anti-HCV	ACd65935	Anti-HCV	13	39.4	37	6	ACN31159	WNV minus
443	13.2	40.0	13	8	ACD66045	Anti-HCV	ACd66045	Anti-HCV	13	39.4	37	6	ACN31159	WNV minus
444	13.2	40.0	13	8	ACD66265	Anti-HCV	ACd66265	Anti-HCV	13	39.4	37	6	ACN19553	WNV minus
445	13.2	40.0	13	8	ACD66183	Anti-HCV	ACd66183	Anti-HCV	13	39.4	37	6	ACN19553	WNV minus
446	13.2	40.0	13	8	ACD66259	Anti-HCV	ACd66259	Anti-HCV	13	39.4	37	6	ACN19553	WNV minus
447	13.2	40.0	13	8	ACD66043	Anti-HCV	ACd66043	Anti-HCV	13	39.4	37	6	ACN19553	WNV minus
448	13.2	40.0	13	8	ACD65992	Anti-HCV	ACd65992	Anti-HCV	13	39.4	37	6	ACN19553	WNV minus
449	13.2	40.0	13	8	ACD66264	Anti-HCV	ACd66264	Anti-HCV	13	39.4	37	6	ACN19092	WNV minus
450	13.2	40.0	13	12	AD187577	Anti-HCV	Adi87577	Anti-HCV	13	39.4	37	6	ACN19741	WNV minus
451	13.2	40.0	13	12	AD187561	Anti-HCV	Adi87561	Anti-HCV	13	39.4	37	6	ACN19741	WNV minus
452	13.2	40.0	13	12	AD187688	Anti-HCV	Adi87688	Anti-HCV	13	39.4	37	6	ACN31688	WNV minus
453	13.2	40.0	13	12	AD187647	Anti-HCV	Adi87647	Anti-HCV	13	39.4	37	11	ADL52661	Human NOG
454	13.2	40.0	13	12	AD187534	Anti-HCV	Adi87534	Anti-HCV	13	39.4	37	11	ADL52661	Human NOG
455	13.2	40.0	13	12	AD187579	Anti-HCV	Adi87579	Anti-HCV	13	39.4	37	11	ADL52653	Human NOG
456	13.2	40.0	13	12	AD187579	Anti-HCV	Adi87579	Anti-HCV	13	39.4	38	4	ADL54440	Human IKK
457	13.2	40.0	13	12	AD187694	Anti-HCV	Adi87694	Anti-HCV	13	39.4	38	4	ABK05711	Human NOG
458	13.2	40.0	13	12	AD187693	Anti-HCV	Adi87693	Anti-HCV	13	39.4	38	4	ABK08618	Human CD2
459	13.2	40.0	15	2	AAQ99414	Hepatitis	Aaq99414	Hepatitis	13	39.4	38	4	ABK08618	Human CD2

C 533	13	39.4	41	6	ABS60501	AbS60501 Human DNA	C 606	12.8	38.8	40	12	ADG93426	Adg93426 Human PDG
C 534	13	39.4	41	6	ABZ43742	AbZ43742 Human alc	C 607	12.8	38.8	41	6	ABA05341	AbA05341 Human cel
C 535	13	39.4	41	6	ABZ49296	AbZ49296 Human alc	C 608	12.8	38.8	41	6	ABA05340	AbA05340 Human cel
C 536	13	39.4	41	10	ADC46973	AdC46973 Synthesis	C 609	12.8	38.8	41	6	ABZ47336	AbZ47336 Human ATP
C 537	13	39.4	42	4	AAH22223	AaH22223 Anti-A33	C 610	12.8	38.8	45	2	AAQ41071	AaQ41071 OmpA sign
C 538	13	39.4	42	5	AAH20088	AaH20088 Chimeric	C 611	12.8	38.8	45	2	AAQ44041	AaQ44041 OmpA sign
C 539	13	39.4	43	12	ADP96878	AdP96878 C. albica	C 612	12.8	38.8	45	6	AAZ66583	AaZ66583 Human map
C 540	13	39.4	45	4	AAH46022	AaH46022 BCG deriv	C 613	12.8	38.8	47	3	AAZ66583	AaZ66583 Human map
C 541	13	39.4	47	6	ABN85153	AbN85153 HIV-1 PR-	C 614	12.8	38.8	47	3	AAZ68063	AaZ68063 Human map
C 542	13	39.4	50	3	AAZ52573	AaZ52573 HCV RNA p	C 615	12.8	38.8	48	2	AAZ34964	AaZ34964 Single st
C 543	13	39.4	50	3	AAH89757	AaH89757 HCV RNA p	C 616	12.8	38.8	48	2	AAZ34964	AaZ34964 Single st
C 544	13	39.4	50	4	AAH78215	AaH78215 Human sil	C 617	12.8	38.8	48	2	AAV74035	AaV74035 Enzymatic
C 545	13	39.4	50	4	AAZ90039	AaZ90039 Oligonucl	C 618	12.8	38.8	48	10	ADF38652	AdF38652 Synchroni
C 546	13	39.4	50	4	AAH23274	AaH23274 Oligonucl	C 619	12.8	38.8	50	6	ABZ07873	AbZ07873 Human leu
C 547	13	39.4	50	5	AAH23740	AaH23740 Oligonucl	C 620	12.8	38.8	50	10	ADG33643	AdG33643 Human DNA
C 548	13	39.4	50	6	AAI68916	AaI68916 Activated	C 621	12.8	38.8	50	10	ADG33643	AdG33643 Human DNA
C 549	13	39.4	50	6	ABZ00962	AbZ00962 Human leu	C 622	12.8	38.8	50	10	ADP10237	AdP10237 50-mer ol
C 550	13	39.4	50	6	ABZ00962	AbZ00962 Human leu	C 623	12.6	38.2	15	6	ABK81574	AbK81574 Human HRH
C 551	12.8	38.8	16	1	AAZ50508	AaZ50508 Sequence	C 624	12.6	38.2	20	4	AAH26150	AaH26150 PCR prime
C 552	12.8	38.8	16	2	AAQ27082	AaQ27082 Oligonucl	C 625	12.6	38.2	20	6	ABQ62408	AbQ62408 Human syn
C 553	12.8	38.8	17	8	ACD65838	AcD65838 HCV minus	C 626	12.6	38.2	20	8	ACC86816	AcC86816 Mouse VEG
C 554	12.8	38.8	17	12	ADI87276	AdI87276 HCV DNAY	C 627	12.6	38.2	20	12	ADG27919	AdG27919 Rice vari
C 555	12.8	38.8	19	10	ADF51466	AdF51466 Hepatitis	C 628	12.6	38.2	20	12	ADJ19244	AdJ19244 Antisense
C 556	12.8	38.8	19	10	ADF52162	AdF52162 Hepatitis	C 629	12.6	38.2	21	12	ADH56171	AdH56171 Human ELO
C 557	12.8	38.8	20	2	ABT80293	AbT80293 Oligo HCV	C 630	12.6	38.2	22	2	AAQ34635	AaQ34635 Human bcr
C 558	12.8	38.8	20	2	AAZ38347	AaZ38347 E. coli K	C 631	12.6	38.2	22	12	ADU93348	AdU93348 PST 1A pr
C 559	12.8	38.8	20	6	ABS65877	AbS65877 Inhibitor	C 632	12.6	38.2	23	4	AAH91406	AaH91406 Human inf
C 560	12.8	38.8	21	2	AAZ37636	AaZ37636 HCV detec	C 633	12.6	38.2	23	4	AAH91406	AaH91406 Human inf
C 561	12.8	38.8	21	6	ABK91422	AbK91422 Hepatitis	C 634	12.6	38.2	24	3	ABZ87377	AbZ87377 Human thr
C 562	12.8	38.8	21	10	ADD67944	AdD67944 Hepatitis	C 635	12.6	38.2	24	3	ABK49331	AbK49331 Nuclear p
C 563	12.8	38.8	21	10	ABX0616	AbX0616 TagMan pr	C 636	12.6	38.2	25	6	ABN10988	AbN10988 Human GDM
C 564	12.8	38.8	23	10	ADF52812	AdF52812 Hepatitis	C 637	12.6	38.2	25	6	ABN10987	AbN10987 Human GDM
C 565	12.8	38.8	24	2	AAZ98072	AaZ98072 Erwinia c	C 638	12.6	38.2	25	9	ACK09013	AcK09013 Human mic
C 566	12.8	38.8	25	9	ACI11495	AcI11495 Human mic	C 639	12.6	38.2	25	9	ACK117405	AcK117405 Human mic
C 567	12.8	38.8	25	9	ACI94260	AcI94260 Human mic	C 640	12.6	38.2	25	9	ACK17959	AcK17959 Human mic
C 568	12.8	38.8	25	9	ACI08326	AcI08326 Human mic	C 641	12.6	38.2	25	9	ACK05676	AcK05676 Human mic
C 569	12.8	38.8	25	9	ACI11285	AcI11285 Human mic	C 642	12.6	38.2	25	9	ACK17959	AcK17959 Human mic
C 570	12.8	38.8	25	9	ACH61875	AcH61875 DNA targe	C 643	12.6	38.2	25	9	ACK07782	AcK07782 Human mic
C 571	12.8	38.8	25	9	ACH58326	AcH58326 DNA targe	C 644	12.6	38.2	25	9	ACH63261	AcH63261 DNA targe
C 572	12.8	38.8	25	12	ADP13714	AdP13714 Renal cel	C 645	12.6	38.2	26	2	AAV94924	AaV94924 Primer #2
C 573	12.8	38.8	26	2	AAQ47448	AaQ47448 Rat G pro	C 646	12.6	38.2	26	2	AAV18030	AaV18030 PrMADS2 s
C 574	12.8	38.8	26	2	AAQ47440	AaQ47440 Rat G pro	C 647	12.6	38.2	26	4	AAZ00913	AaZ00913 Beetle lu
C 575	12.8	38.8	26	6	ABV95576	AbV95576 Human NOV	C 648	12.6	38.2	28	6	AAZ45693	AaZ45693 Salmonell
C 576	12.8	38.8	26	10	ADG32625	AdG32625 PCR prime	C 649	12.6	38.2	28	6	ABK66330	AbK66330 Human gen
C 577	12.8	38.8	26	10	ADG32629	AdG32629 Human PCR	C 650	12.6	38.2	28	6	ABQ76184	AbQ76184 S. typhim
C 578	12.8	38.8	27	2	AAZ89482	AaZ89482 Human mat	C 651	12.6	38.2	28	6	ABQ52575	AbQ52575 PCR prime
C 579	12.8	38.8	27	4	AAH78705	AaH78705 Human pro	C 652	12.6	38.2	28	6	ABK90589	AbK90589 DNA adeni
C 580	12.8	38.8	29	2	AAZ84460	AaZ84460 Heat choc	C 653	12.6	38.2	28	6	ABQ73063	AbQ73063 Salmonell
C 581	12.8	38.8	29	10	ADC36598	AdC36598 Primer of	C 654	12.6	38.2	29	3	AAA04129	AaA04129 Polymorph
C 582	12.8	38.8	30	2	AAQ20891	AaQ20891 Immunosti	C 655	12.6	38.2	29	3	AAA04656	AaA04656 Polynucle
C 583	12.8	38.8	30	2	AAZ17904	AaZ17904 Human TPO	C 656	12.6	38.2	30	6	ACC60596	AcC60596 Polynucle
C 584	12.8	38.8	30	6	ABX72711	AbX72711 Cryptococ	C 657	12.6	38.2	31	4	AAI30328	AaI30328 Human sin
C 585	12.8	38.8	31	2	AAZ45810	AaZ45810 Glucocort	C 658	12.6	38.2	31	4	ABL60324	AbL60324 Human I k
C 586	12.8	38.8	31	10	AAZ56124	AaZ56124 EPO-FC ex	C 659	12.6	38.2	32	12	ADP83576	AdP83576 Mutagenic
C 587	12.8	38.8	32	12	ADQ10521	AdQ10521 KB signal	C 660	12.6	38.2	32	12	ADP83577	AdP83577 Mutagenic
C 588	12.8	38.8	32	4	AAZ75867	AaZ75867 PCR prime	C 661	12.6	38.2	35	2	AAQ36846	AaQ36846 3' UTR, a
C 589	12.8	38.8	33	12	ADZ89694	AdZ89694 Kanamycin	C 662	12.6	38.2	35	5	AAZ64962	AaZ64962 Human c-m
C 590	12.8	38.8	33	12	ADJ65172	AdJ65172 Kanamycin	C 663	12.6	38.2	35	5	AAZ64962	AaZ64962 Human c-m
C 591	12.8	38.8	33	12	ADJ65172	AdJ65172 Kanamycin	C 664	12.6	38.2	35	5	AAZ64962	AaZ64962 Human c-m
C 592	12.8	38.8	33	12	ADJ65882	AdJ65882 Aminophos	C 665	12.6	38.2	35	5	AAZ64962	AaZ64962 Human c-m
C 593	12.8	38.8	37	2	AAQ49021	AaQ49021 Multimeri	C 666	12.6	38.2	37	6	ABK23906	AbK23906 HBCAg-lys
C 594	12.8	38.8	37	2	AAQ81381	AaQ81381 Reverse p	C 667	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 595	12.8	38.8	37	3	AAZ49186	AaZ49186 Murine Ig	C 668	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 596	12.8	38.8	37	8	ACC49424	AcC49424 Oligonucl	C 669	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 597	12.8	38.8	37	8	ACC49428	AcC49428 5' SH-X	C 670	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 598	12.8	38.8	37	8	ACC49428	AcC49428 5' SH-X	C 671	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 599	12.8	38.8	37	12	ADN62674	AdN62674 Reporter	C 672	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 600	12.8	38.8	37	12	ADN62673	AdN62673 Reporter	C 673	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 601	12.8	38.8	38	4	AAI70158	AaI70158 Human uro	C 674	12.6	38.2	37	6	ABZ70990	AbZ70990 48s PCR p
C 602	12.8	38.8	39	2	AAQ42939	AaQ42939 3'-5' seq	C 675	12.6	38.2	37	10	ADD24271	AdD24271 Prion dis
C 603	12.8	38.8	39	2	AAV07542	AaV07542 Human tel	C 676	12.6	38.2	37	10	ADD24271	AdD24271 Prion dis
C 604	12.8	38.8	39	2	AAZ08696	AaZ08696 Human tel	C 677	12.6	38.2	37	11	ADL52617	AdL52617 Human NOG
C 605	12.8	38.8	40	2	AAV57697	AaV57697 Human PDG	C 678	12.6	38.2	37	11	ADL52617	AdL52617 Human NOG

c 679	12.6	38.2	37	11	ADL75588	Adl75588 Human PTG	752	12.4	37.6	24	8	ACC49080	Acc49080 Human NOV
c 680	12.6	38.2	38	12	ADK90710	Adk90710 Cloning c	753	12.4	37.6	25	8	ACC49077	Acc49077 Human NOV
c 681	12.6	38.2	39	6	ADG14579	Adg14579 Vector pM	c 754	12.4	37.6	24	8	ACI48008	ACI48008 Human mic
c 682	12.6	38.2	39	8	ABV93477	Abv93477 Bacillus	c 755	12.4	37.6	25	9	ACI84132	ACI84132 Human mic
c 683	12.6	38.2	39	8	ABV93808	Abv93808 Bacillus	c 756	12.4	37.6	25	9	ACI65258	ACI65258 Human mic
c 684	12.6	38.2	39	8	ABV93478	Abv93478 Bacillus	c 757	12.4	37.6	25	9	ACI88892	ACI88892 Human mic
c 685	12.6	38.2	39	8	ABV93807	Abv93807 Bacillus	c 758	12.4	37.6	25	9	ACI22381	ACI22381 Human mic
c 686	12.6	38.2	39	10	ADH08356	Adh08356 K. lactis	c 759	12.4	37.6	25	9	ACI50347	ACI50347 Human mic
c 687	12.6	38.2	40	3	AAZ95772	Aaz95772 Polynucle	c 760	12.4	37.6	25	9	ACI52455	ACI52455 Human mic
c 688	12.6	38.2	41	6	ABV74462	Abv74462 Human pro	c 761	12.4	37.6	25	9	ACK09418	ACK09418 Human mic
c 689	12.6	38.2	41	6	ABV74461	Abv74461 Human pro	c 762	12.4	37.6	25	9	ACI20234	ACI20234 Human mic
c 690	12.6	38.2	41	12	ADK17862	Adk17862 Cytochrom	c 763	12.4	37.6	25	9	ACI18893	ACI18893 Human mic
c 691	12.6	38.2	42	2	AAQ49175	Aaq49175 IGF-I gen	c 764	12.4	37.6	25	9	ACK15327	ACK15327 Human mic
c 692	12.6	38.2	42	3	AAZ51540	Aaz51540 PCR prime	c 765	12.4	37.6	25	9	ACI43285	ACI43285 Human mic
c 693	12.6	38.2	42	12	ADQ76051	Adq76051 TBEI in r	c 766	12.4	37.6	25	9	ACK26806	ACK26806 Human mic
c 694	12.6	38.2	45	6	ABK67757	Abk67757 Human tra	c 767	12.4	37.6	25	9	ACI65259	ACI65259 Human mic
c 695	12.6	38.2	46	6	ABA90172	Aba90172 Oestrogen	c 768	12.4	37.6	25	9	ACI36925	ACI36925 Human mic
c 696	12.6	38.2	46	6	ABA90093	Aba90093 Oestrogen	c 769	12.4	37.6	25	9	ACI03133	ACI03133 Human mic
c 697	12.6	38.2	46	6	ABA90133	Aba90133 Oestrogen	c 770	12.4	37.6	25	9	ACI60649	ACI60649 Human mic
c 698	12.6	38.2	46	6	ABA90169	Aba90169 Oestrogen	c 771	12.4	37.6	25	9	ACH58833	ACH58833 DNA targe
c 699	12.6	38.2	46	6	ABA90092	Aba90092 Oestrogen	c 772	12.4	37.6	25	9	ACH62910	ACH62910 DNA targe
c 700	12.6	38.2	46	6	ABA90110	Aba90110 Oestrogen	c 773	12.4	37.6	25	9	ACH62625	ACH62625 DNA targe
c 701	12.6	38.2	46	6	ABA90094	Aba90094 Oestrogen	c 774	12.4	37.6	26	2	AAE66491	AAE66491 RhamIso i
c 702	12.6	38.2	46	6	ABA90106	Aba90106 Oestrogen	c 775	12.4	37.6	26	2	AAE56046	AAE56046 HIV-1 Gro
c 703	12.6	38.2	46	6	ABA90170	Aba90170 Oestrogen	c 776	12.4	37.6	26	2	AAE37161	AAE37161 PCR prime
c 704	12.6	38.2	46	6	ABA90171	Aba90171 Oestrogen	c 777	12.4	37.6	26	8	ACD17029	ACD17029 Sample pr
c 705	12.6	38.2	46	6	ABA90136	Aba90136 Oestrogen	c 778	12.4	37.6	27	2	AAV47664	AAV47664 Alpha-fet
c 706	12.6	38.2	46	6	ABQ87878	Abq87878 Human ESR	c 779	12.4	37.6	27	2	AAV53646	AAV53646 Human alp
c 707	12.6	38.2	46	6	ABQ87880	Abq87880 Human ESR	c 780	12.4	37.6	27	2	AAE04761	AAE04761 Sense PCR
c 708	12.6	38.2	46	6	ABQ87881	Abq87881 Human ESR	c 781	12.4	37.6	27	3	AAA46835	AAA46835 PCR prime
c 709	12.6	38.2	46	6	ABQ87879	Abq87879 Human ESR	c 782	12.4	37.6	27	6	ABK99623	ABK99623 Adenoviru
c 710	12.6	38.2	46	6	ABQ87802	Abq87802 Human ESR	c 783	12.4	37.6	27	8	ACD07348	ACD07348 Host cell
c 711	12.6	38.2	46	6	ABQ87819	Abq87819 Human ESR	c 784	12.4	37.6	27	12	ADI36385	ADI36385 PCR prime
c 712	12.6	38.2	46	6	ABQ87842	Abq87842 Human ESR	c 785	12.4	37.6	28	6	ABK66996	ABK66996 Human gen
c 713	12.6	38.2	46	6	ABQ87801	Abq87801 Human ESR	c 786	12.4	37.6	30	2	AAE42489	AAE42489 Primer fo
c 714	12.6	38.2	46	6	ABQ87815	Abq87815 Human ESR	c 787	12.4	37.6	30	12	ADF66097	ADF66097 Mutagenic
c 715	12.6	38.2	46	6	ABQ87803	Abq87803 Human ESR	c 788	12.4	37.6	31	8	ACD65881	ACD65881 HCV DNazy
c 716	12.6	38.2	46	8	ABQ87845	Abq87845 Human ESR	c 789	12.4	37.6	31	12	ADI92043	ADI92043 HCV DNazy
c 717	12.6	38.2	46	8	ABX33914	Abx33914 Human ESR	c 790	12.4	37.6	32	4	AAF81452	AAF81452 PCR prime
c 718	12.6	38.2	46	8	ABX33855	Abx33855 Human ESR	c 791	12.4	37.6	32	6	AAD29238	AAD29238 Soybean f
c 719	12.6	38.2	46	8	ABX33915	Abx33915 Human ESR	c 792	12.4	37.6	32	10	ADC78769	ADC78769 Mouse BOR
c 720	12.6	38.2	46	8	ABX33837	Abx33837 Human ESR	c 793	12.4	37.6	33	6	ABL55300	ABL55300 Human mit
c 721	12.6	38.2	46	8	ABX33916	Abx33916 Human ESR	c 794	12.4	37.6	34	3	AAE63082	AAE63082 Cre recog
c 722	12.6	38.2	46	8	ABX33851	Abx33851 Human ESR	c 795	12.4	37.6	34	6	ABK59282	ABK59282 Human ClC
c 723	12.6	38.2	46	8	ABX33878	Abx33878 Human ESR	c 796	12.4	37.6	37	6	ABK59530	ABK59530 Human ClC
c 724	12.6	38.2	46	8	ABX33881	Abx33881 Human ESR	c 797	12.4	37.6	37	6	ABK59502	ABK59502 Human ClC
c 725	12.6	38.2	46	8	ABX33839	Abx33839 Human ESR	c 798	12.4	37.6	37	6	ACN30657	ACN30657 WNV minus
c 726	12.6	38.2	46	8	ABX33917	Abx33917 Human ESR	c 799	12.4	37.6	37	6	ACN31288	ACN31288 WNV minus
c 727	12.6	38.2	46	8	ABX33838	Abx33838 Human ESR	c 800	12.4	37.6	37	6	ACN18896	ACN18896 WNV Zinzy
c 728	12.6	38.2	47	3	AAZ69202	Aaz69202 Human map	c 801	12.4	37.6	37	6	ACN18941	ACN18941 WNV Zinzy
c 729	12.6	38.2	47	6	ABN71692	Abn71692 Streptoco	c 802	12.4	37.6	37	6	ACN31031	ACN31031 WNV minus
c 730	12.6	38.2	47	6	ABK23908	Abk23908 HBcAg-lys	c 803	12.4	37.6	37	6	ACN18922	ACN18922 WNV Zinzy
c 731	12.6	38.2	47	6	ABK70992	Abk70992 Molecular	c 804	12.4	37.6	37	6	ACN31185	ACN31185 WNV minus
c 732	12.6	38.2	47	6	ABK66418	Abk66418 Hepatitis	c 805	12.4	37.6	37	6	ACN31213	ACN31213 WNV minus
c 733	12.6	38.2	47	10	ADD24273	Add24273 Prion dis	c 806	12.4	37.6	37	6	ACN18880	ACN18880 WNV Zinzy
c 734	12.6	38.2	47	10	ADD15895	Add15895 K-ras tar	c 807	12.4	37.6	37	6	ACN19625	ACN19625 WNV Zinzy
c 735	12.6	38.2	47	10	ADK17284	Adk17284 Primer HB	c 808	12.4	37.6	37	6	ACN31121	ACN31121 WNV minus
c 736	12.6	38.2	47	12	ADJ67235	Adj67235 HBV core	c 809	12.4	37.6	37	6	ACN30839	ACN30839 WNV minus
c 737	12.6	38.2	47	12	ADK52241	Adk52241 Modified	c 810	12.4	37.6	37	6	ACN31156	ACN31156 WNV minus
c 738	12.6	38.2	49	3	ACN97615	Acn97615 DNA inser	c 811	12.4	37.6	37	6	ACN30765	ACN30765 WNV minus
c 739	12.6	38.2	50	4	AAI75693	Aai75693 Human sil	c 812	12.4	37.6	37	6	ACN30778	ACN30778 WNV minus
c 740	12.6	38.2	50	6	ABZ001272	Abz001272 Human sil	c 813	12.4	37.6	37	6	ACN31783	ACN31783 WNV minus
c 741	12.6	38.2	50	6	ABZ00714	Abz00714 Human leu	c 814	12.4	37.6	37	6	ACN31005	ACN31005 WNV minus
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c 745	12.4	37.6	19	10	ADF52172	Adf52172 Hepatitis	c 818	12.4	37.6	37	8	ACA08105	ACA08105 Necrosis
c 746	12.4	37.6	24	6	ABQ03333	Abq03333 Oligonuc	c 819	12.4	37.6	37	8	ACA08185	ACA08185 Necrosis
c 747	12.4	37.6	24	6	ABI83307	Abi83307 Capture o	c 820	12.4	37.6	37	11	ADL54301	ADL54301 Human IKK
c 748	12.4	37.6	24	6	AB192573	Abi92573 Capture o	c 821	12.4	37.6	37	11	ADL75755	ADL75755 Human PTG
c 749	12.4	37.6	24	6	AB192572	Abi92572 Capture o	c 822	12.4	37.6	37	11	ADL52713	ADL52713 Human NOG
c 750	12.4	37.6	24	6	AB183306	Abi83306 Capture o	c 823	12.4	37.6	37	11	ADL75738	ADL75738 Human PTG
c 751	12.4	37.6	24	8	ABX13752	Abx13752 A. oryzae	c 824	12.4	37.6	37	11	ADL54441	ADL54441 Human IKK

C 825	12.4	37.6	37	11	ADL73586	Adl73586 Human PKR	898	12.4	37.6	50	6	ABZ04640	Human leu
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C 827	12.4	37.6	37	11	ADL75649	Adl75649 Human PTG	C 900	12.4	37.6	50	8	ABZ74886	Human acy
C 828	12.4	37.6	38	4	AAH96935	Aah96935 Human Chk	C 901	12.4	37.6	50	10	ADG33537	Human DNA
C 829	12.4	37.6	38	4	AAH96859	Aah96859 Human Chk	C 902	12.4	37.6	50	10	ACD91957	Human col
C 830	12.4	37.6	38	4	ABK08506	Abk08506 Human CD2	C 903	12.2	37.0	17	6	ABN06097	Human GDM
C 831	12.4	37.6	38	6	ABK20940	Abk20940 Human ERG	C 904	12.2	37.0	17	6	ABQ99733	Murine Ik
C 832	12.4	37.6	38	6	ABK21080	Abk21080 Human ERG	C 905	12.2	37.0	17	11	ADL50926	Human PTG
C 833	12.4	37.6	38	6	ABK21068	Abk21068 Human ERG	C 906	12.2	37.0	18	6	ABQ87902	Enteroheae
C 834	12.4	37.6	38	8	ACD53964	AcD53964 HBV zinzy	C 907	12.2	37.0	19	2	AAT40675	Corynebac
C 835	12.4	37.6	38	8	ACD53785	AcD53785 HBV zinzy	C 908	12.2	37.0	19	2	AAT40680	Corynebac
C 836	12.4	37.6	38	8	ACD53696	AcD53696 HBV zinzy	C 909	12.2	37.0	19	6	ABK51745	Oligonucl
C 837	12.4	37.6	38	8	ADA43202	Ada43202 Human ant	C 910	12.2	37.0	20	2	AAV60762	HIV-1 str
C 838	12.4	37.6	38	10	ADC64138	Adc64138 Polyhydro	C 911	12.2	37.0	20	3	AAZ91685	PCR prime
C 839	12.4	37.6	38	12	ADG01903	Adg01903 Carbon bl	C 912	12.2	37.0	20	6	ABZ21433	Corynebac
C 840	12.4	37.6	38	12	ADJ54084	Adj54084 NA05 comb	C 913	12.2	37.0	20	9	ADB68429	PCR prime
C 841	12.4	37.6	38	12	ADJ54036	Adj54036 Combinato	C 914	12.2	37.0	20	10	ADD06158	Bcr-abl f
C 842	12.4	37.6	38	12	ADM62147	Adm62147 Hepatitis	C 915	12.2	37.0	20	10	ADD56725	Human gen
C 843	12.4	37.6	38	12	ADM62284	Adm62284 Hepatitis	C 916	12.2	37.0	20	11	ADL25569	Shiga tox
C 844	12.4	37.6	38	12	ADM62207	Adm62207 Hepatitis	C 917	12.2	37.0	20	12	ADJ85242	Nucleic a
C 845	12.4	37.6	39	2	AAT87228	Aat87228 IL-4 2'NH	C 918	12.2	37.0	20	12	ADP47366	Intellige
C 846	12.4	37.6	39	2	AAT87229	Aat87229 IL-4 2'NH	C 919	12.2	37.0	20	12	ADP83589	Human Ciz
C 847	12.4	37.6	39	2	AAT87251	Aat87251 IL-4 2'NH	C 920	12.2	37.0	21	2	AAT40679	Corynebac
C 848	12.4	37.6	39	2	AAH91823	Aah91823 Porphorym	C 921	12.2	37.0	21	2	AAT40674	Corynebac
C 849	12.4	37.6	40	2	AQ38079	Aeq38079 Oligonucl	C 922	12.2	37.0	21	2	AAT40684	Corynebac
C 850	12.4	37.6	41	3	AAZ28988	Aaz28988 Promoter	C 923	12.2	37.0	21	2	AAT40689	Corynebac
C 851	12.4	37.6	41	3	AAH75683	Aah75683 Human thr	C 924	12.2	37.0	22	2	AAT40688	Corynebac
C 852	12.4	37.6	41	12	ADM32636	Adm32636 2'10-16	C 925	12.2	37.0	22	2	AAT40678	Corynebac
C 853	12.4	37.6	44	2	AAV74307	Aav74307 Streptomy	C 926	12.2	37.0	22	2	AAT40692	Corynebac
C 854	12.4	37.6	44	6	ADI46081	Adi46081 Single st	C 927	12.2	37.0	22	2	AAT40683	Corynebac
C 855	12.4	37.6	44	6	ADI46080	Adi46080 Single st	C 928	12.2	37.0	22	2	AAT40673	Corynebac
C 856	12.4	37.6	44	10	ABZ37321	Abz37321 URE adapt	C 929	12.2	37.0	22	6	ABK52070	Cytokine
C 857	12.4	37.6	46	2	AAV24262	Aav24262 Chimeric	C 930	12.2	37.0	22	12	ADNO2051	Escherich
C 858	12.4	37.6	46	2	AAH91870	Aah91870 Porphorym	C 931	12.2	37.0	22	12	ADNO2044	Escherich
C 859	12.4	37.6	46	2	AAZ00106	Aaz00106 Human ant	C 932	12.2	37.0	23	2	AAT40682	Corynebac
C 860	12.4	37.6	46	3	AAZ58887	Aaz58887 PCR prime	C 933	12.2	37.0	23	2	AAT40687	Corynebac
C 861	12.4	37.6	46	3	AAZ69215	Aaz69215 Human L c	C 934	12.2	37.0	23	2	AAT40677	Corynebac
C 862	12.4	37.6	46	4	AAH69103	Aah69103 Human L c	C 935	12.2	37.0	23	2	AAT40691	Corynebac
C 863	12.4	37.6	46	4	AAH75080	Aah75080 Nucleotid	C 936	12.2	37.0	23	2	AAV72571	Thyroglob
C 864	12.4	37.6	46	4	AAH76618	Aah76618 Human Ig	C 937	12.2	37.0	23	3	AAA60648	Human HNR
C 865	12.4	37.6	46	5	AAH74259	Aah74259 Nucleotid	C 938	12.2	37.0	24	2	AAT40681	Corynebac
C 866	12.4	37.6	46	5	AAH69159	Aah69159 Human L c	C 939	12.2	37.0	24	2	AAT40686	Corynebac
C 867	12.4	37.6	46	6	ABL94795	Abi94795 Joint dis	C 940	12.2	37.0	24	2	AAT40676	Corynebac
C 868	12.4	37.6	46	6	ABA90126	Abag90126 Oestrogen	C 941	12.2	37.0	24	2	AAT40690	Corynebac
C 869	12.4	37.6	46	6	ABA90159	Abag90159 Oestrogen	C 942	12.2	37.0	24	2	AAT98070	Corynebac
C 870	12.4	37.6	46	6	ABA90145	Abag90145 Oestrogen	C 943	12.2	37.0	24	2	AAT98061	Erwinia c
C 871	12.4	37.6	46	6	ABA90127	Abag90127 Oestrogen	C 944	12.2	37.0	24	6	ABQ09354	Oligonucl
C 872	12.4	37.6	46	6	ABA90132	Abag90132 Oestrogen	C 945	12.2	37.0	24	6	ABQ02739	Oligonucl
C 873	12.4	37.6	46	6	ABQ87854	Abq87854 Human ESR	C 946	12.2	37.0	24	6	ABQ09395	Oligonucl
C 874	12.4	37.6	46	6	ABQ87836	Abq87836 Human ESR	C 947	12.2	37.0	25	3	AAV19420	Oligonucl
C 875	12.4	37.6	46	6	ABQ87841	Abq87841 Human ESR	C 948	12.2	37.0	25	3	AAC63528	PCR prime
C 876	12.4	37.6	46	6	ABQ87835	Abq87835 Human ESR	C 949	12.2	37.0	25	4	AAV57395	Human VEG
C 877	12.4	37.6	46	6	ABQ87868	Abq87868 Human ESR	C 950	12.2	37.0	25	6	ABN14610	Human GDM
C 878	12.4	37.6	46	8	ABX33872	Abx33872 Human ESR	C 951	12.2	37.0	25	6	ABN14609	Human GDM
C 879	12.4	37.6	46	8	ABX33904	Abx33904 Human ESR	C 952	12.2	37.0	25	9	ACI645092	Human VEG
C 880	12.4	37.6	46	8	ABX33890	Abx33890 Human ESR	C 953	12.2	37.0	25	9	ACI64624	Human mic
C 881	12.4	37.6	46	8	ABX33877	Abx33877 Human ESR	C 954	12.2	37.0	25	9	ACI67347	Human mic
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C 883	12.4	37.6	46	10	ADC64137	Adc64137 Polyhydro	C 956	12.2	37.0	25	9	ACK30659	Human mic
C 884	12.4	37.6	46	10	ABT31647	Abt31647 Angiogene	C 957	12.2	37.0	25	9	ACK35822	Human mic
C 885	12.4	37.6	46	12	ADG01902	Adg01902 Carbon bl	C 958	12.2	37.0	25	9	ACI78916	Human mic
C 886	12.4	37.6	46	12	ADO33816	Ado33816 Parathyro	C 959	12.2	37.0	25	9	ACI66603	Human mic
C 887	12.4	37.6	47	8	ADC28216	Adc28216 Spirochet	C 960	12.2	37.0	25	9	ACI05778	Human mic
C 888	12.4	37.6	48	2	AAT37509	Aat37509 ECGF olig	C 961	12.2	37.0	25	9	ACI67035	Human mic
C 889	12.4	37.6	48	2	AAV34353	Aav34353 Probe III	C 962	12.2	37.0	25	9	ACK23203	Human mic
C 890	12.4	37.6	48	2	AAH03358	Aah03358 Human ECG	C 963	12.2	37.0	25	9	ACK23203	Human mic
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C 894	12.4	37.6	50	4	AAH33850	Aah33850 Human SNP	C 967	12.2	37.0	25	9	ACH64770	DNA target
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C 896	12.4	37.6	50	4	AAH89659	Aah89659 Human onc	C 969	12.2	37.0	25	10	ADF63219	Human PCC
C 897	12.4	37.6	50	6	ABT12663	Abt12663 Orestes s	C 970	12.2	37.0	26	2	AAV55865	Plasmid v

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c 975	12.2	37.0	26	2	AAT86059	Aat86059	Primer p1
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c 977	12.2	37.0	27	2	AAK26925	Aax26925	Antisense
c 978	12.2	37.0	27	2	AAK19675	Aax19675	Cytomegal
c 979	12.2	37.0	27	3	AAZ35476	Aaz35476	Cytomegal
c 980	12.2	37.0	27	3	AAAS4367	Aaa54367	Primer fo
c 981	12.2	37.0	27	3	AAZ35457	Aaz35457	Cytomegal
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c 983	12.2	37.0	27	3	AAAG4984	Aaa64984	Cytomegal
c 984	12.2	37.0	27	3	AAAG4422	Aaa94422	Cytomegal
c 985	12.2	37.0	27	3	AAAG9804	Aaa99804	SEAP expr
c 986	12.2	37.0	27	3	AZ60497	Aaz60497	Antisense
c 987	12.2	37.0	27	3	AAZ58852	Aaz58852	CMV intro
c 988	12.2	37.0	27	3	AAAG9548	Aaa99548	SEAP expr
c 989	12.2	37.0	27	3	AAAG3340	Aaa63340	Cytomegal
c 990	12.2	37.0	27	3	AAAL3779	Aaa13779	Human SEA
c 991	12.2	37.0	27	3	AAAL3698	Aaa13698	Human SEA
c 992	12.2	37.0	27	3	AAAZ28746	Aaa28746	Mutagenic
c 993	12.2	37.0	27	3	AAAG9567	Aaa99567	SEAP expr
c 994	12.2	37.0	27	3	AAAG9586	Aaa99586	SEAP expr
c 995	12.2	37.0	27	4	AAF82126	Aaf82126	Cytomegal
c 996	12.2	37.0	27	4	AAD13513	Aad13513	Cytomegal
c 997	12.2	37.0	27	4	AH47344	Aah47344	CMV mutat
c 998	12.2	37.0	27	4	AAAS14706	Aaa14706	Antisense
c 999	12.2	37.0	27	4	AAF57895	Aaf57895	Mutant cy
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ALIGNMENTS

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RESULT 1
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ID AAD43285 standard; DNA; 34 BP.
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AAD43285;
XX
14-NOV-2002 (first entry)
DT
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DE ST650 HCV specific probe.
XX
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KW Amplification; target nucleic acid; probe; ss.
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OS Hepatitis C virus.
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XX
XX 04-SEP-2002.
XX
XX 27-FEB-2002; 2002EP-00004483.
XX
XX 02-MAR-2001; 2001EP-00105172.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Jaeger S;
XX
XX WPI; 2002-610695/66.
XX
XX Amplification of a target nucleic acid region using a specific control
XX sequence.
XX
XX Example 1; Fig 2; 28pp; English.
XX
XX The invention relates to a method for amplification of a target nucleic
XX acid region in a sample using a specific control sequence. The invention
XX is also directed to a method of determination of a target nucleic acid
XX using a special control nucleic acid. Nucleic acids of the invention are
XX used as a control in a reaction for amplifying target nucleic acids and
XX as a control in a hybridisation reaction for determination of target
XX nucleic acids. The present sequence is HCV (Hepatitis C virus) type 1 DNA
XX specific probe. This probe is used to illustrate the methods of the
XX invention. Note: This sequence is stated to be same as that shown as SEQ
XX ID NO:3 in sequence listing. However this sequence has additional C at
XX its 3' end
XX
XX SQ Sequence 34 BP; 6 A; 13 C; 8 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 33; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-05;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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XX QY 1 CGGTGTACTACCGTTCGGCAGACCACCTATGGC 33
XX ||||||||||||||||||||||||||||||||||
XX Db 1 CGGTGTACTACCGTTCGGCAGACCACCTATGGC 33
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XX RESULT 2
XX AAD43737
XX ID AAD43737 standard; DNA; 34 BP.
XX
XX AC AAD43737;
XX
XX AC
XX
XX 07-AUG-2003 (revised)
XX Dt 14-NOV-2002 (first entry)
XX
XX DE ST650 HCV specific probe.
XX
XX KW Amplification; target nucleic acid; control nucleic acid; probe; ss.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
XX stem_loop 1..14
XX /*tag= b
XX misc_binding 1..5
XX /*tag= c
XX /bound_moiety= "Nucleotides 14-10"
XX misc feature 1

```

```

FT misc_binding
FT /tag= g
FT /bound motif= "Nucleotides 32-30"
FT 24. :28

```



```

FT      /*tag= a
FT      /note= "Linked to Cy5 where Cy5 is Oligonucleotid-
FT      derivatisation with pentamethin-di-indocarbocyanin using
FT      alkylphosphatidyl-linker"
FT      10. .14
FT      /*tag= d
FT      /bound_moiety= "Nucleotides 5-1"
FT      14. .15
FT      /*tag= e
FT      /note= "Linked via FAMs where FAMs is Oligonucleotid-
FT      derivatisation with 6-carboxy-fluorescein using 2-(Amino-
FT      cyclohexyl-)propan-1,3-diol-linker"
FT      24. .32
FT      /*tag= f
FT      /misc_binding
FT      24. .26
FT      /*tag= g
FT      /bound_moiety= "Nucleotides 32-30"
FT      30. .32
FT      /*tag= h
FT      /bound_moiety= "Nucleotides 24-26"
FT      34
FT      /*tag= i
FT      /mod_base= OTHER
FT      /note= "Phosphorylated"
XX      EPI236804-A1.
XX      04-SEP-2002.
XX      02-MAR-2001; 2001EP-00105172.
XX      02-MAR-2001; 2001EP-00105172.
XX      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      Jaeger S;
XX      WPI; 2002-610694/66.
XX      Amplification of a target nucleic acid region using control sequences.
XX      Example 1; Fig 2; 29pp; English.
XX      The invention relates to a method for amplification of a target nucleic
XX      acid region. The method is useful for amplification of a nucleic acid
XX      molecule using control nucleic acid sequences. The control nucleic acid
XX      sequences are at least in part parallel-complementary to the sequence of
XX      the target nucleic acid. The present sequence is ST650 HCV specific
XX      probe. Note: This sequence is stated to be same as that shown as SEQ ID
XX      NO:3 in sequence listing. However this sequence has additional C at its
XX      3' end. (Updated on 07-AUG-2003 to correct OS field.)
XX      Sequence 34 BP; 6 A; 13 C; 8 G; 7 T; 0 U; 0 Other;
XX      Query Match 100.0%; Score 33; DB 6; Length 34;
XX      Best Local Similarity 100.0%; Pred. No. 5.3e-05;
XX      Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
DB      1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33

RESULT 3
ACF35782
ID      ACF35782 standard; DNA; 31 BP.
XX      ACF35782;
XX      06-NOV-2003 (first entry)
XX      Nucleotide sequence of a HCV-specific probe ST650p2.

```

```

XX      Nucleic acid purification; nucleic acid amplification; cancer;
XX      sickle cell anemia; blood screening; HCV; probe; ss.
XX      Hepatitis C virus.
XX      Key Location/Qualifiers
XX      modified_base 1 /*tag= a
XX      modified_base 14. .15 /note= "Cy5 fluorophore attached to 5' terminus"
XX      /*tag= b
XX      /note= "FAM label incorporated between these nucleotides"
XX      WO2003057910-A2.
XX      17-JUL-2003.
XX      04-JAN-2003; 2003WO-EP0000039.
XX      08-JAN-2002; 2002US-0347327P.
XX      (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX      (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX      Pinsl-Ober J, Wenzig P, Weindel K, Bartl K, Schoenbrunner R;
XX      Malhotra K, O'donnell P, Kyger E;
XX      WPI; 2003-587135/55.
XX      Purification and amplification of target nucleic acid from biological
XX      sample used in diagnosis of cancer or in screening blood, involves
XX      binding target nucleic acid with unmodified silica surface, followed by
XX      amplification.
XX      Example 1; Page 23; 33pp; English.
XX      The invention relates to purification and amplification of target nucleic
XX      acid from biological sample. The method involves and binding target
XX      nucleic acid (TNA) in the sample with a material comprising an unmodified
XX      silica surface, separating the material from the sample and amplifying
XX      TNA in the presence of the material. The method is useful in diagnosis of
XX      certain diseases such as inherited diseases like sickle cell anemia and
XX      certain types of cancer or in screening blood for presence of target
XX      nucleic acid from virus. The method improves reaction efficiency and
XX      detection sensitivity of target nucleic acids. The present sequence
XX      represents a hepatitis C virus (HCV)-specific probe used in the method of
XX      the invention
XX      Sequence 31 BP; 6 A; 11 C; 7 G; 7 T; 0 U; 0 Other;
XX      Query Match 93.9%; Score 31; DB 9; Length 31;
XX      Best Local Similarity 100.0%; Pred. No. 0.00042;
XX      Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
DB      1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31

RESULT 4
AAT39735/c
ID      AAT39735 standard; DNA; 36 BP.
XX      AAT39735;
XX      09-APR-1997 (first entry)
XX      Hepatitis C virus PCR probe S1, based on nucleotides 121-157.
XX      Hepatitis C virus; HCV; polymerase chain reaction; amplification;
XX      replication; non-lymphoblastoid cell; monkey kidney cell;
XX      hybridisation probe; ss.

```

XX OS Synthetic.
 XX PN WO9624662-A1.
 XX PD 15-AUG-1996.
 XX PF 10-FEB-1995; 95WO-IT0000016.
 XX PR 10-FEB-1995; 95WO-IT0000016.
 XX PA (CNR) CONSIGLIO NAZ DELLE RICERCHE.
 XX PI Ravagnan G, Battaglia M, Carloni G, Ponzetto A, Iacovacci S;
 XX DR WPI; 1996-384435/38.
 XX PT Replication of hepatitis C virus in non-lymphoblastoid mammalian cells -
 XX PT useful for studies of HCV replication, prodn. of vaccines or viral
 XX PT antigens, etc.
 XX PS Disclosure; Page 8; 25pp; English.
 XX CC Hepatitis C virus can be replicated in non-lymphoblastoid mammalian cells
 CC by first incubating an HCV sample with the cells until an infecting
 CC amount of HCV has been absorbed. Infected cells are then washed and
 CC incubated under growth conditions. In an example, the presence of HCV in
 CC culture medium of monkey kidney cells inoculated with HCV-infected serum
 CC was verified by PCR amplification using two external primers (OUI and
 CC OUI2, see AAT39731 and AAT39732) and two internal primers (INI and IN2,
 CC see AAT39733 and AAT39734). The amplified products were identified by
 CC hybridisation to labelled probe S1 (see AAT39735). Small amounts of virus
 CC were shown to be released into the culture medium from secondary
 CC cultures. Control (non-inoculated) cells were negative for presence of
 CC viral genome
 XX SQ Sequence 36 BP; 9 A; 9 C; 11 G; 7 T; 0 U; 0 Other;
 Query Match 92.1%; Score 30.4; DB 2; Length 36;
 Best Local Similarity 96.9%; Pred. No. 0.00079;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CGGTGACTCACCGTTCCGACACCACTATGG 32
 Db |||||
 32 CGGTGACTCACCGTTCCGACACCACTATGG 1
 RESULT 5
 AAV15324/c
 ID AAV15324 standard; DNA; 29 BP.
 XX AC AAV15324;
 XX DT 25-MAR-2003 (revised)
 XX DT 28-MAY-1998 (first entry)
 XX DE Hepatitis C virus probe HCV40.
 XX KW Hepatitis C virus; HCV; PCR; detection; reverse transcription; probe;
 KW enzyme immunoassay; viral RNA; ss.
 XX OS Synthetic.
 OS Hepatitis C virus.
 PN WO9746716-A1.
 XX PD 11-DEC-1997.
 XX PF 03-JUN-1997; 97WO-IT000128.
 XX PR 07-JUN-1996; 96IT-RM000404.
 XX PA (WESA) WABCO BV.

XX PI Bosio P, Strumia C, Clemenza F;
 XX DR WPI; 1998-042222/04.
 XX PT Detection of hepatitis C virus - by reverse transcription, single-step
 XX PT PCR and detection by DNA enzyme immunoassay.
 XX PS Disclosure; Page 4; 26pp; English.
 XX CC The present sequence represents a probe involved in the method of the
 CC present invention for detecting hepatitis C virus (HCV). The method
 CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
 CC resulting cDNA by a single polymerase chain reaction in a reaction
 CC mixture having a Mg2+/Taq polymerase ratio of about 100 nmole/enzyme unit
 CC ; and (c) detecting the amplification product by DEIA (DNA enzyme
 CC immunoassay) using an oligonucleotide probe. The sensitivity of this
 CC method is at least equal to that achievable by more complicated assays
 CC using nested PCR. (Updated on 25-MAR-2003 to correct PR field.)
 XX SQ Sequence 29 BP; 7 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
 Query Match 83.0%; Score 27.4; DB 2; Length 29;
 Best Local Similarity 96.6%; Pred. No. 0.017;
 Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 TGTACTCACCGTTCCGACACCACTATGG 32
 Db |||||
 29 TGTACTCACCGTTCCGACACCACTATGG 1
 RESULT 6
 AAL40116
 ID AAL40116 standard; DNA; 41 BP.
 XX AC AAL40116;
 XX DT 13-SEP-2002 (first entry)
 XX DE Pathogenic microorganism detecting PCR primer SEQ ID No 42.
 XX KW Tuberculosis; Mycobacterium; bovis; BCG; africanum; microti; canotti;
 KW monitoring therapy; pathogenic microorganism; PCR; primer; ss.
 XX OS Unidentified.
 XX PN WO200252043-A1.
 XX PD 04-JUL-2002.
 XX PF 26-DEC-2001; 2001WO-JP011422.
 XX PR 26-DEC-2000; 2000JP-00396222.
 XX PR 26-DEC-2000; 2000JP-00396321.
 XX PR 29-JUN-2001; 2001JP-00199552.
 XX PR 13-SEP-2001; 2001JP-00278920.
 XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX PI Shimada M, Hino F, Kato I;
 XX DR WPI; 2002-500769/53.
 XX PT Detecting pathogenic microorganisms with oligonucleotide probes and
 XX PT primers, useful in disease diagnosis and monitoring therapy.
 XX PS Claim 57; Page 97; 106pp; Japanese.
 XX CC The invention relates to a probe containing a 410 or 20 base pair
 CC sequence, given in the specification. It is capable of detecting the
 CC tuberculosis bacterial group including Mycobacterium tuberculosis,
 CC Mycobacterium bovis BCG, Mycobacterium africanum, Mycobacterium microti
 CC and/or Mycobacterium canotti. The method is useful in disease diagnosis

CC and monitoring therapy. This polynucleotide sequence represents a PCR
 CC primer relating to the detection of pathogenic microorganisms of the
 CC invention

XX Sequence 41 BP; 7 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 66.7%; Score 22; DB 6; Length 41;

Best Local Similarity 97.1%; Pred. No. 4.8;

Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTCACC-GTTCCGACGACCACTATGGC 33

Db 5 CGGTGTACTCACC-GTTCCGACGACCACTATGGC 38

RESULT 7

AAX37635/C

ID AAX37635 standard; DNA; 41 BP.

XX AAX37635;

AC AAX37635;

XX 08-JUL-1999 (first entry)

XX HCV detecting primer #5.

XX Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;

XX fluorescence resonance energy transfer; ss.

XX Synthetic.

XX Hepatitis C virus; Virus.

XX JP11103899-A.

XX 20-APR-1999.

XX 30-SEP-1997; 97JP-00283042.

XX 30-SEP-1997; 97JP-00283042.

XX (TOKR-) ZH TOKYO RINGSHO IGAKU SOGO KENKYUSHO.
 XX (SRLS-) SRL KK.

XX WPI; 1999-305862/26.

XX Measurement of HCV gene using real time detecting PCR and primer and
 PT probe - is highly sensitive.

XX Claim 5; Page 6; 8pp; Japanese.

XX This invention describes a method for the measurement of an HCV gene by a
 CC real time detecting PCR. The invention also describes a method where a
 CC reporter fluorescent colour and a quencher fluorescent colour are
 CC combined to an oligonucleotide and the fluorescence of the reporter
 CC fluorescent colour is controlled by fluorescence resonance energy
 CC transfer. The method can measure HCV exactly with high sensitivity

XX Sequence 41 BP; 9 A; 11 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 63.6%; Score 21; DB 2; Length 41;

Best Local Similarity 97.0%; Pred. No. 13;

Matches 32; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CGGTGTACTCACC-GTTCCGACGACCACTATGG 32

Db 33 CGGTGTACTCACC-GTTCCGACGACCACTATGG 1

RESULT 8

AAA74622

ID AAA74622 standard; DNA; 26 BP.

XX AAA74622;

AC AAA74622;

XX

DT 08-JAN-2001 (first entry)

XX HCV-specific amplification primer C133R26.

XX Hepatitis C virus; HCV; HCV detection; amplification primer; ss.

XX Hepatitis C virus.

XX EP1026262-A2.

XX 09-AUG-2000.

XX 01-FEB-2000; 2000EP-00300763.

XX 03-FEB-1999; 99US-0118497P.

XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

XX Linnen JM, Gorman KM;

XX WPI; 2000-507254/46.

XX Detecting hepatitis C virus in biological sample involves amplifying
 CC reverse transcribed products of virus RNA using amplification primers
 CC whose sequences correspond to 5' or 3' non-coding region of the virus
 CC RNA.

XX Claim 30; Page 27; 28pp; English.

XX The present sequence is an amplification primer used in a method for
 CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
 CC is reverse transcribed to generate cDNA. This is then amplified using
 CC primers, including the present sequence, corresponding to the 5' or 3'
 CC non-coding region of HCV. The method is useful for the diagnosis of HCV
 CC infection in patients, in testing the efficacy of anti-HCV therapeutic
 CC regimes, and in screening blood for HCV-infected samples. The method
 CC provides an improved single-round, reverse transcription/amplification
 CC assay which detects low copy levels of HCV RNA. The primers and assay
 CC system are designed to allow the co-amplification of multiple regions of
 CC the HCV genome, multiple viral species, and an internal positive control
 CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
 CC regions of the HCV genome increases assay sensitivity and the co-
 CC amplification of an IPC decreases the likelihood of false negative
 CC results because of PCR inhibition

XX Sequence 26 BP; 4 A; 10 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 20.4; DB 3; Length 26;

Best Local Similarity 95.5%; Pred. No. 23;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CGGTTCGACGACCACTATGGC 33

Db 1 CGGTTCGACGACCACTATGGC 22

RESULT 9

AAT05216

ID AAT05216 standard; DNA; 28 BP.

XX AAT05216;

XX 13-JUN-1996 (first entry)

XX Hepatitis C virus antisense oligonucleotide A161.

XX Inhibition; expression; hepatitis C virus; HCV; non-A; non-B; RNA;
 KW translation; in vivo; ex vivo; in vitro; treatment; prevention;
 KW infection; antisense; non coding; region; NCR; core region; ss.

XX Synthetic.

XX WO9530746-A1.

PN

```

XX 16-NOV-1995.
PD
XX
PF 08-MAY-1995; 95WO-US005812.
PR 10-MAY-1994; 94US-00240382.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Wakita T, Wands JR;
XX
XX WPI; 1995-404113/51.
DR
XX
PT New anti:sense hepatitis C virus oligo:nucleotide(s) - used for
PT inhibiting HCV RNA translation, for the treatment or prevention of HCV
PT infection.
XX
XX Claim 1; Page 27; 50pp; English.
XX
CC The present oligonucleotide (ON) inhibits the expression of hepatitis C
CC virus (HCV) RNA, specifically HCV type II and type III protein synthesis
CC is inhibited by 81% and 76%, respectively. The ONs of the invention
CC inhibit translation of HCV types I-V RNA in vivo, ex vivo or in vitro,
CC and can therefore be used to treat or prevent HCV infection. The
CC antisense ONs comprise 10-28 nucleotides complementary to the entire HCV
CC 5'-non-coding and part of the core region. The A or S in the ONs name
CC denotes antisense or sense, and the no. indicates the position of the 5'-
CC end of the ON. The ON was tested at 10 fold molar excess to HCV RNA
XX
SQ Sequence 28 BP; 5 A; 11 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 20.4; DB 2; Length 28;
Best Local Similarity 95.5%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCGTTCGCGAGACCACTATGGC 33
Db 4 CCGTTCGCGAGACCACTATGGC 25

RESULT 10
AAZ57751
ID AAZ57751 standard; DNA; 28 BP.
AC
XX
XX AAZ57751;
XX
DT 05-APR-2000 (first entry)
XX
DE Hepatitis C virus antisense inhibitor oligonucleotide A161.
XX
KW Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss;
KW anti-inflammatory; translation inhibition; HCV infection; virucide.
XX
OS Hepatitis C virus.
XX
XX US6001990-A.
XX
XX 14-DEC-1999.
XX
XX 07-JUN-1995; 95US-00474700.
XX
XX 10-MAY-1994; 94US-00240382.
XX
XX (GEO ) GEN HOSPITAL CORP.
XX
PI Moradpour D, Wands JR, Wakita T;
XX
XX WPI; 2000-104900/09.
DR
PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
PT Hepatitis C virus infections.
XX
XX Claim 4; Col 21; 31pp; English.

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XX This sequence is an antisense oligonucleotide that hybridises to
CC Hepatitis C virus (HCV) RNA, under physiological conditions. The
CC invention relates to HCV antisense oligonucleotides, and also for a
CC vector comprising a nucleotide sequence which is transcribed in an animal
CC cell to generate an antisense oligonucleotide. The oligonucleotides have
CC virucide, hepatotropic and anti-inflammatory activity, and are useful for
CC treating HCV infection by inhibiting translation of type I-V HCV RNA.
CC Hepatitis C virus is a positive strand RNA virus, and is the major
CC causative agent of post-transfusion hepatitis. Persistent HCV infection
CC can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma
XX
SQ Sequence 28 BP; 5 A; 11 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.8%; Score 20.4; DB 3; Length 28;
Best Local Similarity 95.5%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCGTTCGCGAGACCACTATGGC 33
Db 4 CCGTTCGCGAGACCACTATGGC 25

RESULT 11
ADC54071/c
ID ADC54071 standard; DNA; 28 BP.
XX
AC ADC54071;
XX
DT 18-DEC-2003 (first entry)
XX
DE HCV 5'UTR signal amplification probe, SEQ ID NO:22.
XX
KW HCV; hepatitis C virus; classification; interferon therapy; 5'UTR;
KW signal amplification; probe; ss.
XX
OS Hepatitis C virus.
XX
XX JP2002345467-A.
XX
PD 03-DEC-2002.
XX
PF 17-APR-2001; 2001JP-00118810.
XX
PR 23-OCT-2000; 2000JP-00322567.
XX
PA (SRLS-) SRL KK.
XX
XX WPI; 2003-460879/44.
XX
PT Probe and method for classification of hepatitis C virus (HCV) types used
PT for forecast of therapeutic effect of interferon administration.
XX
PS Disclosure; SEQ ID NO 22; 15pp; Japanese.
XX
XX The invention relates to a nucleic acid probe for the classification of
CC hepatitis C virus (HCV) into 3 genotypes. The 3 HCV genotypes are MH1Am1
CC (type 1), MH2Am1 (type 2) and MH3G3C-MH1G3C' (type 3). The probe can be
CC used to classify HCV type to enable prediction of the success or
CC otherwise of interferon therapy in a patient. Sequences ADC54068-ADC54073
CC represent HCV 5'UTR signal amplification probes. Note: The present
CC sequence is given in the sequence listing, but is not further referred to
CC in the specification.
XX
SQ Sequence 28 BP; 6 A; 6 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 61.8%; Score 20.4; DB 10; Length 28;
Best Local Similarity 95.5%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCGTTCGCGAGACCACTATGGC 33
Db 26 CCGTTCGCGAGACCACTATGGC 5

```


CC agents (antibodies, peptides and other non-peptidyl agents) that may be
CC administered to treat hepatitis, cirrhosis or hepatocellular carcinomas
CC and to diagnose these disease. The present sequence represents a primer
CC used in a hybridisation assay to detect HCV RNA
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTTCGCAGACCACTATGGC 33
Db 25 GTTCGCAGACCACTATGGC 6
|||||
|||

RESULT 17
ADH79952/c
ID ADH79952 standard; DNA; 25 BP.
XX
AC ADH79952;
XX
DT 22-APR-2004 (first entry)
XX
DE HCV RT-PCR primer RJD-6.
XX
KW DC-SIGN; HCV infection; liver disease; hepatocellular carcinoma;
KW hepatitis; cirrhosis; DC-SIGN; HCV envelope glycoprotein; cytostatic;
KW antiinflammatory; hepatotropic; virucide; RT-PCR; reverse transcriptase;
KW primer; ss; RJD-6.
XX
OS Hepatitis C virus.
XX
XX US2003232745-A1.
XX
XX 18-DEC-2003.
XX
XX 24-DEC-2002; 2002US-00328997.
XX
XX 26-JUN-2001; 2001US-0300971P.
XX
XX (OLSO/) OLSON W C.
XX
XX (MADD/) MADDON P J.
XX
XX (GARD/) GARDNER J P.
XX
XX Olson WC, Maddon PJ, Gardner JP;
XX
XX WPI; 2004-061306/06.
XX
XX Use of DC-SIGN and DC-SIGNR proteins for inhibiting, preventing or
XX treating HCV infection and liver disease e.g. hepatitis or cirrhosis or
XX hepatocellular carcinoma.
XX
XX Disclosure; Page 33; 55pp; English.
XX
XX The invention relates to the use of DC-SIGN and DC-SIGNR proteins for
XX inhibiting, treating or preventing HCV infection and liver diseases such
XX as hepatocellular carcinoma, hepatitis or cirrhosis. The DC-SIGN and DC-
XX SIGNR protein are useful for inhibiting HCV infection, treating HCV
XX infection or treating or preventing liver disease e.g. hepatitis,
XX cirrhosis or hepatocellular carcinoma. Antibodies to the polypeptides,
XX the polypeptides or non-peptidyl agents can be used for inhibiting
XX binding of a DC-SIGNR or DC-SIGN protein to an HCV envelope glycoprotein.
XX This sequence represents an HCV reverse transcriptase PCR (RT-PCR) primer
XX used in the scope of the invention.
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC agents (antibodies, peptides and other non-peptidyl agents) that may be
CC administered to treat hepatitis, cirrhosis or hepatocellular carcinomas
CC and to diagnose these disease. The present sequence represents a primer
CC used in a hybridisation assay to detect HCV RNA
XX
SQ Sequence 25 BP; 6 A; 5 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;

Qy 14 GTTCGCAGACCACTATGGC 33
Db 25 GTTCGCAGACCACTATGGC 6
|||||
|||

RESULT 18
ADP87799
ID ADP87799 standard; DNA; 26 BP.
XX
AC ADP87799;
XX
DT 09-SEP-2004 (first entry)
XX
DE TEX on microarray template N2.
XX
KW TEX; thermodynamic equilibrium extension of primers; template; ss.
XX
OS Synthetic.
XX
XX US2004115643-A1.
XX
XX 17-JUN-2004.
XX
XX 12-DEC-2002; 2002US-00318416.
XX
XX 12-DEC-2002; 2002US-00318416.
XX
XX (LIZA/) LIZARDI P M.
XX
XX (GRIB/) GRIBANOV O G.
XX
XX Lizardi PM, Gribanov OG;
XX
XX WPI; 2004-468050/44.
XX
XX Amplifying nucleic acid for detecting nucleic acid, by extension of one
XX or more primers using target templates having replication terminating
XX feature, dissociation of primer from templates to produce multiple
XX extended primers.
XX
XX Example; SEQ ID NO 32; 75pp; English.
XX
XX The invention relates to amplifying (M1) a nucleic acid, involving
XX contacting one or more extension primers (EP) and target templates (TT)
XX and incubating under conditions to promote interaction of (EP) and
XX templates, extension of (EP) using the interacting (TT), and dissociation
XX of the extended (EP) from (TT), to produce multiple extended (EP) from at
XX least one (TT), where each (TT) comprise a replication terminating
XX feature. In (M1), (EP) and target templates are incubated under
XX isothermal conditions or single set of conditions. The target templates
XX are nucleic acid sequences of interest. Each of (EP) comprises or
XX consists of a target complement portion, preferably nucleotides, where
XX the nucleotides consist of the target complement portion. Each (EP)
XX further comprises non-target complement portion. The method is known as
XX TEX (thermodynamic equilibrium extension of primers). The method is
XX useful for amplifying nucleic acid and for detecting nucleic acid
XX sequences which involves performing (M1), and detecting one or more of
XX the extended (EP). In (M1), only those sequences targeted by (EP) are
XX amplified, thus allowing specific sequences to be targeted for
XX amplification. Flexibility in the location of replication terminating
XX feature allows flexibility in targeting sequences. If a targeted sequence
XX is not present, the sequence will not be amplified. Multiple sequences
XX can be amplified in the same reaction by targeting multiple sequences
XX with (EP). Simultaneous amplification and detection is facilitated using
XX detection probes associated with a substrate. Multiplex detection can be
XX facilitated by an array of detection probes with different detection
XX probes at different locations of a substrate. The present sequence is a
XX synthetic template sequence used to demonstrate the method of the
XX invention.
XX
SQ Sequence 26 BP; 4 A; 11 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 12; Length 26;
Best Local Similarity 100.0%; Pred. No. 35;

```

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGACCACTATGCG 33
DB 1 GTTCGCGACCACTATGCG 20

RESULT 19
AAH25418
ID AAH25418 standard; DNA; 32 BP.
XX
AC AAH25418;
XX
DT 22-AUG-2001 (first entry)
XX
DE Detection probe for a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "derivatisation with a pentamethine-di-
FT indocarbocyanine via an alkylphosphatidyl linker"
FT 15
FT /*tag= b
FT /note= "2-(amino-cyclohexyl)-propane-1,3-diol-linker
FT derivatised with 6-carboxy-fluorescein"
FT 31
FT modified_base 1
FT /*tag= c
FT /note= "derivatised with a 3'-terminal phosphate group"
XX
PN WO200137291-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-BP011459.
XX
PR 17-NOV-1999; 99EP-00122853.
XX
PR 12-MAY-2000; 2000EP-00110165.
XX
PA (HOFF ) ROCHE DIAGNOSTICS GMEH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
WPI; 2001-381247/40.
XX
Novel composition of magnetic glass particles for purification of DNA or
RNA in automated processes.
XX
Example 7; Page 100; 105pp; English.
XX
The specification describes a composition of magnetic glass particles,
CC which contain at least one magnetic object with a mean diameter between 5
CC -500 nm. The composition is useful for the purification of nucleic acids.
CC The composition can be used to process large quantities of nucleic acid
CC samples, because it does not involve the particles being centrifuged or
CC the fluids being drawn through glass fiber filters. The present sequence
CC represents a probe for a HCV DNA fragment. The DNA fragment can be
CC purified using the method of the invention
XX
SQ Sequence 32 BP; 6 A; 11 C; 7 G; 7 T; 0 U; 1 Other;

Query Match 60.6%; Score 20; DB 4; Length 32;
Best Local Similarity 96.9%; Pred. No. 36;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGGTGTACTCACCAG-TTCGCGACCACTATG 31
DB 1 CGGTGTACTCACCAGTTCGCGACCACTATG 32

```

```

RESULT 20
AAH37631/c
ID AAX37631 standard; DNA; 37 BP.
XX
AC AAX37631;
XX
DT 08-JUL-1999 (first entry)
XX
DE HCV detecting primer #1.
XX
KW Detection; HCV; real time; PCR; reporter; fluorescent; primer; quencher;
KW fluorescence resonance energy transfer; ss.
XX
OS Synthetic.
OS Hepatitis C virus; Virus.
XX
PN JP11103899-A.
XX
PD 20-APR-1999.
XX
PF 30-SEP-1997; 97JP-00283042.
XX
PF 30-SEP-1997; 97JP-00283042.
XX
PA (TOKR-) ZH TOKYO RINSHO IGAKU SOGO KENKYUSHO.
PA (SRLS-) SRL KK.
XX
WPI; 1999-305862/26.
XX
Measurement of HCV gene using real time detecting PCR and primer and
probe - is highly sensitive.
XX
Claim 1; Page 6; 8pp; Japanese.
XX
This invention describes a method for the measurement of an HCV gene by a
real time detecting PCR. The invention also describes a method where a
reporter fluorescent colour and a quencher fluorescent colour are
combined to an oligonucleotide and the fluorescence of the reporter
fluorescent colour is controlled by fluorescence resonance energy
transfer. The method can measure HCV exactly with high sensitivity
XX
SQ Sequence 37 BP; 6 A; 15 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 60.6%; Score 20; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGACCACTATGCG 33
DB 37 GTTCGCGACCACTATGCG 18

RESULT 21
AAH2490/c
ID AAT12490 standard; DNA; 38 BP.
XX
AC AAT12490;
XX
DT 18-JUL-1996 (first entry)
XX
DE Labelled oligonucleotide probe used in fluorescence quenching method.
XX
KW Probe length; fluorescence quenching; DNA binding; detection; cleavage;
KW fluorescein; FAM; DNA intercalator; ethidium bromide; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "labelled with FAM"
XX
modified_base 37

```


DR WPI; 1997-525681/48.
XX
PT Cell line comprising B or T lymphocytes infected with HCV - for
PT production of HCV proteins for use in immunoassays, vaccines and drug
PT screening.
XX
XX Disclosure; Col 27; 22pp; English.
XX
CC A novel cell line has been developed which is infected with hepatitis C
CC virus (HCV). The cells in the cell line are B or T lymphocytes and are
CC capable of replicating HCV. The present sequence represents an
CC oligonucleotide probe used in the detection of HCV RNA by strand specific
CC RT-PCR. The cell line may be used for producing HCV proteins for use in
CC immunoassays for anti-HCV antibodies; for producing HCV protein-
CC containing fractions for use in vaccines; and for drug screening to
CC develop antiviral agents for treating hepatitis C. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACTATGG 32
Db 21 CGGTTCCGCGAGACCACTATGG 1
RESULT 24
AAZ27492/c
ID AAZ27492 standard; DNA; 30 BP.
XX
AC AAZ27492;
XX
XX 27-AUG-2003 (revised).
DT 20-MAR-2003 (revised)
DT 13-DEC-1999 (first entry)
XX
XX Probe for HCV RNA.
DE
XX
XX Probe; HCV; detection; diagnosis; HCV infection; therapy;
KW antiviral agent; viral replication; ss.
XX
XX Hepatitis C virus.
OS
XX
XX US5968775-A.
PN
XX
XX 19-OCT-1999.
PD
XX
XX 10-MAY-1995; 95US-00438435.
PF
XX
XX 18-NOV-1987; 87US-00122714.
PR 30-DEC-1987; 87US-00139886.
PR 26-FEB-1988; 88US-00161072.
PR 06-MAY-1988; 88US-00191263.
PR 26-OCT-1988; 88US-00263584.
PR 14-NOV-1988; 88US-00271450.
PR 18-NOV-1988; 88WO-US004125.
PR 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 21-APR-1989; 89US-00353896.
PR 18-MAY-1989; 89US-00355002.
PR 18-MAY-1989; 89US-00355961.
PR 25-AUG-1989; 89US-00398667.
PR 21-DEC-1989; 89US-00456637.
PR 08-NOV-1990; 90US-00611965.
PR 27-JUL-1993; 93US-00097853.
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Weiner AJ, Steimer KS, Houghton M;
XX

DR WPI; 1999-590406/50.
XX
PT Use of extracorporeal cell systems infected with hepatitis C virus in the
PT detection of an anti-HCV antibody.
XX
XX Example; Col 27; 21pp; English.
XX
CC This sequence represents a probe for hepatitis C virus (HCV) RNA. The
CC invention relates to a method of preparing a composition for the
CC detection of an anti-HCV antibody comprises: (a) purifying or partially
CC purifying HCV virus particles or polypeptides from a cell line infected
CC with HCV, where the cells in the cell line are B lymphocytes or T
CC lymphocytes, and are capable of replicating HCV; and (b) fixing the
CC particles or polypeptides to a solid phase. The method is useful in the
CC diagnosis, treatment and prevention of HCV infection. The HCV infected
CC cell systems can also be used screening programs to develop antiviral
CC agents for treating HCV. The antiviral agents identified this way may
CC block infection of the cell systems or may prevent viral replication in
CC infected cells. (Updated on 20-MAR-2003 to correct PR field.) (Updated on
CC 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 67;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCGTTCGCGAGACCACTATGG 32
Db 21 CGGTTCCGCGAGACCACTATGG 1
RESULT 25
AAA75276/c
ID AAA75276 standard; DNA; 30 BP.
XX
AC AAA75276;
XX
XX 15-JAN-2001 (first entry)
DT
XX
XX Probe used to isolate HCV CDNA clone 18g.
DE
XX
XX Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
KW viral infectivity; viral replication; probe; ss.
XX
XX Hepatitis C virus.
OS
XX
XX EP1034785-A2.
PN
XX
XX 13-SEP-2000.
PD
XX
XX 16-MAR-1990; 2000EP-00109602.
PF
XX
XX 17-MAR-1989; 89US-00325338.
PR 20-APR-1989; 89US-00341334.
PR 18-MAY-1989; 89US-00355002.
PR 16-MAR-1990; 90EP-00302866.
XX
XX (CHIR) CHIRON CORP.
PA
XX
XX Houghton M, Choo Q, Kuo G;
PI
XX
XX WPI; 2000-566891/53.
DR
XX
XX Novel composition comprising a hepatitis C virus antisense polynucleotide
PT which is complementary to or corresponds to a sense strand of the virus
PT genome, and selectively hybridizes to it.
PT
XX
XX Example; Page 25; 75pp; English.
PS
XX
XX The specification describes a pharmaceutical composition which comprises
CC a hepatitis C virus (HCV) antisense polynucleotide. The HCV is
CC characterized by a positive stranded RNA genome which has 40% homology at

CC the polypeptide level to a HCV polypeptide. The antisense polynucleotide
 CC binds to cellular polynucleotides which enhance and/or are required for
 CC viral infectivity, replicative ability or chronicity. The antisense
 CC polynucleotides may also be designed to bind with high specificity, to be
 CC of increased stability, to be stable and to have low toxicity. The
 CC composition also comprises an agent which causes viral RNA to be
 CC inactive. The composition is used for preventing HCV replication in a
 CC system. The present sequence represents a probe which was used to isolate
 CC a novel HCV cDNA sequence

XX SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 3; Length 30;
 Best Local Similarity 95.2%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACACCACTATGG 32
 Db 21 CCGTTCGCGACCACTATGG 1

RESULT 26
 ADN35930/c
 ID ADN35930 standard; DNA; 30 BP.

XX AC ADN35930;

XX DT 17-JUN-2004 (first entry)

XX DE HCV cDNA clone 189 probe.

XX KW Antiviral; Vaccine; hepatitis C virus infection; HCV infection; probe;
 XX ss.

XX OS Hepatitis C virus.

XX FN EPI394255-A2.

XX PD 03-MAR-2004.

XX PF 16-MAR-1990; 2003EP-00016585.

XX PR 17-MAR-1989; 89US-00325338.

XX PR 20-APR-1989; 89US-00341334.

XX PR 18-MAY-1989; 89US-00355002.

XX PR 16-MAR-1990; 90EP-00302866.

XX PA (CHIR) CHIRON CORP.

XX PI Houghton M, Choo Q, Kuo G;

XX DR WPI; 2004-193149/19.

XX PT Novel purified hepatitis C virus polypeptide comprising epitope encoded
 XX by hepatitis C virus cDNA, useful as vaccine for treating hepatitis C
 XX virus.

XX PS Example 1; Page 26; 79pp; English.

XX CC The present invention relates to hepatitis C virus (HCV) proteins and
 XX cDNA sequences. The sequences are useful in immunoassays for detecting
 XX antibodies directed against HCV antigen; preparing host cells transformed
 XX with a recombinant polynucleotide; screening antiviral agents and
 XX determining the effect of antiviral agent in inhibiting viral replication
 XX in cell culture system; and developing vaccine for treating HCV
 XX infection. The present sequence was used to isolate a HCV cDNA clone of
 XX the invention.

XX SQ Sequence 30 BP; 7 A; 7 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 12; Length 30;

Best Local Similarity 95.2%; Pred. No. 67;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACACCACTATGG 32
 Db 21 CCGTTCGCGACCACTATGG 1

RESULT 27

AAZ99214/c

ID AAZ99214 standard; DNA; 31 BP.

XX AC AAZ99214;

XX DT 19-JUN-2000 (first entry)

XX DE Primer for primer-specific and mispair extension analysis of HCV.

XX KW Primer-specific and mispair extension assay; PSMEA;

XX KW genotype determination; HCV; gene variation; PCR primer; ss.

XX OS Hepatitis C virus.

XX FN WO200009745-A1.

XX PD 24-FEB-2000.

XX PF 09-AUG-1999; 99WO-CA000733.

XX PR 13-AUG-1998; 98CA-02245039.

XX PA (CABL-) CANADIAN BLOOD SERVICES.

XX PA (HEMA-) HEMA-QUEBEC.

XX PI Hu Y;

XX DR WPI; 2000-224367/19.

XX PT Primer-specific and mispair extension assay for identifying gene
 XX variations, comprises specific primer amplification of unknown nucleic
 XX acid sequences of patients using incomplete dNTP sets.

XX PS Disclosure; Page 13; 65pp; English.

XX CC AAZ99212-26 represent PCR primers used in a primer-specific and mispair
 XX extension assay (PSMEA) for genotype determination of Hepatitis C virus
 XX (HCV). The method comprises extending an unknown nucleic acid sequence
 XX (from a patient) using a primer specific for particular genotype and
 XX incomplete set of dNTPs under suitable conditions followed by
 XX characterizing and comparing the extension products with known nucleic
 XX acid sequences of various genotypes. The present primers are used for
 XX detecting nucleotide variations in the 5' untranslated region of the HCV
 XX genome. PSMEA is capable of accurately detecting heterozygotes and
 XX nucleotide mutations in a nucleic acid sequence. The PSMEA is useful for
 XX identifying gene variations such as in different genotypes or subtypes of
 XX a given genotype, especially Hepatitis C virus genotypes and subtypes

XX SQ Sequence 31 BP; 7 A; 8 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 58.8%; Score 19.4; DB 3; Length 31;

Best Local Similarity 95.2%; Pred. No. 67;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACACCACTATGG 32

Db 21 CCGTTCGCGACCACTATGG 1

RESULT 28

ADD67939

ID ADD67939 standard; DNA; 19 BP.

XX AC ADD67939;

XX DT 15-JAN-2004 (first entry)

XX	Hepatitis C virus RT-PCR primer seq id 11.
DE	antiviral; hepatitis C virus; HCV; viral replication inhibitor;
XX	replication competent HCV; 3' non-translated region;
KW	reverse transcriptase PCR; RT-PCR; primer; ss; lightcycler RT-PCR.
KM	
XX	
OS	Hepatitis C virus.
XX	
PN	US2003125541-A1.
XX	
PD	03-JUL-2003.
XX	
PF	27-SEP-2002; 2002US-00259275.
XX	
PR	23-DEC-1999; 99US-0171909P.
XX	
PR	23-DEC-2000; 2000US-00747419.
XX	
PR	27-SEP-2001; 2001US-0325236P.
XX	
PR	13-NOV-2001; 2001US-0338123P.
XX	
PA	(TEXA) UNIV TEXAS SYSTEM.
XX	
PI	Lemon SM, Yi M;
XX	
XX	WPI; 2003-811006/76.
XX	
PT	Identifying a compound that inhibits replication of a hepatitis C virus
PT	(HCV) RNA comprises contacting a cell comprising a replication competent
PT	HCV RNA containing a heterologous polynucleotide encoding a
PT	transactivator, with a compound.
XX	
PS	Example 6; SEQ ID NO 11; 95pp; English.
XX	
XX	The invention describes a method of identifying a compound that inhibits
CC	replication of a hepatitis C virus (HCV) RNA. The method comprises
CC	contacting a cell comprising a replication competent HCV RNA containing a
CC	heterologous polynucleotide having a first coding sequence encoding a
CC	transactivator, with a compound. The method is useful for identifying a
CC	compound that inhibits replication of HCV RNA. The kit is useful for
CC	detecting replication competent HCV RNA. This sequence represents a
CC	primer used to isolate DNA encoding HCV in order to detect the production
CC	of the viral RNA in cell lines.
XX	
SQ	Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
	Query Match 57.6%; Score 19; DB 10; Length 19;
	Best Local Similarity 100.0%; Pred. No. 95;
	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	14 GTTCCGACAGACCACTATGG 32
DB	1 GTTCCGACAGACCACTATGG 19
	RESULT 29
	ADF51498/c
ID	ADF51488 standard; RNA; 19 BP.
XX	
AC	ADF51488;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Hepatitis C virus short interfering nucleic acid sense strand SeqID78.
XX	
KW	short interfering nucleic acid; siNA; virus replication inhibition;
KW	hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW	hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW	hepatocellular cancer; cirrhosis; ss.
XX	
OS	Hepatitis C virus.
XX	
PN	WO2003070750-A2.
XX	

PD	28-AUG-2003.
XX	
PF	20-FEB-2003; 2003WO-US005043.
PF	
XX	
XX	20-FEB-2002; 2002US-0358580P.
PR	11-MAR-2002; 2002US-0363124P.
PR	26-MAR-2002; 2002WO-US009187.
PR	06-JUN-2002; 2002US-0386782P.
PR	05-AUG-2002; 2002US-0401104P.
PR	29-AUG-2002; 2002US-0406784P.
PR	05-SEP-2002; 2002US-0408378P.
PR	09-SEP-2002; 2002US-0409233P.
PR	15-JAN-2003; 2003US-0440129P.
XX	
XX	(SIRN-) SIRNA THERAPEUTICS INC.
XX	
PI	Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX	
DR	WPI; 2003-689778/65.
XX	
XX	New double-stranded short interfering nucleic acid comprises sugar-
PT	modified pyrimidine bases useful for treating infection with hepatitis C
PT	virus.
XX	
PS	Example 3; SEQ ID NO 78; 183pp; English.
XX	
CC	This invention relates to novel double-stranded short interfering nucleic
CC	acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC	one strand is an antisense strand (ASS) that is complementary to (part
CC	of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC	ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC	modification. The invention may allow development of compounds with
CC	virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC	modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC	interference. The siNA's of the invention may be used to inhibit
CC	replication of HCV, in cells, tissue explants or organisms, for treating
CC	HCV infection and its consequences (liver failure; hepatocellular cancer
CC	and cirrhosis), and also for drug screening, diagnosis, target
CC	identification and validation, genetic engineering, pharmacogenomics,
CC	studying gene function and gene mapping (for example of single-nucleotide
CC	polymorphisms). The chemical modification improves stability, activity,
CC	cellular uptake and/or binding affinity. The siNA can be directed to
CC	conserved regions of HCV genes, so are active against many different
CC	strains.
XX	
SQ	Sequence 19 BP; 4 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
Query Match	57.6%; Score 19; DB 10; Length 19;
Best Local Similarity	100.0%; Pred. No. 95;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	15 TTCCGCAGACCACTATGTC 33
Db	19 TTCCGCAGACCACTATGTC 1
RESULT 30	
ADF51492/c	
ID	ADF51492 standard; RNA; 19 BP.
XX	
AC	ADF51492;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Hepatitis C virus short interfering nucleic acid sense strand SeqID82.
XX	
KW	short interfering nucleic acid; siNA; virus replication inhibition;
KW	Hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW	hepatotropic; cytosstatic; RNA interference; HCV infection; liver failure;
KW	hepatocellular cancer; cirrhosis; ss.
XX	
OS	Hepatitis C virus.
XX	

```

PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 82; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
SQ Sequence 19 BP; 4 A; 5 C; 6 G; 0 T; 4 U; 0 Other;
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 GTTCGCGAGACCACTATGG 32
Db 19 GTTCGCGAGACCACTATGG 1
RESULT 31
ADFS2184
ID ADFS2184 standard; RNA; 19 BP.
XX
AC ADFS2184;
XX
XX 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siNA antisense strand SeqID774.
XX
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW hepatocellular cancer; cirrhosis; ss.

```

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OS Hepatitis C virus.
XX
PN WO2003070750-A2.
XX
PD 28-AUG-2003.
XX
PF 20-FEB-2003; 2003WO-US005043.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 26-MAR-2002; 2002WO-US009187.
PR 06-JUN-2002; 2002US-0386782P.
PR 05-AUG-2002; 2002US-0401104P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX WPI; 2003-689778/65.
XX
PT New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
XX virus.
XX
PS Example 3; SEQ ID NO 774; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
XX acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
XX one strand is an antisense strand (ASS) that is complementary to (part
XX of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
XX ASS, and where most of the pyrimidine nucleotides comprise a sugar
XX modification. The invention may allow development of compounds with
XX virucide, antiinflammatory, hepatotropic or cytostatic activities by
XX modulation (inhibition) of expression or activity of HCV RNA, by RNA
XX interference. The siNA's of the invention may be used to inhibit
XX replication of HCV, in cells, tissue explants or organisms, for treating
XX HCV infection and its consequences (liver failure; hepatocellular cancer
XX and cirrhosis), and also for drug screening, diagnosis, target
XX identification and validation, genetic engineering, pharmacogenomics,
XX studying gene function and gene mapping (for example of single-nucleotide
XX polymorphisms). The chemical modification improves stability, activity,
XX cellular uptake and/or binding affinity. The siNA can be directed to
XX conserved regions of HCV genes, so are active against many different
XX strains.
XX
SQ Sequence 19 BP; 4 A; 7 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 95;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TTCCGCGAGACCACTATGGC 33
Db 1 UUCCGCGAGACCACTATGGC 19
RESULT 32
ADFS2188
ID ADFS2188 standard; RNA; 19 BP.
XX
AC ADFS2188;
XX
XX 12-FEB-2004 (first entry)
XX
DE Hepatitis C virus siNA antisense strand SeqID778.
XX
KW short interfering nucleic acid; siNA; virus replication inhibition;
KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;

```

hepatocellular cancer; cirrhosis; ss.
Hepatitis C virus.
WO2003070750-A2.
28-AUG-2003.
20-FEB-2003; 2003WO-US005043.
20-FEB-2002; 2002US-0358580P.
11-MAR-2002; 2002US-0363124P.
26-MAR-2002; 2002WO-US009187.
06-JUN-2002; 2002US-0386782P.
05-AUG-2002; 2002US-0401104P.
29-AUG-2002; 2002US-0406784P.
05-SEP-2002; 2002US-0408378P.
09-SEP-2002; 2002US-0409293P.
15-JAN-2003; 2003US-0440129P.
(SIRN-) SIRNA THERAPEUTICS INC.
Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
WPI; 2003-689778/65.
New double-stranded short interfering nucleic acid comprises sugar-modified pyrimidine bases useful for treating infection with hepatitis C virus.
Example 3; SEQ ID NO 778; 183pp; English.
This invention relates to novel double-stranded short interfering nucleic acids (siNA) that inhibits replication of hepatitis C virus (HCV), where one strand is an antisense strand (ASS) that is complementary to (part of) an HCV RNA (portion) and a sense strand (SS) that is complementary to ASS, and where most of the pyrimidine nucleotides comprise a sugar modification. The invention may allow development of compounds with virucide, antiinflammatory, hepatotropic or cytostatic activities by modulation (inhibition) of expression or activity of HCV RNA, by RNA interference. The siNA's of the invention may be used to inhibit replication of HCV in cells, tissue explants or organisms, for treating HCV infection and its consequences (liver failure; hepatocellular cancer and cirrhosis), and also for drug screening, diagnosis, target identification and validation, genetic engineering, pharmacogenomics, studying gene function and gene mapping (for example of single-nucleotide polymorphisms). The chemical modification improves stability, activity, cellular uptake and/or binding affinity. The siNA can be directed to conserved regions of HCV genes, so are active against many different strains.
Sequence 19 BP; 4 A; 6 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 78.9%; Pred. No. 95;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 14 GTTCGCGACACCATGTGG 32
|:|||||:|||||:|
DB 1 GUUCCGCGACACCATUAGG 19
|:|||||:|||||:|
RESULT 33
ABX10611
ID ABX10611 standard; DNA; 19 BP.
XX
AC ABX10611;
XX
DT 11-APR-2003 (first entry)
XX
DE Light Cycler reverse PCR primer used to detect Viral RNA.
XX
KW PCR; primer; ss; replication competent; hepatitis C virus; HCV;

3' non-translated RNA; 3'NTR; chronic viral hepatitis; hepatic fibrosis; cirrhosis; hepatocellular carcinoma; secretory alkaline phosphatase; SEAP.
Hepatitis c virus.
US2002155582-A1.
24-OCT-2002.
23-DEC-2000; 2000US-00747419.
23-DEC-1999; 99US-0171909P.
(LEMO/) LEMON S M.
(YIMW/) YI M.
Lemon SM, Yi M;
WPI; 2003-182640/18.
Novel replication competent hepatitis C virus for producing infectious viral particles and as antigen for detecting hepatitis C virus antibodies, comprises hepatitis C virus genome and heterologous polynucleotide.
Example 6; Page 16; 37pp; English.
The invention discloses a replication competent hepatitis C virus (HCV) comprising a HCV virus genome and a heterologous polynucleotide, where the HCV genome comprises a 3' non-translated RNA and the heterologous polynucleotide is present in the 3' non-translated RNA. HCV is a cause of chronic viral hepatitis, hepatic fibrosis, cirrhosis and/or the development of hepatocellular carcinoma. A cell comprising the HCV is useful for selecting or detecting a replication competent HCV, for identifying a compound that inhibits replication of HCV, for producing infectious viral particles which are useful as a source of virus particles for various assays, including evaluating methods for inactivating particles, excluding particles from serum, identifying a neutralising compound and as an antigen for use in detecting anti-HCV antibodies in an animal. The cell comprising the HCV is also useful for identifying a variant HCV. An HCV particle is useful as an antigen, as a positive-control in assays that test for the presence of anti-HCV antibodies, to produce antibodies to detect the presence of viral particles in biological samples (e.g. blood products and cell-free blood products) and as a source of viral antigen to measure the presence and amount of antibody present in an animal. The sequence presented is the Light Cycler reverse PCR primer which was used to detect viral RNA in Huh -secretory alkaline phosphatase (SEAP) -010 cell lines
Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 57.6%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 14 GTTCGCGACACCATGTGG 32
|:|||||:|||||:|
DB 1 GTTCGCGACACCATGTGG 19
|:|||||:|||||:|
RESULT 34
AAQ65023
ID AAQ65023 standard; DNA; 20 BP.
XX
AC AAQ65023;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide SMS21 complementary to HCV genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.

```

XX OS Synthetic.
XX FH Key
XX FT misc_feature Location/Qualifiers
XX FT 1..20
XX FT /tag= a
XX FT /note= "phosphorothioate linkages between these
XX FT nucleotides"
XX PN CA2104649-A.
XX PD 26-FEB-1994.
XX XX 23-AUG-1993; 93CA-02104649.
XX XX 25-AUG-1992; 92JP-00248796.
XX PR 03-MAR-1993; 93JP-00042736.
XX XX (SEKI/) SEKI M.
XX PI Seki M, Honda Y, Yamada E;
XX WPI; 1994-151836/19.
XX DR
XX XX Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus
XX FT genome - are useful as antiviral agents.
XX PS Example 3; Page 112; 262pp; English.
XX CC This oligonucleotide is an example of an antisense compound designed to
XX CC hybridise to a hepatitis C virus sequence. Such antisense
XX CC oligonucleotides are useful for inhibiting translation of HCV genes
XX XX
XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCCTATGG 32
DB 2 GTTCGCGAGACCCTATGG 20

RESULT 35
AAZ88590/c
ID AA288590 standard; DNA; 20 BP.
XX AC AAZ88590;
XX DT 04-MAY-2000 (first entry)
XX DE Hepatitis C genome PCR primer 3.
XX KW Detection; serum; plasma; probe; infection; PCR primer; ss.
XX OS Hepatitis C virus.
XX PN DE19832050-A1.
XX PD 27-JAN-2000.
XX PF 16-JUL-1998; 98DE-01032050.
XX PR 16-JUL-1998; 98DE-01032050.
XX XX (BIOT ) BIOTEST PHARMA GMBH.
XX PI Jochum C;
XX WPI; 2000-148478/14.
XX DR Detection of Hepatitis C and B viral genomes in serum or plasma using
XX FT

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PT specific oligonucleotide primers and probes.
XX Claim 1c; Page 2; 7pp; German.
XX CC This invention describes a novel method to detect Hepatitis C (HCV)
XX CC and/or Hepatitis B (HBV) viral genomes in a serum or plasma sample using
XX CC specific primers and probes. The method and oligonucleotide primers and
XX CC probes are useful for the specific detection of Hepatitis C and/or
XX CC Hepatitis B viral sequences in plasma and serum samples. This may be
XX CC useful for preventing Hepatitis B and/or C infection in patients through
XX CC contaminated blood and/or serum products. The method is able to detect
XX CC all reference samples of HBV subtypes AD and AY and HCV subtypes 1 - 5
XX CC with 100% accuracy. AA288588-288591 represent PCR primers used to detect
XX CC HCV virus in a sample
XX SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCCTATGG 32
DB 19 GTTCGCGAGACCCTATGG 1

RESULT 36
AAQ67619/c
ID AAQ67619 standard; DNA; 22 BP.
XX AC AAQ67619;
XX DT 31-JAN-1995 (first entry)
XX DE Primer for amplifying hepatitis C virus 5' non-coding region.
XX KW Hepatitis C virus; HCV; testing; detection; probe; linker;
XX KW non-coding region; acridinium N-hydroxy succinimide; ss.
XX OS Synthetic.
XX PN JP06121700-A.
XX PD 06-MAY-1994.
XX PF 13-OCT-1992; 92JP-00274273.
XX PR 13-OCT-1992; 92JP-00274273.
XX PA (CHUS ) CHUGAI PHARM CO LTD.
XX DR WPI; 1994-185929/23.
XX PT Method of detecting Hepatitis C virus - using a labelled DNA probe.
XX PS Disclosure; Page 2; 13pp; Japanese.
XX CC 7 Primers (AAQ67617-20, AAQ67622-24) were used to amplify regions of the
XX CC hepatitis C virus 5' non-coding (5'NC) region. A probe (See AAQ67615, 5',
XX CC AAQ67616) which is specific for a conserved base sequence within the 5'
XX CC non-coding (5'NC) region of hepatitis C virus (HCV) gene was then used to
XX CC detect amplification products. The probe was labelled using an acridinium
XX CC N-hydroxy succinimide ester which is attached to the probe via a linker
XX SQ Sequence 22 BP; 6 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCCTATGGC 33
DB 22 TTCCGCGAGACCCTATGGC 4

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RESULT 37
AAAD19054/c
ID AAAD19054 standard; DNA; 24 BP.
XX
XX
AC AAAD19054;
XX
XX 18-DEC-2001 (first entry)
XX
XX Hepatitis C virus (HCV) DNA amplifying forward PCR primer #29.
XX
XX Hepatitis C virus; HCV; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.
XX
XX Hepatitis C virus.
OS
XX WO200168921-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 14-MAR-2001; 2001WO-US008110.
PF
XX
XX 14-MAR-2000; 2000US-0189344P.
PR
XX
XX (INVE-) INVESTIGEN.
PA
XX Koshinsky H, Zwick MS, Mccue KF;
PI
XX WPI; 2001-611396/70.
DR
XX
XX Simultaneous detection of biological entities such as bacteria, fungi and
PT viruses by specific nucleic acid amplification.
XX
XX Disclosure; Page 31; 55pp; English.
XX
XX The invention relates to a method and apparatus for the simultaneous
CC detection of multiple biological entities such as bacteria, fungi and
CC viruses by specific nucleic acid amplification. The invention also
CC relates to a kit for simultaneous detection of biological entities. The
CC kit is employed for detecting blood-borne pathogens, associated with a
CC variety of infectious diseases such as respiratory and sexually
CC transmitted diseases. The methods and apparatus are used for the
CC simultaneous detection of biological entities present in biological and
CC environment samples. In particular, they are used for monitoring diseases
CC cause by microorganisms associated with a respiratory or sexually
CC transmitted disease such as a bacterium (Staphylococcus, Pneumococcus,
CC Gonococcus, Haemophilus, Bacteroides, Escherichia or Salmonella), virus
CC (DNA or RNA virus, such as adenovirus, adeno-associated virus, HAV, HCV,
CC HDV, HEV, HGV or TTV), fungus (Aspergillus fumigatus, Blastomycosis,
CC dermatitis, Candida albicans) or protozoa (Entamoeba histolytica). The
CC present sequence is a PCR primer used for amplifying Hepatitis C virus
CC (HCV) DNA.
XX
XX Sequence 24 BP; 6 A; 4 C; 10 G; 4 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGCG 33
DB 24 TTCCGCAGACCACTATGCG 6

RESULT 38
AAA96551/c
ID AAA96551 standard; DNA; 25 BP.
XX
XX
AC AAA96551;
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Forward PCR primer used to amplify a HCV fragment.
DE
XX
XX HCV; HIV; viral detection; PCR primer; ss.
KW
XX
XX Hepatitis C virus.
OS
XX
XX CA2296044-A1.
PN
XX
XX 03-AUG-2000.
PD
XX
XX 01-FEB-2000; 2000CA-02296044.
PF
XX
XX 03-FEB-1999; 99US-0118498P.
PR
XX
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX
XX Linnen JM, Song K, Patterson DR, Gorman KM;
PI

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XX
DE
XX Forward PCR primer used to amplify a 5' noncoding region of HCV.
KW HCV; HIV; viral detection; PCR primer; ss.
XX
XX Hepatitis C virus.
OS
XX
XX CA2296044-A1.
PN
XX
XX 03-AUG-2000.
PD
XX
XX 01-FEB-2000; 2000CA-02296044.
PF
XX
XX 03-FEB-1999; 99US-0118498P.
PR
XX
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX
XX Linnen JM, Song K, Patterson DR, Gorman KM;
PI
WPI; 2000-594741/57.
DR
XX
XX New methods for the simultaneous detection of hepatitis C virus and human
PT immunodeficiency virus in biological samples from humans.
XX
XX Claim 1; Page 21; 45pp; English.
XX
XX The specification describes a method for co-detecting Hepatitis C Virus
CC (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological
CC sample. The method uses HCV and HIV specific reverse transcription
CC primers, either separately or in combination. The reverse transcribed
CC products are then amplified using primers specific for the 5' noncoding
CC region of HCV and/or HIV. The presence of specific products indicates the
CC presence of the appropriate RNA in the sample. The method is used for the
CC simultaneous detection of the presence of HCV RNA and HIV RNA in a
CC sample. PCR primers AAA96551-52 are used to the amplify 5' noncoding
CC region of HCV
XX
XX Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGCG 33
DB 25 TTCCGCAGACCACTATGCG 7

RESULT 39
AAA96560/c
ID AAA96560 standard; DNA; 25 BP.
XX
XX
AC AAA96560;
XX
XX 08-FEB-2001 (first entry)
DT
XX
XX Forward PCR primer used to amplify a HCV fragment.
DE
XX
XX HCV; HIV; viral detection; PCR primer; ss.
KW
XX
XX Hepatitis C virus.
OS
XX
XX CA2296044-A1.
PN
XX
XX 03-AUG-2000.
PD
XX
XX 01-FEB-2000; 2000CA-02296044.
PF
XX
XX 03-FEB-1999; 99US-0118498P.
PR
XX
XX (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
PA
XX
XX Linnen JM, Song K, Patterson DR, Gorman KM;
PI

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XX WPI; 2000-594741/57.
XX
XX New methods for the simultaneous detection of hepatitis C virus and human
PT immunodeficiency virus in biological samples from humans.
XX
XX Claim 16; Page 27; 45pp; English.
XX
XX The specification describes a method for co-detecting Hepatitis C Virus
CC (HCV) RNA and human immunodeficiency virus (HIV) RNA in a biological
CC sample. The method uses HCV and HIV specific reverse transcription
CC primers, either separately or in combination. The reverse transcribed
CC products are then amplified using primers specific for the 5' noncoding
CC region of HCV and/or HIV. The presence of specific products indicates the
CC presence of the appropriate RNA in the sample. The method is used for the
CC simultaneous detection of the presence of HCV RNA and HIV RNA in a
CC sample. PCR primers AAA96560-61 are used to the amplify a fragment of HCV
XX
XX Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;
SQ
Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 TTCCGCGAGACCACTATGGC 33
Db 25 TTCCGCGAGACCACTATGGC 7
RESULT 40
AAA74620/c
ID AAA74620 standard; DNA; 25 BP.
XX
XX AAA74620;
XX
XX 08-JAN-2001 (first entry)
XX
XX HCV-specific amplification primer C131F25.
XX
XX Hepatitis C virus; HCV; HCV detection; amplification primer; ss.
XX
XX Hepatitis C virus.
XX
XX EP1026262-A2.
XX
XX 09-AUG-2000.
XX
XX 01-FEB-2000; 2000EP-00300763.
XX
XX 03-FEB-1999; 99US-0118497P.
XX
XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
XX Linnen JM, Gorman KM;
XX
XX WPI; 2000-507254/46.
XX
XX Detecting hepatitis C virus in biological sample involves amplifying
PT reverse transcribed products of virus RNA using amplification primers
PT whose sequences correspond to 5' or 3' non-coding region of the virus
PT RNA.
XX
XX Claim 30; Page 27; 28pp; English.
XX
XX The present sequence is an amplification primer used in a method for
CC detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA
CC is reverse transcribed to generate cDNA. This is then amplified using
CC primers, including the present sequence, corresponding to the 5' or 3'
CC non-coding region of HCV. The method is useful for the diagnosis of HCV
CC infection in patients, in testing the efficacy of anti-HCV therapeutic
CC regimes, and in screening blood for HCV-infected samples. The method
CC provides an improved single-round, reverse transcription/amplification
CC assay which detects low copy levels of HCV RNA. The primers and assay

CC system are designed to allow the co-amplification of multiple regions of
CC the HCV genome, multiple viral species, and an internal positive control
CC (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple
CC regions of the HCV genome increases assay sensitivity and the co-
CC amplification of an IPC decreases the likelihood of false negative
CC results because of PCR inhibition
XX
SQ Sequence 25 BP; 6 A; 4 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 57.6%; Score 19; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGAGACCACTATGGC 33
Db 25 TTCCGCGAGACCACTATGGC 7

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Job time : 201.112 secs

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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 38.191 Seconds
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	61.8	26	4	US-09-493-353-4
2	20.4	61.8	28	3	US-08-474-700B-6
3	20.4	61.8	28	5	PCT-US95-05812-6
C 4	20.4	61.8	36	4	US-09-153-242-39
C 5	20	60.6	38	1	US-08-299-682-9
C 6	20	60.6	38	1	US-08-299-682-10
C 7	19.4	58.8	30	1	US-08-097-853-2
C 8	19.4	58.8	30	2	US-08-438-435-3
C 9	19.4	58.8	30	3	US-08-444-818-217
C 10	19	57.6	25	4	US-09-494-332A-1
C 11	19	57.6	25	4	US-09-494-332A-10
C 12	19	57.6	25	4	US-09-493-353-2
C 13	18.4	55.8	20	1	US-08-533-820A-6
C 14	18.4	55.8	20	4	US-08-150-204E-125
C 15	18.4	55.8	26	1	US-08-299-682-11
C 16	18.4	55.8	26	1	US-08-240-547-43
C 17	17.4	52.7	20	3	US-08-397-220B-50
C 18	17.4	52.7	20	3	US-08-650-093C-50
C 19	16	48.5	16	3	US-08-954-210-9
C 20	16	48.5	16	4	US-09-431-419A-9
C 21	16	48.5	16	4	US-09-474-432B-24
C 22	16	48.5	16	4	US-09-476-387-24
C 23	16	48.5	33	1	US-08-438-639-46
C 24	16	48.5	33	1	US-07-813-338A-46
C 25	16	48.5	33	2	US-08-470-124-79
C 26	16	48.5	33	3	US-08-441-971-122
C 27	16	48.5	33	3	US-08-221-653-122

28	16	48.5	33	3	US-08-442-144A-122	Sequence 122, App
29	16	48.5	33	3	US-08-441-970-122	Sequence 122, App
30	16	48.5	33	3	US-08-435-568A-28	Sequence 28, Appl
31	16	48.5	33	3	US-08-417-551-5	Sequence 5, Appli
32	16	48.5	39	4	US-08-316-385-5	Sequence 5, Appli
C 33	15.4	46.7	18	3	US-09-034-205-52	Sequence 52, Appl
C 34	15.4	46.7	18	3	US-09-677-218B-52	Sequence 52, Appl
C 35	15.4	46.7	18	3	US-09-677-192-52	Sequence 52, Appl
C 36	15.4	46.7	18	4	US-09-402-618B-52	Sequence 52, Appl
C 37	15.4	46.7	37	6	5166057-36	Patent No. 5166057
38	15.4	46.7	38	2	US-08-316-439A-21	Sequence 21, Appl
39	15.2	46.1	33	3	US-09-039-982A-54	Sequence 54, Appl
40	15.2	46.1	33	3	US-09-039-762A-54	Sequence 54, Appl
41	15.2	46.1	33	3	US-09-194-285-46	Sequence 46, Appl
42	15.2	46.1	33	3	US-09-042-492D-54	Sequence 54, Appl
43	15.2	46.1	33	4	US-08-913-612A-60	Sequence 60, Appl
44	15.2	46.1	38	3	US-08-974-022-31	Sequence 31, Appl
45	15.2	46.1	38	3	US-08-974-022-33	Sequence 33, Appl
46	15.2	46.1	38	3	US-08-795-445A-31	Sequence 31, Appl
47	15.2	46.1	38	3	US-08-795-445A-33	Sequence 33, Appl
48	15.2	46.1	38	3	US-08-795-447A-31	Sequence 31, Appl
49	15.2	46.1	38	3	US-08-795-447A-33	Sequence 33, Appl
50	15.2	46.1	38	3	US-08-974-186-31	Sequence 31, Appl
51	15.2	46.1	38	3	US-08-974-186-33	Sequence 33, Appl
52	15.2	46.1	38	3	US-08-795-446B-31	Sequence 31, Appl
53	15.2	46.1	38	3	US-08-795-446B-33	Sequence 33, Appl
54	15.2	46.1	38	3	US-08-706-945D-26	Sequence 26, Appl
55	15.2	46.1	38	3	US-08-706-945D-28	Sequence 28, Appl
56	15.2	46.1	38	4	US-08-577-788C-31	Sequence 31, Appl
57	15.2	46.1	38	4	US-08-577-788C-33	Sequence 33, Appl
C 58	15	45.5	15	1	US-08-182-968A-4	Sequence 4, Appli
C 59	15	45.5	15	2	US-08-774-306A-4	Sequence 4, Appli
C 60	15	45.5	15	3	US-09-064-156A-4	Sequence 4, Appli
C 61	15	45.5	26	4	US-10-029-907-19	Sequence 19, Appl
C 62	15	45.5	27	1	US-08-688-649-11	Sequence 11, Appl
C 63	14.8	44.8	21	3	US-08-397-220B-13	Sequence 13, Appl
64	14.8	44.8	21	3	US-08-650-093C-13	Sequence 13, Appl
65	14.8	44.8	21	4	US-08-823-895A-13	Sequence 13, Appl
66	14.8	44.8	25	1	US-08-361-442-4	Sequence 4, Appli
67	14.8	44.8	25	2	US-08-823-516-121	Sequence 121, App
68	14.8	44.8	25	3	US-08-759-038-96	Sequence 96, Appl
69	14.8	44.8	25	4	US-08-758-314-96	Sequence 96, Appl
70	14.8	44.8	25	4	US-09-684-938-96	Sequence 96, Appl
71	14.8	44.8	25	4	US-09-308-825A-96	Sequence 96, Appl
C 72	14.8	44.8	26	1	US-08-379-078-664	Sequence 664, App
73	14.8	44.8	28	3	US-08-474-700B-7	Sequence 7, Appli
C 74	14.8	44.8	28	3	US-08-474-700B-33	Sequence 33, Appl
C 75	14.8	44.8	28	5	PCT-US95-05812-7	Sequence 7, Appli
C 76	14.8	44.8	28	5	PCT-US95-05812-33	Sequence 33, Appl
C 77	14.8	44.8	30	5	PCT-US93-00928-3	Sequence 3, Appli
78	14.8	44.8	33	1	US-08-438-639-47	Sequence 47, Appl
79	14.8	44.8	33	1	US-07-813-338A-47	Sequence 47, Appl
80	14.8	44.8	33	2	US-08-470-124-80	Sequence 80, Appl
81	14.8	44.8	33	3	US-08-441-971-123	Sequence 123, App
82	14.8	44.8	33	3	US-08-221-653-123	Sequence 123, App
83	14.8	44.8	33	3	US-09-034-205-63	Sequence 63, Appl
84	14.8	44.8	33	3	US-08-442-144A-123	Sequence 123, App
85	14.8	44.8	33	3	US-08-441-970-123	Sequence 123, App
86	14.8	44.8	33	3	US-09-677-218B-63	Sequence 63, Appl
87	14.8	44.8	33	3	US-09-677-192-63	Sequence 63, Appl
88	14.8	44.8	33	4	US-09-402-618B-63	Sequence 63, Appl
89	14.8	44.8	46	1	US-08-347-029-12	Sequence 12, Appl
90	14.8	44.8	46	5	PCT-US95-14932-12	Sequence 12, Appl
C 91	14.4	43.6	22	3	US-08-938-033-1	Sequence 1, Appli
C 92	14.4	43.6	22	4	US-09-311-487-1	Sequence 3, Appli
C 93	14.4	43.6	26	4	US-09-493-353-3	Sequence 3, Appli
C 94	14.4	43.6	41	3	US-08-813-507-79	Sequence 79, Appl
C 95	14.4	43.6	41	3	US-09-464-453-79	Sequence 79, Appl
C 96	14.2	43.0	30	4	US-09-151-409-9	Sequence 9, Appli
C 97	14.2	43.0	36	5	PCT-US91-02942-71	Sequence 71, Appl
C 98	14	42.4	26	4	US-10-353-589-3	Sequence 3, Appli
C 99	14	42.4	37	4	US-09-770-158-1	Sequence 1, Appli
C 100	14	42.4	38	4	US-09-474-432B-1107	Sequence 1107, Ap

c 101	14	42.4	38	4	US-09-476-387-1106	Sequence 1106, Ap	174	12.8	38.8	31	3	US-08-653-648A-39	Sequence 39, Appl
c 102	14	42.4	47	4	US-09-561-490E-27	Sequence 27, Appl	175	12.8	38.8	31	4	US-09-564-418-34	Sequence 34, Appl
c 103	13.8	41.8	20	3	US-08-397-220B-51	Sequence 51, Appl	c 176	12.8	38.8	32	1	US-07-882-838E-48	Sequence 48, Appl
c 104	13.8	41.8	20	3	US-08-650-093C-51	Sequence 51, Appl	c 177	12.8	38.8	37	3	US-08-479-744A-33	Sequence 33, Appl
c 105	13.8	41.8	25	4	US-08-866-108A-10985	Sequence 10985, A	c 178	12.8	38.8	37	3	US-08-280-757B-33	Sequence 33, Appl
c 106	13.8	41.8	34	3	US-09-257-584-30	Sequence 30, Appl	c 179	12.8	38.8	37	4	US-09-425-762-33	Sequence 33, Appl
c 107	13.8	41.8	37	5	US-08-341-560B-14	Sequence 14, Appl	c 180	12.8	38.8	39	3	US-09-018-545-5	Sequence 11, Appl
c 108	13.8	41.8	37	5	PCT-US93-03895-14	Sequence 14, Appl	c 181	12.8	38.8	39	4	US-09-940-173A-11	Sequence 11, Appl
c 109	13.8	41.8	40	2	US-09-485-737B-74	Sequence 74, Appl	c 182	12.8	38.8	39	4	US-09-730-893-11	Sequence 11, Appl
c 110	13.6	41.2	47	4	US-09-641-638-708	Sequence 708, App	c 183	12.8	38.8	40	1	US-08-258-283-1	Sequence 1, Appl
c 111	13.6	41.2	47	4	US-10-170-097-708	Sequence 708, App	c 184	12.8	38.8	40	5	PCT-US92-10359-1	Sequence 1, Appl
c 112	13.6	41.2	48	4	US-09-136-801-29	Sequence 29, Appl	c 185	12.8	38.8	41	3	US-08-813-507-80	Sequence 80, Appl
c 113	13.6	41.2	48	4	US-09-202-088A-29	Sequence 29, Appl	c 186	12.8	38.8	41	3	US-09-464-453-80	Sequence 80, Appl
c 114	13.4	40.6	27	3	US-09-149-922-46	Sequence 46, Appl	c 187	12.8	38.8	44	1	US-08-259-148A-28	Sequence 28, Appl
c 115	13.4	40.6	33	4	US-09-311-784A-104	Sequence 104, App	c 188	12.8	38.8	44	2	US-07-876-941A-44	Sequence 44, Appl
c 116	13.4	40.6	40	3	US-09-275-850-154	Sequence 154, App	c 189	12.8	38.8	48	3	US-08-849-567A-98	Sequence 98, Appl
c 117	13.4	40.6	47	4	US-09-422-978-1903	Sequence 1903, Ap	c 190	12.6	38.2	20	4	US-09-688-313A-164	Sequence 164, App
c 118	13.2	40.0	24	4	US-09-940-244-121	Sequence 121, App	c 191	12.6	38.2	20	4	US-09-953-318-111	Sequence 111, App
c 119	13.2	40.0	26	2	US-08-859-998-396	Sequence 396, App	c 192	12.6	38.2	22	1	US-08-152-621-11	Sequence 11, App
c 120	13.2	40.0	26	3	US-09-225-928-396	Sequence 396, App	c 193	12.6	38.2	22	5	PCT-US92-05035-11	Sequence 11, Appl
c 121	13.2	40.0	26	4	US-09-225-201B-396	Sequence 396, App	c 194	12.6	38.2	25	4	US-09-866-108A-10979	Sequence 10979, A
c 122	13.2	40.0	45	3	US-09-232-478-26	Sequence 26, Appl	c 195	12.6	38.2	25	4	US-09-866-108A-10980	Sequence 10980, A
c 123	13.2	40.0	45	4	US-09-785-055-26	Sequence 26, Appl	c 196	12.6	38.2	26	4	US-09-396-154-56	Sequence 56, Appl
c 124	13.2	40.0	47	4	US-09-422-978-3114	Sequence 3114, Ap	c 197	12.6	38.2	27	3	US-09-447-356-10	Sequence 10, Appl
c 125	13	39.4	15	1	US-08-182-968A-5	Sequence 5, Appl	c 198	12.6	38.2	28	2	US-08-859-998-418	Sequence 418, App
c 126	13	39.4	15	2	US-08-774-306A-5	Sequence 5, Appl	c 199	12.6	38.2	28	3	US-09-225-928-418	Sequence 418, App
c 127	13	39.4	15	3	US-09-064-156A-5	Sequence 5, Appl	c 200	12.6	38.2	28	4	US-09-225-201B-418	Sequence 418, App
c 128	13	39.4	20	3	US-08-397-220B-49	Sequence 49, Appl	c 201	12.6	38.2	29	4	US-09-304-232-329	Sequence 329, App
c 129	13	39.4	20	3	US-08-650-093C-49	Sequence 49, Appl	c 202	12.6	38.2	29	4	US-09-304-232-856	Sequence 856, App
c 130	13	39.4	24	3	US-09-521-668B-15	Sequence 15, Appl	c 203	12.6	38.2	34	4	US-09-474-432B-304	Sequence 304, App
c 131	13	39.4	25	4	US-09-866-108A-10981	Sequence 10981, A	c 204	12.6	38.2	35	2	US-07-829-461A-14	Sequence 14, Appl
c 132	13	39.4	25	4	US-09-866-108A-10982	Sequence 10982, A	c 205	12.6	38.2	35	3	US-09-197-649-15	Sequence 15, Appl
c 133	13	39.4	25	4	US-09-866-108A-10983	Sequence 10983, A	c 206	12.6	38.2	36	4	US-09-476-387-303	Sequence 303, App
c 134	13	39.4	25	4	US-09-866-108A-10984	Sequence 10984, A	c 207	12.6	38.2	36	4	US-09-474-432B-305	Sequence 305, App
c 135	13	39.4	25	4	US-09-866-108A-10986	Sequence 10986, A	c 208	12.6	38.2	36	4	US-09-125-491C-6	Sequence 6, Appl
c 136	13	39.4	25	4	US-09-866-108A-10987	Sequence 10987, A	c 209	12.6	38.2	37	4	US-09-476-387-304	Sequence 304, App
c 137	13	39.4	25	4	US-09-866-108A-10988	Sequence 10988, A	c 210	12.6	38.2	38	4	US-09-474-432B-1292	Sequence 1292, Ap
c 138	13	39.4	25	4	US-09-866-108A-10989	Sequence 10989, A	c 211	12.6	38.2	38	4	US-09-474-432B-1408	Sequence 1408, Ap
c 139	13	39.4	26	1	US-08-363-233B-6	Sequence 6, Appl	c 212	12.6	38.2	38	4	US-09-474-432B-1474	Sequence 1474, Ap
c 140	13	39.4	29	4	US-09-770-158-16	Sequence 16, Appl	c 213	12.6	38.2	38	4	US-09-476-387-1291	Sequence 1291, Ap
c 141	13	39.4	31	1	US-08-049-264C-47	Sequence 47, Appl	c 214	12.6	38.2	38	4	US-09-476-387-1407	Sequence 1407, Ap
c 142	13	39.4	31	1	US-08-049-264C-53	Sequence 47, Appl	c 215	12.6	38.2	38	4	US-09-388-089B-14	Sequence 1473, Ap
c 143	13	39.4	31	1	US-08-476-562-47	Sequence 53, Appl	c 216	12.6	38.2	42	5	PCT-US93-02457-4	Sequence 4, Appl
c 144	13	39.4	31	1	US-08-476-562-53	Sequence 53, Appl	c 217	12.6	38.2	42	5	PCT-US93-11458-5	Sequence 5, Appl
c 145	13	39.4	31	1	US-08-479-723A-47	Sequence 47, Appl	c 218	12.6	38.2	47	4	US-09-422-978-3558	Sequence 3558, Ap
c 146	13	39.4	31	1	US-08-479-723A-53	Sequence 53, Appl	c 219	12.6	38.2	47	4	US-09-474-432B-6	Sequence 6, Appl
c 147	13	39.4	31	5	PCT-US94-04310-47	Sequence 47, Appl	c 220	12.4	37.6	16	4	US-09-476-387-6	Sequence 6, Appl
c 148	13	39.4	31	5	PCT-US94-04310-53	Sequence 53, Appl	c 221	12.4	37.6	16	4	US-09-476-387-6	Sequence 6, Appl
c 149	13	39.4	32	4	US-09-322-409-138	Sequence 138, App	c 222	12.4	37.6	26	2	US-08-912-129A-19	Sequence 19, Appl
c 150	13	39.4	32	4	US-09-451-527-138	Sequence 138, App	c 223	12.4	37.6	26	4	US-08-547-602-1	Sequence 1, Appl
c 151	13	39.4	38	4	US-09-474-432B-915	Sequence 915, App	c 224	12.4	37.6	27	3	US-09-033-428-11	Sequence 11, Appl
c 152	13	39.4	38	4	US-09-474-432B-1160	Sequence 1160, Ap	c 225	12.4	37.6	27	4	US-09-033-556-24	Sequence 24, Appl
c 153	13	39.4	38	4	US-09-770-158-2	Sequence 2, Appl	c 226	12.4	37.6	27	4	US-09-474-699-17	Sequence 17, Appl
c 154	13	39.4	38	4	US-09-476-387-914	Sequence 914, App	c 227	12.4	37.6	27	4	US-09-898-883-11	Sequence 11, Appl
c 155	13	39.4	38	4	US-09-476-387-1159	Sequence 1159, Ap	c 228	12.4	37.6	27	4	US-09-151-376-49	Sequence 49, Appl
c 156	13	39.4	42	3	US-09-425-638A-6	Sequence 6, Appl	c 229	12.4	37.6	28	2	US-08-859-998-1084	Sequence 1084, Ap
c 157	13	39.4	42	3	US-09-543-004-6	Sequence 6, Appl	c 230	12.4	37.6	28	3	US-09-225-928-1084	Sequence 1084, Ap
c 158	13	39.4	47	4	US-09-422-978-3439	Sequence 3439, Ap	c 231	12.4	37.6	28	4	US-09-225-201B-1084	Sequence 1084, Ap
c 159	13	39.4	50	4	US-09-576-537-2	Sequence 2, Appl	c 232	12.4	37.6	30	2	US-08-860-882A-22	Sequence 22, Appl
c 160	13	39.4	50	4	US-09-519-859A-2	Sequence 2, Appl	c 233	12.4	37.6	30	4	US-09-011-769A-18	Sequence 18, Appl
c 161	13	39.4	50	4	US-09-519-859A-3	Sequence 3, Appl	c 234	12.4	37.6	32	1	US-08-055-390-8	Sequence 8, Appl
c 162	12.8	38.8	16	1	US-07-639-684A-4	Sequence 4, Appl	c 235	12.4	37.6	32	4	US-09-665-189A-49	Sequence 49, Appl
c 163	12.8	38.8	16	4	US-09-474-432B-7	Sequence 7, Appl	c 236	12.4	37.6	33	2	US-08-734-591A-105	Sequence 105, App
c 164	12.8	38.8	16	4	US-09-476-387-7	Sequence 7, Appl	c 237	12.4	37.6	33	3	US-08-470-335-105	Sequence 105, App
c 165	12.8	38.8	20	4	US-09-112-580-60	Sequence 60, Appl	c 238	12.4	37.6	33	3	US-08-734-664A-105	Sequence 105, App
c 166	12.8	38.8	26	1	US-08-379-078-559	Sequence 559, App	c 239	12.4	37.6	33	3	US-08-470-339-105	Sequence 105, App
c 167	12.8	38.8	26	3	US-07-974-409C-182	Sequence 182, App	c 240	12.4	37.6	33	4	US-08-467-602-105	Sequence 920, App
c 168	12.8	38.8	26	3	US-07-974-409C-228	Sequence 228, App	c 241	12.4	37.6	38	4	US-09-474-432B-939	Sequence 939, App
c 169	12.8	38.8	26	5	PCT-US93-00977-182	Sequence 182, App	c 242	12.4	37.6	38	4	US-09-474-432B-955	Sequence 955, App
c 170	12.8	38.8	26	5	PCT-US93-00977-228	Sequence 228, App	c 243	12.4	37.6	38	4	US-09-474-432B-980	Sequence 980, App
c 171	12.8	38.8	27	4	US-08-832-488-6	Sequence 6, Appl	c 244	12.4	37.6	38	4	US-09-474-432B-1007	Sequence 1007, Ap
c 172	12.8	38.8	27	4	US-08-832-488-10	Sequence 10, Appl	c 245	12.4	37.6	38	4	US-09-474-432B-1086	Sequence 1086, Ap
c 173	12.8	38.8	30	4	US-09-946-678-19	Sequence 19, Appl	c 246	12.4	37.6	38	4		

C 247	12.4	37.6	38	4	US-09-474-432B-1099	Sequence 1099, Appl	320	12.2	37.0	36	4	US-09-403-422-8	Sequence 8, Appli
C 248	12.4	37.6	38	4	US-09-474-432B-1237	Sequence 1237, Ap	321	12.2	37.0	37	1	US-08-423-691-5	Sequence 5, Appli
C 249	12.4	37.6	38	4	US-09-474-432B-1256	Sequence 1256, Ap	322	12.2	37.0	37	3	US-08-867-260-5	Sequence 5, Appli
C 250	12.4	37.6	38	4	US-09-474-432B-1404	Sequence 1404, Ap	323	12.2	37.0	37	3	US-08-706-945D-38	Sequence 38, Appl
C 251	12.4	37.6	38	4	US-09-476-387-919	Sequence 919, App	C 324	12.2	37.0	38	1	US-08-384-708A-188	Sequence 188, App
C 252	12.4	37.6	38	4	US-09-476-387-938	Sequence 938, App	C 325	12.2	37.0	38	2	US-08-455-976A-6	Sequence 6, Appli
C 253	12.4	37.6	38	4	US-09-476-387-954	Sequence 954, App	C 326	12.2	37.0	38	2	US-08-982-412-6	Sequence 6, Appli
C 254	12.4	37.6	38	4	US-09-476-387-979	Sequence 979, App	C 327	12.2	37.0	38	3	US-08-687-421-188	Sequence 188, App
C 255	12.4	37.6	38	4	US-09-476-387-1006	Sequence 1006, Ap	C 328	12.2	37.0	38	4	US-08-442-423-188	Sequence 188, App
C 256	12.4	37.6	38	4	US-09-476-387-1085	Sequence 1085, Ap	C 329	12.2	37.0	39	2	US-08-343-923-14	Sequence 14, Appl
C 257	12.4	37.6	38	4	US-09-476-387-1098	Sequence 1098, Ap	C 330	12.2	37.0	40	2	US-08-425-684-54	Sequence 54, Appl
C 258	12.4	37.6	38	4	US-09-476-387-1236	Sequence 1236, Ap	C 331	12.2	37.0	40	2	US-08-675-502-54	Sequence 54, Appl
C 259	12.4	37.6	38	4	US-09-476-387-1255	Sequence 1255, Ap	C 332	12.2	37.0	40	4	US-09-538-709-1192	Sequence 1192, Ap
C 260	12.4	37.6	38	4	US-09-476-387-1403	Sequence 1403, Ap	C 333	12.2	37.0	40	4	US-08-445-802-54	Sequence 54, Appl
C 261	12.4	37.6	41	4	US-09-674-677-33	Sequence 33, Appl	C 334	12.2	37.0	40	4	US-08-811-492-126	Sequence 126, App
C 262	12.4	37.6	47	4	US-09-671-317-830	Sequence 832, App	C 335	12.2	37.0	47	4	US-09-671-317-776	Sequence 776, App
C 263	12.4	37.6	47	4	US-09-422-978-930	Sequence 930, App	C 336	12.2	37.0	47	4	US-09-422-978-519	Sequence 519, App
C 264	12.4	37.6	47	4	US-09-422-978-2410	Sequence 2410, Ap	C 337	12.2	37.0	47	4	US-08-422-978-3353	Sequence 3353, Ap
C 265	12.2	37.0	17	3	US-08-946-138-27	Sequence 27, Appl	C 338	12.2	37.0	48	3	US-08-675-566-102	Sequence 102, App
C 266	12.2	37.0	17	4	US-09-907-795-2	Sequence 2, Appli	C 339	12.2	37.0	48	3	US-09-020-846-34	Sequence 34, Appl
C 267	12.2	37.0	17	4	US-09-865-108A-6089	Sequence 6089, Ap	C 340	12	36.4	20	3	US-09-034-205-60	Sequence 60, Appl
C 268	12.2	37.0	20	4	US-09-319-588C-21	Sequence 21, Appl	C 341	12	36.4	20	3	US-09-677-218B-60	Sequence 60, Appl
C 269	12.2	37.0	20	4	US-09-319-588C-88	Sequence 88, Appl	C 342	12	36.4	20	3	US-09-677-192-60	Sequence 60, Appl
C 270	12.2	37.0	22	3	US-09-339-622-8	Sequence 8, Appli	C 343	12	36.4	20	4	US-08-944-410-9	Sequence 9, Appli
C 271	12.2	37.0	23	3	US-08-840-551-2	Sequence 2, Appli	C 344	12	36.4	20	4	US-09-402-618B-60	Sequence 60, Appl
C 272	12.2	37.0	25	4	US-09-395-448-18	Sequence 18, Appl	C 345	12	36.4	21	1	US-08-379-078-581	Sequence 581, App
C 273	12.2	37.0	25	4	US-09-865-108A-14601	Sequence 14601, A	C 346	12	36.4	21	3	US-07-974-409C-204	Sequence 204, App
C 274	12.2	37.0	25	4	US-09-866-108A-14602	Sequence 14602, A	C 347	12	36.4	21	5	PCT-US93-00977-204	Sequence 204, App
C 275	12.2	37.0	25	4	US-09-925-796-18	Sequence 18, Appl	C 348	12	36.4	24	3	US-09-302-812-18	Sequence 18, Appl
C 276	12.2	37.0	25	4	US-09-941-450-18	Sequence 18, Appl	C 349	12	36.4	24	3	US-09-511-477-18	Sequence 18, Appl
C 277	12.2	37.0	26	3	US-08-859-998-575	Sequence 575, App	C 350	12	36.4	24	4	US-09-511-507-18	Sequence 18, Appl
C 278	12.2	37.0	26	3	US-09-225-928-575	Sequence 575, App	C 351	12	36.4	24	4	US-09-651-374A-10	Sequence 10, Appl
C 279	12.2	37.0	26	4	US-09-225-201B-575	Sequence 575, App	C 352	12	36.4	25	4	US-09-641-259B-33	Sequence 33, Appl
C 280	12.2	37.0	27	3	US-09-332-769-8	Sequence 8, Appli	C 353	12	36.4	25	4	US-09-866-108A-10990	Sequence 10990, A
C 281	12.2	37.0	27	3	US-09-257-584-14	Sequence 14, Appl	C 354	12	36.4	27	4	US-09-254-180C-61	Sequence 61, Appl
C 282	12.2	37.0	27	3	US-09-456-153-8	Sequence 8, Appli	C 355	12	36.4	27	4	US-08-284-180C-106	Sequence 106, App
C 283	12.2	37.0	27	3	US-09-456-627-8	Sequence 8, Appli	C 356	12	36.4	29	2	US-08-889-909A-14	Sequence 14, Appl
C 284	12.2	37.0	27	3	US-09-426-533-8	Sequence 8, Appli	C 357	12	36.4	29	3	US-09-156-163A-14	Sequence 14, Appl
C 285	12.2	37.0	27	3	US-09-609-205-9	Sequence 9, Appli	C 358	12	36.4	29	4	US-09-304-232-748	Sequence 748, App
C 286	12.2	37.0	27	3	US-09-516-945-8	Sequence 8, Appli	C 359	12	36.4	29	4	US-09-982-308B-14	Sequence 14, Appl
C 287	12.2	37.0	27	3	US-09-757-218-9	Sequence 9, Appli	C 360	12	36.4	30	1	US-08-186-229-30	Sequence 30, Appl
C 288	12.2	37.0	27	3	US-09-516-757-8	Sequence 8, Appli	C 361	12	36.4	30	2	US-08-470-124-30	Sequence 30, Appl
C 289	12.2	37.0	27	3	US-09-516-750-8	Sequence 8, Appli	C 362	12	36.4	32	4	US-09-586-216C-9	Sequence 9, Appli
C 290	12.2	37.0	27	3	US-09-342-577-9	Sequence 9, Appli	C 363	12	36.4	33	3	US-09-232-071-18	Sequence 18, Appl
C 291	12.2	37.0	27	3	US-09-516-756-8	Sequence 8, Appli	C 364	12	36.4	33	3	US-09-292-071-19	Sequence 19, Appl
C 292	12.2	37.0	27	3	US-09-828-061A-9	Sequence 9, Appli	C 365	12	36.4	33	3	US-09-292-069A-18	Sequence 18, Appl
C 293	12.2	37.0	27	3	US-09-463-917-8	Sequence 8, Appli	C 366	12	36.4	33	3	US-09-232-069A-19	Sequence 19, Appl
C 294	12.2	37.0	27	4	US-09-347-673-9	Sequence 9, Appli	C 367	12	36.4	33	3	US-09-418-721-18	Sequence 18, Appl
C 295	12.2	37.0	27	4	US-09-757-213-9	Sequence 9, Appli	C 368	12	36.4	33	3	US-09-155-107-42	Sequence 42, Appl
C 296	12.2	37.0	27	4	US-09-656-653-8	Sequence 8, Appli	C 369	12	36.4	33	3	US-09-767-013-18	Sequence 18, Appl
C 297	12.2	37.0	27	4	US-09-757-251-9	Sequence 9, Appli	C 370	12	36.4	33	4	US-09-767-013-19	Sequence 19, Appl
C 298	12.2	37.0	27	4	US-09-828-259A-9	Sequence 9, Appli	C 371	12	36.4	33	4	US-09-232-072-18	Sequence 18, Appl
C 299	12.2	37.0	27	4	US-09-713-878-9	Sequence 9, Appli	C 372	12	36.4	33	4	US-09-232-072-19	Sequence 19, Appl
C 300	12.2	37.0	27	4	US-09-757-217A-9	Sequence 9, Appli	C 373	12	36.4	33	4	US-09-232-072-19	Sequence 19, Appl
C 301	12.2	37.0	27	4	US-09-828-325A-9	Sequence 9, Appli	C 374	12	36.4	34	4	US-09-474-432B-207	Sequence 207, App
C 302	12.2	37.0	27	4	US-09-756-248-8	Sequence 8, Appli	C 375	12	36.4	35	2	US-08-889-909A-11	Sequence 11, Appl
C 303	12.2	37.0	28	3	US-09-341-955-2	Sequence 2, Appli	C 376	12	36.4	35	3	US-09-156-163A-11	Sequence 11, Appl
C 304	12.2	37.0	28	4	US-09-779-881-2	Sequence 2, Appli	C 377	12	36.4	35	4	US-09-982-308B-11	Sequence 11, Appl
C 305	12.2	37.0	29	2	US-08-859-998-410	Sequence 410, App	C 378	12	36.4	35	4	US-09-476-387-207	Sequence 207, App
C 306	12.2	37.0	29	3	US-09-225-928-410	Sequence 410, App	C 379	12	36.4	36	4	US-09-474-432B-208	Sequence 208, App
C 307	12.2	37.0	29	4	US-09-225-201B-410	Sequence 410, App	C 380	12	36.4	37	1	US-08-244-378A-25	Sequence 25, Appl
C 308	12.2	37.0	30	1	US-08-384-708A-50	Sequence 50, Appl	C 381	12	36.4	37	4	US-09-476-387-208	Sequence 208, App
C 309	12.2	37.0	30	3	US-08-687-421-50	Sequence 50, Appl	C 382	12	36.4	38	3	US-09-476-299-8	Sequence 8, Appli
C 310	12.2	37.0	30	4	US-08-442-423-50	Sequence 50, Appl	C 383	12	36.4	38	3	US-09-609-154-8	Sequence 8, Appli
C 311	12.2	37.0	31	2	US-08-484-933B-54	Sequence 54, Appl	C 384	12	36.4	38	4	US-09-474-432B-937	Sequence 937, App
C 312	12.2	37.0	31	2	US-08-484-158B-54	Sequence 54, Appl	C 385	12	36.4	38	4	US-09-474-432B-988	Sequence 988, App
C 313	12.2	37.0	31	2	US-08-484-596A-54	Sequence 54, Appl	C 386	12	36.4	38	4	US-09-474-432B-1333	Sequence 1333, Ap
C 314	12.2	37.0	31	2	US-08-480-150A-54	Sequence 54, Appl	C 387	12	36.4	38	4	US-09-474-432B-1362	Sequence 1362, Ap
C 315	12.2	37.0	31	3	US-08-458-731-54	Sequence 54, Appl	C 388	12	36.4	38	4	US-09-371-772B-11362	Sequence 11362, A
C 316	12.2	37.0	31	3	US-08-149-223A-54	Sequence 54, Appl	C 389	12	36.4	38	4	US-09-371-772B-11420	Sequence 11420, A
C 317	12.2	37.0	32	4	US-09-837-644-4	Sequence 4, Appli	C 390	12	36.4	38	4	US-09-371-772B-11559	Sequence 11559, A
C 318	12.2	37.0	33	4	US-08-706-945D-36	Sequence 36, Appl	C 391	12	36.4	38	4	US-09-371-772B-13652	Sequence 13652, A
C 319	12.2	37.0	34	4	US-09-491-522-13	Sequence 13, Appl	C 392	12	36.4	38	4	US-09-476-387-936	Sequence 936, App

C 393	12	36.4	38	4	US-09-476-387-987	Sequence 987, App	466	11.8	35.8	35	3	US-09-199-149-21	Sequence 21, Appl
C 394	12	36.4	38	4	US-09-476-387-1332	Sequence 1332, Ap	C 467	11.8	35.8	37	4	US-09-813-781-19	Sequence 19, Appl
C 395	12	36.4	38	4	US-09-476-387-1361	Sequence 1361, Ap	468	11.8	35.8	37	4	US-09-842-164A-19	Sequence 19, Appl
C 396	12	36.4	39	3	US-09-476-299-7	Sequence 7, Appl	469	11.8	35.8	37	5	PCT-US93-08067-11	Sequence 11, Appl
C 397	12	36.4	39	3	US-09-609-154-7	Sequence 7, Appl	C 470	11.8	35.8	38	4	US-09-968-255-15	Sequence 15, Appl
C 398	12	36.4	40	1	US-08-049-264C-31	Sequence 31, Appl	471	11.8	35.8	38	4	US-07-623-611-15	Sequence 15, Appl
C 399	12	36.4	40	1	US-08-476-562-31	Sequence 31, Appl	472	11.8	35.8	39	5	PCT-US91-09108-15	Sequence 15, Appl
C 400	12	36.4	40	1	US-08-479-723A-31	Sequence 31, Appl	473	11.8	35.8	41	4	US-08-962-281-24	Sequence 24, Appl
C 401	12	36.4	40	2	US-08-425-684-13	Sequence 13, Appl	474	11.8	35.8	41	4	US-08-962-281-26	Sequence 26, Appl
C 402	12	36.4	40	2	US-08-675-502-13	Sequence 13, Appl	475	11.8	35.8	41	4	US-08-962-281-28	Sequence 28, Appl
C 403	12	36.4	40	4	US-09-245-803-13	Sequence 13, Appl	476	11.8	35.8	41	4	US-08-962-281-36	Sequence 36, Appl
C 404	12	36.4	40	5	PCT-US94-04310-31	Sequence 31, Appl	C 477	11.8	35.8	42	3	US-09-146-319-3	Sequence 3, Appl
C 405	12	36.4	42	3	US-09-306-405-28	Sequence 28, Appl	C 478	11.8	35.8	42	3	US-09-175-973-3	Sequence 3, Appl
C 406	12	36.4	45	4	US-09-518-914-18	Sequence 18, Appl	479	11.8	35.8	42	3	US-09-425-638A-5	Sequence 5, Appl
C 407	12	36.4	47	4	US-09-671-317-712	Sequence 712, App	480	11.8	35.8	42	3	US-09-543-004-5	Sequence 5, Appl
C 408	12	36.4	48	4	US-10-165-857-4	Sequence 4, Appl	C 481	11.8	35.8	46	3	US-08-916-576B-25	Sequence 25, Appl
C 409	12	36.4	50	4	US-09-443-199C-4	Sequence 4, Appl	C 482	11.8	35.8	47	1	US-07-720-222-42	Sequence 42, Appl
C 410	12	36.4	50	5	PCT-US93-01901-26	Sequence 26, Appl	C 483	11.8	35.8	47	1	US-09-641-638-1069	Sequence 1069, Ap
C 411	11.8	35.8	15	1	US-08-502-185-22	Sequence 22, Appl	484	11.8	35.8	47	4	US-09-538-709-127	Sequence 127, App
C 412	11.8	35.8	15	1	US-08-398-945-22	Sequence 22, Appl	485	11.8	35.8	47	4	US-09-538-709-1294	Sequence 831, App
C 413	11.8	35.8	15	1	US-08-501-779-22	Sequence 22, Appl	C 486	11.8	35.8	47	4	US-09-671-317-831	Sequence 831, App
C 414	11.8	35.8	15	1	US-08-501-713-22	Sequence 22, Appl	C 487	11.8	35.8	47	4	US-09-422-978-1323	Sequence 1323, Ap
C 415	11.8	35.8	15	1	US-08-378-860-22	Sequence 22, Appl	C 488	11.8	35.8	47	4	US-09-422-978-1414	Sequence 1414, Ap
C 416	11.8	35.8	15	1	US-08-501-356-22	Sequence 22, Appl	C 489	11.8	35.8	47	4	US-09-422-978-1414	Sequence 2548, Ap
C 417	11.8	35.8	15	1	US-08-501-356-22	Sequence 22, Appl	C 490	11.8	35.8	47	4	US-09-422-978-1414	Sequence 1069, Ap
C 418	11.8	35.8	16	2	US-08-292-620A-1617	Sequence 1617, Ap	C 491	11.8	35.8	48	1	US-08-399-412A-104	Sequence 104, App
C 419	11.8	35.8	16	3	US-09-071-845-1617	Sequence 1617, Ap	C 492	11.8	35.8	48	2	US-08-615-961-13	Sequence 13, Appl
C 420	11.8	35.8	17	2	US-08-757-653-152	Sequence 152, App	493	11.8	35.8	48	3	US-09-485-737B-23	Sequence 23, Appl
C 421	11.8	35.8	17	3	US-08-520-948-152	Sequence 152, App	494	11.8	35.8	50	1	US-08-207-901-90	Sequence 90, Appl
C 422	11.8	35.8	17	4	US-09-655-378A-152	Sequence 152, App	495	11.6	35.2	18	2	US-09-156-424-25	Sequence 25, Appl
C 423	11.8	35.8	17	4	US-09-866-108A-6087	Sequence 6087, Ap	496	11.6	35.2	18	4	US-03-387-341-39	Sequence 39, Appl
C 424	11.8	35.8	17	4	US-09-866-108A-6088	Sequence 6088, Ap	497	11.6	35.2	19	4	US-09-387-341-7	Sequence 7, Appl
C 425	11.8	35.8	20	1	US-08-502-185-21	Sequence 21, Appl	C 499	11.6	35.2	20	3	US-09-392-580-25	Sequence 25, Appl
C 426	11.8	35.8	20	1	US-08-398-945-21	Sequence 21, Appl	C 500	11.6	35.2	20	4	US-09-780-173A-26	Sequence 26, Appl
C 427	11.8	35.8	20	1	US-08-501-779-21	Sequence 21, Appl	C 501	11.6	35.2	20	4	US-08-894-454-60	Sequence 60, Appl
C 428	11.8	35.8	20	1	US-08-501-713-21	Sequence 21, Appl	C 502	11.6	35.2	21	3	US-09-153-947-5	Sequence 5, Appl
C 429	11.8	35.8	20	1	US-08-378-860-21	Sequence 21, Appl	503	11.6	35.2	21	4	US-09-657-472-1611	Sequence 1611, Ap
C 430	11.8	35.8	20	1	US-08-531-556-71	Sequence 71, Appl	504	11.6	35.2	22	1	US-08-283-203-13	Sequence 13, Appl
C 431	11.8	35.8	20	1	US-08-472-416-71	Sequence 71, Appl	505	11.6	35.2	22	3	US-09-475-316A-102	Sequence 102, App
C 432	11.8	35.8	20	1	US-08-501-626-21	Sequence 21, Appl	506	11.6	35.2	22	4	US-09-704-640-102	Sequence 102, App
C 433	11.8	35.8	20	1	US-08-501-356-21	Sequence 21, Appl	C 507	11.6	35.2	23	4	US-09-527-030G-155	Sequence 155, App
C 434	11.8	35.8	20	2	US-08-753-979A-25	Sequence 25, Appl	C 508	11.6	35.2	23	4	US-09-928-385B-15	Sequence 15, Appl
C 435	11.8	35.8	20	3	US-09-296-280-36	Sequence 36, Appl	509	11.6	35.2	23	4	US-09-379-888B-19	Sequence 19, Appl
C 436	11.8	35.8	20	3	US-09-686-179A-11	Sequence 11, Appl	C 510	11.6	35.2	24	1	US-08-758-626-10	Sequence 10, Appl
C 437	11.8	35.8	20	4	US-09-198-452A-5638	Sequence 5638, Ap	C 511	11.6	35.2	24	2	US-08-912-976-19	Sequence 19, Appl
C 438	11.8	35.8	20	4	US-09-509-595-36	Sequence 36, Appl	512	11.6	35.2	24	2	US-08-632-575B-56	Sequence 56, Appl
C 439	11.8	35.8	20	4	US-09-981-621-11	Sequence 11, Appl	513	11.6	35.2	24	4	US-09-199-542B-56	Sequence 56, Appl
C 440	11.8	35.8	22	4	US-09-528-348-5	Sequence 5, Appl	514	11.6	35.2	24	4	US-09-514-907A-4	Sequence 4, Appl
C 441	11.8	35.8	24	3	US-08-891-292A-90	Sequence 90, Appl	515	11.6	35.2	24	4	US-09-896-994-4	Sequence 4, Appl
C 442	11.8	35.8	24	4	US-09-927-737C-90	Sequence 90, Appl	C 516	11.6	35.2	24	5	PCT-US94-07684-10	Sequence 10, Appl
C 443	11.8	35.8	25	1	US-08-502-185-23	Sequence 23, Appl	C 517	11.6	35.2	25	4	US-09-866-108A-10978	Sequence 10978, A
C 444	11.8	35.8	25	1	US-08-398-945-23	Sequence 23, Appl	C 518	11.6	35.2	26	5	PCT-US92-04426-2	Sequence 2, Appl
C 445	11.8	35.8	25	1	US-08-501-779-23	Sequence 23, Appl	C 519	11.6	35.2	27	5	US-08-758-626-31	Sequence 31, Appl
C 446	11.8	35.8	25	1	US-08-501-713-23	Sequence 23, Appl	C 520	11.6	35.2	27	5	PCT-US94-07684-31	Sequence 31, Appl
C 447	11.8	35.8	25	1	US-08-378-860-23	Sequence 23, Appl	C 521	11.6	35.2	28	3	US-08-933-358-14	Sequence 14, Appl
C 448	11.8	35.8	25	1	US-08-501-626-23	Sequence 23, Appl	C 522	11.6	35.2	29	1	US-07-642-734C-8	Sequence 8, Appl
C 449	11.8	35.8	25	3	US-08-501-356-23	Sequence 23, Appl	C 523	11.6	35.2	29	3	US-08-439-009A-8	Sequence 8, Appl
C 450	11.8	35.8	25	3	US-09-103-577A-10	Sequence 10, Appl	C 524	11.6	35.2	29	3	US-08-613-298-2	Sequence 2, Appl
C 451	11.8	35.8	26	1	US-08-460-344-17	Sequence 17, Appl	C 525	11.6	35.2	29	4	US-09-810-506-4	Sequence 4, Appl
C 452	11.8	35.8	26	1	US-08-133-598A-17	Sequence 17, Appl	C 526	11.6	35.2	29	4	US-09-810-506-4	Sequence 4, Appl
C 453	11.8	35.8	26	1	US-08-886-999-17	Sequence 17, Appl	C 527	11.6	35.2	29	5	PCT-US95-04971-2	Sequence 2, Appl
C 454	11.8	35.8	26	3	US-09-117-860-47	Sequence 47, Appl	C 528	11.6	35.2	30	1	US-07-854-596B-21	Sequence 21, Appl
C 455	11.8	35.8	26	5	PCT-US93-05085-17	Sequence 17, Appl	C 529	11.6	35.2	30	2	US-08-676-378-1	Sequence 1, Appl
C 456	11.8	35.8	28	3	US-08-839-624-35	Sequence 35, Appl	C 530	11.6	35.2	30	3	US-08-899-595-10	Sequence 10, Appl
C 457	11.8	35.8	28	3	US-09-150-812-35	Sequence 35, Appl	C 531	11.6	35.2	31	3	US-09-248-588-20	Sequence 20, Appl
C 458	11.8	35.8	29	2	US-08-721-684C-5	Sequence 5, Appl	C 532	11.6	35.2	31	3	US-09-651-656-54	Sequence 54, Appl
C 459	11.8	35.8	29	2	US-09-005-970-5	Sequence 5, Appl	C 533	11.6	35.2	31	3	US-09-650-855-54	Sequence 54, Appl
C 460	11.8	35.8	29	3	US-09-407-715-5	Sequence 5, Appl	534	11.6	35.2	31	5	PCT-US94-04208-9	Sequence 9, Appl
C 461	11.8	35.8	31	1	US-08-578-649-6	Sequence 6, Appl	C 535	11.6	35.2	31	5	PCT-US94-04208-10	Sequence 10, Appl
C 462	11.8	35.8	33	1	US-08-050-319B-13	Sequence 13, Appl	C 536	11.6	35.2	32	4	US-09-410-935B-12	Sequence 12, Appl
C 463	11.8	35.8	33	2	US-08-465-982-13	Sequence 13, Appl	C 537	11.6	35.2	32	4	US-09-780-403A-12	Sequence 12, Appl
C 464	11.8	35.8	34	4	US-09-617-548-10	Sequence 10, Appl	C 538	11.6	35.2	33	1	US-08-051-935A-27	Sequence 27, Appl
C 465	11.8	35.8	35	1	US-08-361-337-49	Sequence 49, Appl							

C 539	11.6	35.2	33	3	US-08-840-062-11	Sequence 11, Appl	612	11.4	34.5	24	5	PCT-US95-16766-16	Sequence 16, Appl
C 540	11.6	35.2	33	4	US-09-302-765-2	Sequence 2, Appl	C 613	11.4	34.5	25	2	US-08-743-637B-124	Sequence 124, App
C 541	11.6	35.2	34	4	US-09-474-432B-270	Sequence 270, Appl	C 614	11.4	34.5	25	2	US-08-743-637B-270	Sequence 270, App
C 542	11.6	35.2	34	5	PCT-US93-00031-2	Sequence 2, Appl	C 615	11.4	34.5	25	3	US-08-526-840B-124	Sequence 124, Appl
C 543	11.6	35.2	35	1	US-08-464-531-62	Sequence 62, Appl	C 616	11.4	34.5	25	3	US-09-306-595C-41	Sequence 41, Appl
C 544	11.6	35.2	35	2	US-08-461-598-62	Sequence 62, Appl	C 617	11.4	34.5	25	4	US-09-925-388-41	Sequence 41, Appl
C 545	11.6	35.2	35	3	US-08-322-137-62	Sequence 62, Appl	C 618	11.4	34.5	25	4	US-08-866-108A-14597	Sequence 14597, A
C 546	11.6	35.2	35	3	US-08-936-632B-18	Sequence 18, Appl	C 619	11.4	34.5	25	4	US-09-866-108A-14598	Sequence 14598, A
C 547	11.6	35.2	35	3	US-08-582-333A-70	Sequence 70, Appl	C 620	11.4	34.5	25	4	US-09-866-108A-14599	Sequence 14599, A
C 548	11.6	35.2	35	4	US-09-476-387-269	Sequence 269, Appl	C 621	11.4	34.5	25	4	US-08-866-108A-14600	Sequence 14600, A
C 549	11.6	35.2	36	2	US-08-782-760-1	Sequence 1, Appl	C 622	11.4	34.5	26	1	US-08-469-202-5	Sequence 5, Appl
C 550	11.6	35.2	36	4	US-09-940-244-404	Sequence 404, Appl	C 623	11.4	34.5	26	1	US-08-484-434C-5	Sequence 5, Appl
C 551	11.6	35.2	36	5	PCT-US96-00995-1	Sequence 1, Appl	C 624	11.4	34.5	26	4	US-09-384-361-5	Sequence 5, Appl
C 552	11.6	35.2	37	3	US-08-435-568A-29	Sequence 29, Appl	C 625	11.4	34.5	27	4	US-09-758-282B-137	Sequence 137, Appl
C 553	11.6	35.2	37	3	US-08-822-516-9	Sequence 9, Appl	C 626	11.4	34.5	27	4	US-09-577-304A-137	Sequence 137, Appl
C 554	11.6	35.2	37	3	US-09-131-684-9	Sequence 9, Appl	C 627	11.4	34.5	28	4	US-09-331-793-39	Sequence 39, Appl
C 555	11.6	35.2	38	1	US-08-418-859-37	Sequence 37, Appl	C 628	11.4	34.5	29	1	US-08-307-444A-20	Sequence 20, Appl
C 556	11.6	35.2	38	2	US-08-643-181-37	Sequence 37, Appl	C 629	11.4	34.5	29	1	US-08-587-389-20	Sequence 20, Appl
C 557	11.6	35.2	38	4	US-09-474-432B-1090	Sequence 1090, Appl	C 630	11.4	34.5	29	3	US-08-403-066A-6	Sequence 6, Appl
C 558	11.6	35.2	38	4	US-09-474-432B-1121	Sequence 1121, Appl	C 631	11.4	34.5	29	4	US-09-470-276-43	Sequence 43, Appl
C 559	11.6	35.2	38	4	US-09-474-432B-1224	Sequence 1224, Appl	C 632	11.4	34.5	30	3	US-08-444-818-180	Sequence 180, Appl
C 560	11.6	35.2	38	4	US-09-474-432B-1316	Sequence 1316, Appl	C 633	11.4	34.5	30	4	US-09-733-042-41	Sequence 41, Appl
C 561	11.6	35.2	38	4	US-09-474-432B-1345	Sequence 1345, Appl	C 634	11.4	34.5	30	4	US-09-747-391-274	Sequence 274, Appl
C 562	11.6	35.2	38	4	US-09-371-772B-12294	Sequence 12294, A	C 635	11.4	34.5	30	5	PCT-US95-14418-16	Sequence 16, Appl
C 563	11.6	35.2	38	4	US-09-476-387-1089	Sequence 1089, Appl	C 636	11.4	34.5	30	5	PCT-US95-15327-16	Sequence 16, Appl
C 564	11.6	35.2	38	4	US-09-476-387-1120	Sequence 1120, Appl	C 637	11.4	34.5	30	5	PCT-US95-15327-17	Sequence 17, Appl
C 565	11.6	35.2	38	4	US-09-476-387-1223	Sequence 1223, Appl	C 638	11.4	34.5	31	2	US-08-961-749-5	Sequence 5, Appl
C 566	11.6	35.2	38	4	US-09-476-387-1315	Sequence 1315, Appl	C 639	11.4	34.5	31	2	US-08-164-664-2	Sequence 2, Appl
C 567	11.6	35.2	38	4	US-09-476-387-1344	Sequence 1344, Appl	C 640	11.4	34.5	31	3	US-09-569-601A-8	Sequence 8, Appl
C 568	11.6	35.2	40	2	US-08-031-538-15	Sequence 15, Appl	C 641	11.4	34.5	32	4	US-08-538-875-71	Sequence 71, Appl
C 569	11.6	35.2	40	2	US-08-031-538-16	Sequence 16, Appl	C 642	11.4	34.5	33	1	US-08-469-526A-105	Sequence 105, Appl
C 570	11.6	35.2	40	6	5519127-27	Patent No. 5519127	C 643	11.4	34.5	33	1	US-08-951-822-8	Sequence 8, Appl
C 571	11.6	35.2	41	3	US-09-142-355B-3	Sequence 3, Appl	C 644	11.4	34.5	33	2	US-09-368-951-8	Sequence 8, Appl
C 572	11.6	35.2	41	4	US-09-699-931-3	Sequence 3, Appl	C 645	11.4	34.5	33	3	US-09-229-947-8	Sequence 8, Appl
C 573	11.6	35.2	41	7	US-08-814-806-26	Sequence 26, Appl	C 646	11.4	34.5	33	4	US-08-829-931-3	Sequence 3, Appl
C 574	11.6	35.2	45	3	US-09-217-228-4	Sequence 4, Appl	C 647	11.4	34.5	33	4	US-08-569-150A-20	Sequence 20, Appl
C 575	11.6	35.2	45	3	US-09-410-935B-17	Sequence 17, Appl	C 648	11.4	34.5	34	2	US-08-537-402-2	Sequence 2, Appl
C 576	11.6	35.2	45	4	US-09-293-854-26	Sequence 26, Appl	C 649	11.4	34.5	35	2	US-09-014-416-12	Sequence 12, Appl
C 577	11.6	35.2	45	4	US-09-784-403A-17	Sequence 17, Appl	C 650	11.4	34.5	35	3	PCT-US96-06224-5	Sequence 5, Appl
C 578	11.6	35.2	47	1	US-07-990-303A-1	Sequence 1, Appl	C 651	11.4	34.5	35	5	US-08-154-916-7	Sequence 7, Appl
C 579	11.6	35.2	47	1	US-08-196-103A-1	Sequence 1, Appl	C 652	11.4	34.5	36	1	US-08-455-860-6	Sequence 6, Appl
C 580	11.6	35.2	47	1	US-08-357-396-1	Sequence 1, Appl	C 653	11.4	34.5	36	1	US-08-383-749-6	Sequence 6, Appl
C 581	11.6	35.2	47	1	US-08-386-141-1	Sequence 1, Appl	C 654	11.4	34.5	36	1	US-08-600-908A-8	Sequence 8, Appl
C 582	11.6	35.2	47	2	US-08-659-567-16	Sequence 16, Appl	C 655	11.4	34.5	36	2	US-08-683-838A-8	Sequence 8, Appl
C 583	11.6	35.2	47	4	US-09-422-978-345	Sequence 345, Appl	C 656	11.4	34.5	36	3	US-09-182-859-11	Sequence 11, Appl
C 584	11.6	35.2	47	4	US-09-422-978-1841	Sequence 1841, Appl	C 657	11.4	34.5	36	3	US-09-537-168-10	Sequence 10, Appl
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C 586	11.6	35.2	47	4	US-09-409-926-33	Sequence 33, Appl	C 659	11.4	34.5	36	4	US-09-636-252A-8	Sequence 8, Appl
C 587	11.6	35.2	49	3	US-09-109-063-28	Sequence 28, Appl	C 660	11.4	34.5	36	4	US-09-169-205D-18	Sequence 18, Appl
C 588	11.6	35.2	49	3	US-09-109-063-29	Sequence 29, Appl	C 661	11.4	34.5	36	4	US-09-474-432B-200	Sequence 200, Appl
C 589	11.6	35.2	49	4	US-09-448-310-28	Sequence 28, Appl	C 662	11.4	34.5	36	4	US-09-474-432B-219	Sequence 219, Appl
C 590	11.6	35.2	49	4	US-09-448-310-29	Sequence 29, Appl	C 663	11.4	34.5	36	4	US-09-474-432B-249	Sequence 249, Appl
C 591	11.6	35.2	50	3	US-09-390-867A-12	Sequence 12, Appl	C 664	11.4	34.5	36	4	US-09-474-432B-255	Sequence 255, Appl
C 592	11.6	35.2	50	3	US-09-548-260-12	Sequence 12, Appl	C 665	11.4	34.5	36	4	US-10-186-042-11	Sequence 11, Appl
C 593	11.4	34.5	21	2	US-08-832-449A-2	Sequence 2, Appl	C 666	11.4	34.5	37	1	US-08-709-912-47	Sequence 47, Appl
C 594	11.4	34.5	21	4	US-09-447-103A-11	Sequence 11, Appl	C 667	11.4	34.5	37	1	US-09-047-370-47	Sequence 47, Appl
C 595	11.4	34.5	22	1	US-08-400-580A-7	Sequence 7, Appl	C 668	11.4	34.5	37	2	US-09-477-135A-150	Sequence 150, Appl
C 596	11.4	34.5	22	2	US-08-068-729-2	Sequence 2, Appl	C 669	11.4	34.5	37	4	US-09-476-387-200	Sequence 200, Appl
C 597	11.4	34.5	22	3	US-09-255-671-2	Sequence 2, Appl	C 670	11.4	34.5	37	4	US-09-476-387-219	Sequence 219, Appl
C 598	11.4	34.5	22	4	US-09-393-366-2	Sequence 2, Appl	C 671	11.4	34.5	37	4	US-09-476-387-248	Sequence 248, Appl
C 599	11.4	34.5	22	4	US-09-371-615A-4	Sequence 4, Appl	C 672	11.4	34.5	37	4	US-09-476-387-254	Sequence 254, Appl
C 600	11.4	34.5	22	4	US-09-589-560B-80	Sequence 80, Appl	C 673	11.4	34.5	37	4	US-08-811-463-10	Sequence 10, Appl
C 601	11.4	34.5	23	5	PCT-US94-05085A-16	Sequence 16, Appl	C 674	11.4	34.5	38	3	US-09-474-432B-908	Sequence 908, Appl
C 602	11.4	34.5	23	5	PCT-US94-05085-16	Sequence 16, Appl	C 675	11.4	34.5	38	4	US-09-474-432B-1134	Sequence 1134, Appl
C 603	11.4	34.5	24	1	US-08-360-096-7	Sequence 7, Appl	C 676	11.4	34.5	38	4	US-09-474-432B-1152	Sequence 1152, Appl
C 604	11.4	34.5	24	1	US-08-538-875-35	Sequence 35, Appl	C 677	11.4	34.5	38	4	US-09-474-432B-1168	Sequence 1168, Appl
C 605	11.4	34.5	24	2	US-08-812-003-6	Sequence 6, Appl	C 678	11.4	34.5	38	4	US-09-474-432B-1265	Sequence 1265, Appl
C 606	11.4	34.5	24	2	US-08-899-371-18	Sequence 18, Appl	C 679	11.4	34.5	38	4	US-09-474-432B-1416	Sequence 1416, Appl
C 607	11.4	34.5	24	2	US-08-859-998-754	Sequence 754, Appl	C 680	11.4	34.5	38	4	US-09-371-772B-7971	Sequence 7971, Appl
C 608	11.4	34.5	24	3	US-08-576-202-16	Sequence 16, Appl	C 681	11.4	34.5	38	4	US-09-371-772B-7980	Sequence 7980, Appl
C 609	11.4	34.5	24	3	US-09-225-928-754	Sequence 754, Appl	C 682	11.4	34.5	38	4	US-09-371-772B-10799	Sequence 10799, A
C 610	11.4	34.5	24	4	US-09-538-709-262	Sequence 262, Appl	C 683	11.4	34.5	38	4	US-09-371-772B-10896	Sequence 10896, A
C 611	11.4	34.5	24	4	US-09-225-201B-754	Sequence 754, Appl	C 684	11.4	34.5	38	4		

C 831	11.2	33.9	32	4	US-09-440-781-1	Sequence 1, Appli	C 904	11.2	33.9	47	4	US-09-422-978-1214	Sequence 1214, Ap
C 832	11.2	33.9	33	1	US-08-045-284A-2	Sequence 2, Appli	C 905	11.2	33.9	47	4	US-09-422-978-3860	Sequence 3860, Ap
C 833	11.2	33.9	33	1	US-08-328-592-6	Sequence 6, Appli	C 906	11.2	33.9	47	4	US-08-454-898G-79	Sequence 79, Appl
C 834	11.2	33.9	33	3	US-08-464-514-23	Sequence 23, Appl	C 907	11.2	33.9	49	4	US-09-538-709-1020	Sequence 1020, Ap
C 835	11.2	33.9	33	3	US-08-486-403-23	Sequence 23, Appl	C 908	11.2	33.9	50	3	US-09-336-643A-67	Sequence 67, Appl
C 836	11.2	33.9	34	3	US-08-469-318-170	Sequence 170, App	C 909	11.2	33.9	50	4	US-08-706-054A-7	Sequence 7, Appli
C 837	11.2	33.9	34	3	US-08-468-609A-170	Sequence 170, App	C 910	11.2	33.9	50	4	US-09-313-299-7	Sequence 7, Appli
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C 839	11.2	33.9	34	3	US-08-469-712A-51	Sequence 51, Appl	C 912	11.2	33.9	50	4	US-08-781-986A-5135	Sequence 5135, Ap
C 840	11.2	33.9	34	3	US-08-974-549A-482	Sequence 482, App	C 913	11.2	33.9	50	4	US-09-034-205-12	Sequence 12, Appl
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C 843	11.2	33.9	34	3	US-08-446-872A-170	Sequence 170, App	C 916	11.2	33.9	50	4	US-08-677-218B-12	Sequence 12, Appl
C 844	11.2	33.9	34	3	US-08-468-910-51	Sequence 51, Appl	C 917	11.2	33.9	50	4	US-09-677-192-12	Sequence 12, Appl
C 845	11.2	33.9	34	4	US-08-761-907-51	Sequence 51, Appl	C 918	11.2	33.9	50	4	US-09-402-618B-12	Sequence 12, Appl
C 846	11.2	33.9	34	4	US-08-762-227A-170	Sequence 170, App	C 919	11.2	33.9	50	4	US-09-825-574-12	Sequence 12, Appl
C 847	11.2	33.9	34	4	US-08-912-951-249	Sequence 249, App	C 920	11.2	33.9	50	4	US-09-676-768-12	Sequence 12, Appl
C 848	11.2	33.9	34	4	US-09-402-181B-482	Sequence 482, App	C 921	11.2	33.9	50	4	US-09-034-205-62	Sequence 62, Appl
C 849	11.2	33.9	34	4	US-09-721-456-482	Sequence 482, App	C 922	11.2	33.9	50	4	US-09-677-218B-62	Sequence 62, Appl
C 850	11.2	33.9	34	5	PCT-US95-01185-170	Sequence 170, App	C 923	11.2	33.9	50	4	US-09-677-192-62	Sequence 62, Appl
C 851	11.2	33.9	36	1	US-08-173-497-29	Sequence 29, Appl	C 924	11.2	33.9	50	4	US-09-402-618B-62	Sequence 62, Appl
C 852	11.2	33.9	36	1	US-08-286-889-29	Sequence 29, Appl	C 925	11.2	33.9	50	4	US-08-485-942A-80	Sequence 80, Appl
C 853	11.2	33.9	36	1	US-08-485-618-29	Sequence 29, Appl	C 926	11.2	33.9	50	4	US-08-488-214A-80	Sequence 80, Appl
C 854	11.2	33.9	36	1	US-08-309-512-59	Sequence 59, Appl	C 927	11.2	33.9	50	4	US-08-488-208A-80	Sequence 80, Appl
C 855	11.2	33.9	36	1	US-08-362-652-29	Sequence 29, Appl	C 928	11.2	33.9	50	4	US-08-483-211A-80	Sequence 80, Appl
C 856	11.2	33.9	36	1	US-08-602-672-29	Sequence 29, Appl	C 929	11.2	33.9	50	4	US-08-488-223A-80	Sequence 80, Appl
C 857	11.2	33.9	36	2	US-08-482-293A-29	Sequence 29, Appl	C 930	11.2	33.9	50	4	US-08-438-431A-80	Sequence 80, Appl
C 858	11.2	33.9	36	2	US-08-943-363-29	Sequence 29, Appl	C 931	11.2	33.9	50	4	US-08-488-225A-80	Sequence 80, Appl
C 859	11.2	33.9	36	3	US-09-193-043-29	Sequence 29, Appl	C 932	11.2	33.9	50	4	US-08-104-072B-23	Sequence 23, Appl
C 860	11.2	33.9	36	3	US-09-275-850-219	Sequence 219, App	C 933	11.2	33.9	50	4	US-08-371-001-1	Sequence 1, Appli
C 861	11.2	33.9	36	4	US-08-688-307A-29	Sequence 29, Appl	C 934	11.2	33.9	50	4	US-08-640-672-12	Sequence 12, Appl
C 862	11.2	33.9	36	4	US-08-350-259-29	Sequence 29, Appl	C 935	11.2	33.9	50	4	US-08-684-498A-12	Sequence 12, Appl
C 863	11.2	33.9	37	1	US-09-931-103-5	Sequence 5, Appli	C 936	11.2	33.9	50	4	US-08-577-858A-12	Sequence 12, Appl
C 864	11.2	33.9	37	1	US-08-086-428B-134	Sequence 134, App	C 937	11.2	33.9	50	4	US-08-776-900C-25	Sequence 25, Appl
C 865	11.2	33.9	37	1	US-08-431-080-10	Sequence 10, Appl	C 938	11.2	33.9	50	4	US-09-289-267-107	Sequence 107, App
C 866	11.2	33.9	37	2	US-08-468-570-134	Sequence 134, App	C 939	11.2	33.9	50	4	US-09-288-195C-25	Sequence 25, Appl
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C 868	11.2	33.9	37	2	US-08-938-534-10	Sequence 5, Appli	C 941	11.2	33.9	50	4	US-08-397-220B-52	Sequence 52, Appl
C 869	11.2	33.9	37	2	US-08-737-271-5	Sequence 5, Appli	C 942	11.2	33.9	50	4	US-09-502-600-10	Sequence 10, Appl
C 870	11.2	33.9	37	3	US-09-058-555-5	Sequence 5, Appli	C 943	11.2	33.9	50	4	US-09-039-211C-10	Sequence 10, Appl
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C 872	11.2	33.9	37	4	US-08-466-601A-134	Sequence 134, App	C 945	11.2	33.9	50	4	US-08-650-093C-52	Sequence 52, Appl
C 873	11.2	33.9	37	4	US-09-485-147A-30	Sequence 30, App	C 946	11.2	33.9	50	4	US-09-167-109-59	Sequence 59, Appl
C 874	11.2	33.9	37	5	PCT-US95-10398-238	Sequence 238, App	C 947	11.2	33.9	50	4	US-09-861-966-10	Sequence 10, Appl
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C 876	11.2	33.9	39	2	US-08-244-548-2	Sequence 2, Appli	C 949	11.2	33.9	50	4	US-09-918-243-10	Sequence 10, Appl
C 877	11.2	33.9	39	3	US-08-850-961-41	Sequence 41, Appl	C 950	11.2	33.9	50	4	US-09-232-785-367	Sequence 367, App
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C 879	11.2	33.9	39	3	US-08-564-805-152	Sequence 152, App	C 952	11.2	33.9	50	4	PCT-US96-00331-1	Sequence 1, Appli
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C 881	11.2	33.9	39	4	US-09-335-011-14	Sequence 14, Appl	C 954	11.2	33.9	50	4	US-08-317-432A-27	Sequence 27, Appl
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C 883	11.2	33.9	40	1	US-08-284-516C-66	Sequence 66, Appl	C 956	11.2	33.9	50	4	US-09-023-082A-86	Sequence 86, Appl
C 884	11.2	33.9	40	3	US-08-952-793-228	Sequence 228, App	C 957	11.2	33.9	50	4	US-09-371-710-14	Sequence 14, Appl
C 885	11.2	33.9	40	4	US-09-537-911A-66	Sequence 66, App	C 958	11.2	33.9	50	4	US-09-371-710-15	Sequence 15, Appl
C 886	11.2	33.9	40	4	US-09-849-928-228	Sequence 228, App	C 959	11.2	33.9	50	4	US-09-543-106-5	Sequence 5, Appli
C 887	11.2	33.9	40	5	PCT-US96-09455A-228	Sequence 228, App	C 960	11.2	33.9	50	4	US-08-397-220B-14	Sequence 14, Appl
C 888	11.2	33.9	41	1	US-08-211-202-90	Sequence 90, Appl	C 961	11.2	33.9	50	4	US-09-648-386-14	Sequence 14, Appl
C 889	11.2	33.9	41	1	US-08-211-202-94	Sequence 94, Appl	C 962	11.2	33.9	50	4	US-09-648-386-15	Sequence 15, Appl
C 890	11.2	33.9	41	1	US-08-437-538-23	Sequence 23, Appl	C 963	11.2	33.9	50	4	US-08-706-945D-32	Sequence 32, Appl
C 891	11.2	33.9	41	3	US-08-952-793-239	Sequence 239, App	C 964	11.2	33.9	50	4	US-08-706-945D-34	Sequence 34, Appl
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C 893	11.2	33.9	41	4	US-09-005-286B-21	Sequence 21, Appl	C 966	11.2	33.9	50	4	US-08-706-945D-44	Sequence 44, Appl
C 894	11.2	33.9	41	5	PCT-US96-09455A-239	Sequence 239, App	C 967	11.2	33.9	50	4	US-08-650-093C-14	Sequence 14, Appl
C 895	11.2	33.9	43	4	US-09-358-321C-45	Sequence 45, Appl	C 968	11.2	33.9	50	4	US-08-823-895A-14	Sequence 14, Appl
C 896	11.2	33.9	44	4	US-08-669-656A-25	Sequence 25, Appl	C 969	11.2	33.9	50	4	US-09-248-998-86	Sequence 86, Appl
C 897	11.2	33.9	45	4	US-09-486-241-4	Sequence 4, Appli	C 970	11.2	33.9	50	4	US-09-610-651-86	Sequence 86, Appl
C 898	11.2	33.9	47	3	US-09-338-907-324	Sequence 324, App	C 971	11.2	33.9	50	4	US-09-109-916-64	Sequence 64, Appl
C 899	11.2	33.9	47	3	US-09-218-207-324	Sequence 324, App	C 972	11.2	33.9	50	4	US-09-886-156-64	Sequence 64, Appl
C 900	11.2	33.9	47	4	US-09-671-317-799	Sequence 799, App	C 973	11.2	33.9	50	4	US-09-886-149-64	Sequence 64, Appl
C 901	11.2	33.9	47	4	US-09-671-317-817	Sequence 817, App	C 974	11.2	33.9	50	4	US-09-886-150-64	Sequence 64, Appl
C 902	11.2	33.9	47	4	US-09-671-317-823	Sequence 823, App	C 975	11.2	33.9	50	4	US-09-886-159-64	Sequence 64, Appl
C 903	11.2	33.9	47	4	US-09-422-978-466	Sequence 466, App	C 976	11.2	33.9	50	4	US-10-326-090-64	Sequence 64, Appl

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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05812-6

Query Match 61.8%; Score 20.4; DB 5; Length 28;
Best Local Similarity 95.5%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 4 CCGTTCGCGACCACTATGGC 25

RESULT 4
US-09-153-242-39/c
Sequence 39, Application US/09153242
Patent No. 6482592
GENERAL INFORMATION:
APPLICANT: Lundberg, Joakim
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: MODULAR PROBES II
CURRENT APPLICATION NUMBER: US/09/153,242
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PRIOR FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 36
TYPE: DNA
ORGANISM: Hepatitis C virus
US-09-153-242-39

Query Match 61.8%; Score 20.4; DB 4; Length 36;
Best Local Similarity 95.5%; Pred. No. 2.3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGGC 33
Db 27 CCGTTCGCGACCACTATGGC 6

RESULT 5
US-08-299-682-9/c
Sequence 9, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-299-682-9

Query Match 60.6%; Score 20; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CCGGTGTACTACCGTTCGCGACCACTATG 31
Db 32 CCGGTGTACTACCGTTCGCGACCACTATG 1

RESULT 6
US-08-299-682-10/C
Sequence 10, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-299-682-10

Query Match 60.6%; Score 20; DB 1; Length 38;
Best Local Similarity 96.9%; Pred. No. 3.6;
Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGGTGTACTCACC-GTTCGCGACACCTATG 31
|||||
DB 32 CGGTGTACTCACC-GTTCGCGACACCTATG 1

RESULT 7

US-08-097-853-3/c
; Sequence 3, Application US/08097853
; Patent No. 5679342
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG H.
; APPLICANT: YOO, BYONG J.
; APPLICANT: SUH, BYUNG S.
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTED CELL SYSTEMS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,853
; FILING DATE: 19930727
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0088.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: n/a

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-097-853-3

Query Match 58.8%; Score 19.4; DB 1; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCGCGACACCTATGG 32
|||||
DB 21 CGGTTCGCGACACCTATGG 1

RESULT 8

US-08-438-435-3/c
; Sequence 3, Application US/08438435
; Patent No. 5968775
; GENERAL INFORMATION:
; APPLICANT: HAN, JANG H.
; APPLICANT: YOO, BYONG J.
; APPLICANT: SUH, BYUNG S.
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTED CELL SYSTEMS
; NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

; ADDRESSEE: CHIRON CORPORATION
; STREET: 4560 Horton Street, R-440
; CITY: Emeryville
; STATE: California
; COUNTRY: USA
; ZIP: 94608

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,435
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,853
; FILING DATE: 27-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDMAN, KENNETH M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0088.003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: n/a

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-438-435-3

Query Match 58.8%; Score 19.4; DB 2; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCGCGACACCTATGG 32
|||||
DB 21 CGGTTCGCGACACCTATGG 1

RESULT 9

US-08-444-818-217/c
; Sequence 217, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic polynucleotide
DESCRIPTION: probe used for isolation of clone 18g."
US-08-444-818-217

Query Match 58.8%; Score 19.4; DB 3; Length 30;
Best Local Similarity 95.2%; Pred. No. 6.5;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTATGG 32
Db 21 CCGTTCGCGACCACTATGG 1

RESULT 10
US-09-494-332A-1/c
Sequence 1, Application US/09494332A
Patent No. 6623919
GENERAL INFORMATION:
APPLICANT: GORMAN, Kevin
APPLICANT: PATTERSON, David
APPLICANT: LINNEN, Jeffrey
APPLICANT: SONG, Keming
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEPATITIS C VIRUS (HCV) AND HUMAN IMMUNODEFICIENCY VIRUS (HIV) AND METHODS OF USE
FILE REFERENCE: 2049/1E285-US1
CURRENT APPLICATION NUMBER: US/09/494,332A
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,498
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-494-332A-1

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 11
US-09-494-332A-10/c
Sequence 10, Application US/09494332A
Patent No. 6623919
GENERAL INFORMATION:
APPLICANT: GORMAN, Kevin
APPLICANT: PATTERSON, David
APPLICANT: LINNEN, Jeffrey
APPLICANT: SONG, Keming
TITLE OF INVENTION: OLIGONUCLEOTIDE PRIMERS FOR EFFICIENT MULTIPLEX DETECTION OF HEPATITIS C VIRUS (HCV) AND HUMAN IMMUNODEFICIENCY VIRUS (HIV) AND METHODS OF USE

FILE REFERENCE: 2049/1E285-US1
CURRENT APPLICATION NUMBER: US/09/494,332A
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/118,498 -
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-494-332A-10

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 12
US-09-493-353-2/c
Sequence 2, Application US/09493353
Patent No. 6638714
GENERAL INFORMATION:
APPLICANT: Johnson & Johnson
APPLICANT: Linnen, J.M.
APPLICANT: Gorman, K.M.
TITLE OF INVENTION: DETECTION OF HEPATITIS C VIRUS (HCV) AND METHODS OF USE
FILE REFERENCE: 2094/1E286-US1
CURRENT APPLICATION NUMBER: US/09/493,353
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/118,497
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer
US-09-493-353-2

Query Match 57.6%; Score 19; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCGACCACTATGGC 33
Db 25 TTCCGCGACCACTATGGC 7

RESULT 13
US-08-533-820A-6
Sequence 6, Application US/08533820A
Patent No. 5789153
GENERAL INFORMATION:
APPLICANT: FALKNER, Falko-Guenther
APPLICANT: HAEMMERLE, Thomas
APPLICANT: HIMMELSPACH, Michele
APPLICANT: KOHL, Johann
APPLICANT: DORNER, Friedrich
TITLE OF INVENTION: A METHOD OF QUANTITATING NUCLEIC ACIDS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,820A
FILING DATE: 26-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 1831/94
FILING DATE: 26-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 2245/94
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40433/140/SOPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-533-820A-5

Query Match 55.8%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGACACCACTATG 31
DB 1 CGGTTCCGACACCACTATG 20

RESULT 14
US-08-150-204E-125/c
Sequence 125, Application US/08150204E
Patent No. 6538126
GENERAL INFORMATION:
APPLICANT: CHO, Joong Myung
LEE, Yong Beom
PARK, Young Woo
LIM, Kook Jin
CHOI, Deog Young
SO, Hong Seob
KIM, Chun Hyung
KIM, Sung Taek
YANG, Jae Young
TITLE OF INVENTION: HEPATITIS C DIAGNOSTICS AND VACCINES
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: YANG, Jae Young
STREET: 386-1, Doryong-dong, Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
COMPUTER: IBM PC/pentium
OPERATING SYSTEM: Windows
SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,204E
FILING DATE: 20-Apr-1994
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 91-9510
FILING DATE: 10-JUN-1991
APPLICATION NUMBER: KR 91-13601
FILING DATE: 6-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam, Esq.
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: 2695/FLK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 940-8564
TELEFAX: (212) 940-8776
INFORMATION FOR SEQ ID NO: 125
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: primer A
SEQUENCE DESCRIPTION: SEQ ID NO: 125
US-08-150-204E-125

Query Match 55.8%; Score 18.4; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGACACCACTATG 31
DB 20 CGGTTCCGACACCACTATG 1

RESULT 15
US-08-299-682-11/c
Sequence 11, Application US/08299682
Patent No. 5491063
GENERAL INFORMATION:
APPLICANT: Fisher, Mary Ellen
APPLICANT: Watson, Robert Malcom
TITLE OF INVENTION: Methods for In-Solution Quenching of
Fluorescently Labeled Oligonucleotide Probes
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,682
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-299-682-11

Query Match      55.8%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCACTATG 31
Db      20  CCGTTCCGCAGACCACTATG 1

RESULT 16
US-08-240-547-43/c
; Sequence 43, Application US/08240547
; Patent No. 5527869
; GENERAL INFORMATION:
; APPLICANT: Resnick, Robert M.
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Primers and Probes for Detection of
; TITLE OF INVENTION: Hepatitis C and No. 5527669el Variants
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,547
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias Ph.D., Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-240-547-43

Query Match      55.8%; Score 18.4; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCACTATG 31
Db      20  CCGTTCCGCAGACCACTATG 1

RESULT 17
US-08-397-220B-50
; Sequence 50, Application US/08397220B
; Patent No. 6284458
```

```
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment
; TITLE OF INVENTION: Of Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,220B
; FILING DATE: 09-Mar-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/01293
; FILING DATE: 10-Sep-93
; APPLICATION NUMBER: JP 5-87195
; FILING DATE: 14-Apr-93
; APPLICATION NUMBER: 07/945,289
; FILING DATE: 10-Sep-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-397-220B-50

Query Match      52.7%; Score 17.4; DB 3; Length 20;
Best Local Similarity 94.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12  CCGTTCCGCAGACCACTAT 30
Db      2  CCGTTCCGCAGACCACTAT 20

RESULT 18
US-08-650-093C-50
; Sequence 50, Application US/08650093C
; Patent No. 6391542
; GENERAL INFORMATION:
; APPLICANT: Kevin P. Anderson et al.
; TITLE OF INVENTION: Compositions And Methods For Treatment Of
; TITLE OF INVENTION: Hepatitis C Virus-Associated Diseases
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LICATA & TYRELL P.C.
; STREET: 66 E. Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM Compatible
```

OPERATING SYSTEM: Windows 95
SOFTWARE: WORDPERFECT 6.1 for Windows
CURRENT APPLICATION DATA: US/08/650,093C
APPLICATION NUMBER: US/08/650,093C
FILING DATE: 17-May-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452,841
FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-08-650-093C-50

Query Match 52.7%; Score 17.4; DB 3; Length 20;
Best Local Similarity 94.7%; Pred. No. 50;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCGTTCGCGAGACCCTAT 30
|||||
DB 2 CCGTTCGCGAGACCCTAT 20

RESULT 19
US-08-954-210-9/c
; Sequence 9, Application US/08954210
; Patent No. 6043077
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yei, Soompin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,210
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480124.403C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-954-210-9

Query Match 48.5%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTA 29
|||||
DB 16 GTTCGCGAGACCACTA 1

RESULT 20
US-09-431-419A-9/c
; Sequence 9, Application US/09431419A
; Patent No. 6458567
; GENERAL INFORMATION:
; APPLICANT: Barber, Jack R.
; APPLICANT: Welch, Peter J.
; APPLICANT: Tritz, Richard
; APPLICANT: Yei, Soompin
; APPLICANT: Yu, Mang
; TITLE OF INVENTION: HEPATITIS C VIRUS RIBOZYMES
; FILE REFERENCE: 480124.403C3
; CURRENT APPLICATION NUMBER: US/09/431,419A
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Hepatitis C Virus
US-09-431-419A-9

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTA 29
|||||
DB 16 GTTCGCGAGACCACTA 1

RESULT 21
US-09-474-432B-24/c
; Sequence 24, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511

; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Hepatitis C Virus
US-09-474-432B-24

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTAT 30
| | | | | | | | | | | | | | | | | |
Db 16 TTCCGCAGACCACTAT 1

RESULT 22

US-09-476-387-24/c
; Sequence 24, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Svedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
; FILE REFERENCE: MBH00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476.387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus

US-09-476-387-24

Query Match 48.5%; Score 16; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCCGCAGACCACTAT 30
| | | | | | | | | | | | | | | | | |
Db 16 TTCCGCAGACCACTAT 1

RESULT 23

US-08-438-639-46
; Sequence 46, Application US/08438639
; Patent No. 5712383
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID

; TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,639
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,338
; FILING DATE: 23-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Kenneth, M.
; REGISTRATION NUMBER: 34,174
; REFERENCE/DOCKET NUMBER: 0232.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2719
; TELEFAX: (510) 655-3542
; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-438-639-46

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CGCAGACCACTATGCC 33
| | | | | | | | | | | | | | | | | |
Db 1 CGCAGACCACTATGCC 16

RESULT 24

US-07-813-338A-46
; Sequence 46, Application US/07813338A
; Patent No. 5747244
; GENERAL INFORMATION:
; APPLICANT: Sheridan, Patrick
; APPLICANT: Chang, Chu-An
; APPLICANT: Running, Joyce
; APPLICANT: Urdea, Michael S.
; TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION - R440
; STREET: P.O. Box 8097
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/813,338A
; FILING DATE: 23-DEC-1991

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Kenneth, M.
REGISTRATION NUMBER: 34,174
REFERENCE/DOCKET NUMBER: 0232.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2719
TELEFAX: (510) 655-3542
TELEX: N/A
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-813-338A-46

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 25
US-08-470-124-79
Sequence 79, Application US/08470124
Patent No. 5849481
GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Forster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,588
FILING DATE: 23 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clotti, Thomas E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20104.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-124-79

Query Match 48.5%; Score 16; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 25
US-08-470-124-79
Sequence 79, Application US/08470124
Patent No. 5849481
GENERAL INFORMATION:
APPLICANT: Urdea, Michael S.
APPLICANT: Horn, Thomas
APPLICANT: Chang, Chu-An
APPLICANT: Warner, Brian
APPLICANT: Fultz, Timothy J.
TITLE OF INVENTION: LARGE COMB-TYPE BRANCHED
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Forster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/813,588
FILING DATE: 23 December 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clotti, Thomas E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20104.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-124-79

Query Match 48.5%; Score 16; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 26
US-08-441-971-122
Sequence 122, Application US/08441971
Patent No. 6071693
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,971
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,653
FILING DATE:
APPLICATION NUMBER: US/07/881,528
FILING DATE:
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441
TELEX: EZEKIEL
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-441-971-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
DB 1 CGCAGACCACTATGGC 16

RESULT 27
US-08-221-653-122
Sequence 122, Application US/08221653
Patent No. 6190864
GENERAL INFORMATION:

APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: US/08/221,653
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/881,528
FILING DATE: APRIL 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yatko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CHIR-0121
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-08-221-653-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGCG 33
DB 1 CGCAGACCACCTATGCG 16

RESULT 28
US-08-442-144A-122
Sequence 122, Application US/08442144A
Patent No. 6297370
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
APPLICANT: Eileen Beall
APPLICANT: Bruce Irvine
APPLICANT: Janice Kolberg
APPLICANT: Michael S. Urdea
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 Inch

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,144A
FILING DATE: MAY 16, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,653
FILING DATE: APRIL 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Doreen Yatko Trujillo
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CHIR-0121
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
TELEX:
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 Nucleotides
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
US-08-442-144A-122

Query Match 48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACCTATGCG 33
DB 1 CGCAGACCACCTATGCG 16

RESULT 29
US-08-441-970-122
Sequence 122, Application US/08441970
Patent No. 6297370
GENERAL INFORMATION:
APPLICANT: Tai-An Cha
TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,970
FILING DATE: 16-MAY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,528
FILING DATE: 08-MAY-1992
APPLICATION NUMBER: 07/697,326
FILING DATE: 8 May 1991
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J.
REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: C0772/7000
TELEPHONE: (617) 720-3500
TELEFAX: (617) 720-2441

```
; TELEX: EZEKIEL
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-441-970-122

Query Match      48.5%; Score 16; DB 3; Length 33;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   18 CGCAGACCACTATGGC 33
     |||||
DB    1 CGCAGACCACTATGGC 16

RESULT 30
US-08-435-568A-28 .
Sequence 28, Application US/08435568A
Patent No. 6143298
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
APPLICANT: Davis, Gary
TITLE OF INVENTION: Soluble Truncated Forms of ICAM-1
FILE REFERENCE: MCI 208 4C2D2
CURRENT APPLICATION NUMBER: US/08/435,568A
CURRENT FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 39
TYPE: DNA
ORGANISM: Homo sapiens
US-08-435-568A-28

Query Match      48.5%; Score 16; DB 3; Length 39;
Best Local Similarity 79.2%; Pred.No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY   6 TACTCACCGTTCGCAGACCACCTA 29
     |||||
DB   11 TCCTCACCGTTCTGGAGTCCAGTA 34

RESULT 31
US-08-417-551-5
Sequence 5, Application US/08417551
Patent No. 6326004
GENERAL INFORMATION:
APPLICANT: Greve, Jeffrey M.
APPLICANT: McClelland, Alan
APPLICANT: Davis, Gary
TITLE OF INVENTION: Antiviral Methods Using Fragments Of Human Rhinovirus Receptor (ICAM-1)
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Bayer Corporation
STREET: 400 Morgan Lane
CITY: West Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: Dell Latitude CP
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,551
```

STATE: Connecticut
COUNTRY: USA
ZIP: 06516
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb storage
COMPUTER: Dell Latitude CP
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316.385
FILING DATE: 30-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/103.303
FILING DATE: 6-AUG-1993
APPLICATION NUMBER: 07/631.313
FILING DATE: 20-DEC-1990
APPLICATION NUMBER: 07/556.238
FILING DATE: 20-JUL-1990
APPLICATION NUMBER: 07/390.662
FILING DATE: 10-AUG-1989
APPLICATION NUMBER: 07/262.428
FILING DATE: 25-OCT-1988
APPLICATION NUMBER: 07/239.571
FILING DATE: 1-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: SHIMEI, BARBARA A.
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 208.3C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FEATURE:
NAME/KEY: XbaI site
LOCATION: bases 2-7
NAME/KEY: BamHI site
LOCATION: bases 8-13
NAME/KEY: complement to stop codon
LOCATION: bases 14-16 are complementary to stop
LOCATION: codon on sense strand
NAME/KEY: complement to codons for amino acids 81-
NAME/KEY: 88 of ICAM-1
LOCATION: bases 17-39 are complementary to
LOCATION: nucleotides on sense strand coding for amino acid
LOCATION: residues 81-88 of ICAM-1
PUBLICATION INFORMATION:
AUTHORS: Staunton, D.
AUTHORS: Marlin, S.
AUTHORS: Stratowa, C.
AUTHORS: Dustin, M.
AUTHORS: Springer, T.
TITLE: Primary structure of ICAM-1 demonstrates
TITLE: interaction between members of the immunoglobulin
TITLE: and integrin supergene families
JOURNAL: Cell
VOLUME: 52
PAGES: 925-933
DATE: 25-MAR-1988
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 17 TO 39
US-08-316-385-5
Query Match 48.5%; Score 16; DB 4; Length 39;
Best Local Similarity 79.2%; Pred No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TACTCACCCTCCGACGACCACTA 29
Db 11 TCCTCACCCTTCGGAGTCCAGTA 34
RESULT 33
US-09-034-205-52/c
; Sequence 52, Application US/09034205
; Patent No. 6194149
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,205
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-03268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-09-034-205-52
Query Match 46.7%; Score 15.4; DB 3; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CCGTTCGCGACCACT 28
Db 17 CCGTTCGCGACCACT 1
RESULT 34
US-09-677-218B-52/c
; Sequence 52, Application US/09677218B
; Patent No. 6355437
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-677-218B-52

Query Match 46.7%; Score 15.4; DB 3; Length 18;

Best Local Similarity 94.1%; Pred. No. 4.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGACCACT 28

DB 17 CGGTTCCGCGACCACT 1

RESULT 35

US-09-677-192-52/c

Sequence 52, Application US/09677192

Patent No. 6358691

GENERAL INFORMATION:

APPLICANT: Lyamichev, Victor I.

APPLICANT: Brow, Mary Ann D.

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

TITLE OF INVENTION: OLIGONUCLEOTIDES

FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 52

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-677-192-52

Query Match 46.7%; Score 15.4; DB 3; Length 18;

Best Local Similarity 94.1%; Pred. No. 4.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGACCACT 28

DB 17 CGGTTCCGCGACCACT 1

RESULT 36

US-09-402-618B-52/c

Sequence 52, Application US/09402618B

Patent No. 6709815

GENERAL INFORMATION:

APPLICANT: Dong, Fang

APPLICANT: Lyamichev, Victor

APPLICANT: Prudent, James

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce

APPLICANT: Brow, Mary Ann

APPLICANT: Anderson, Todd

APPLICANT: Dahlberg, James

TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotic

FILE REFERENCE: FORS-04012

CURRENT APPLICATION NUMBER: US/09/402,618B

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: PCT/US98/03194

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.0

SEQ ID NO 52

LENGTH: 18

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-402-618B-52

Query Match 46.7%; Score 15.4; DB 4; Length 18;

Best Local Similarity 94.1%; Pred. No. 4.1e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CGGTTCCGCGACCACT 28

DB 17 CGGTTCCGCGACCACT 1

RESULT 37

5166057-36

Patent No. 5166057

APPLICANT: PALESE, PETER; PARVIN, JEFFREY D.; KRYSTAL, MARK

TITLE OF INVENTION: RECOMBIANT NEGATIVE STRAND RNA VIRUS

EXPRESSION-SYSTEMS

NUMBER OF SEQUENCES: 43

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/527,237

FILING DATE: 22-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 440,053

FILING DATE: 21-NOV-1989

APPLICATION NUMBER: 399,728

FILING DATE: 28-AUG-1989

SEQ ID NO:36;

LENGTH: 37

5166057-36

Query Match 46.7%; Score 15.4; DB 6; Length 37;

Best Local Similarity 76.0%; Pred. No. 4.7e+02;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 6 TACTCAGCTTCGCGCGCATAT 30

RESULT 38

US-08-316-439A-21
; Sequence 21, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PALSESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GORDWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.439A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/440,053
; FILING DATE: No. 5840520ember 21, 1989
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, LUANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5165
; TELEFAX: (415) 857-0663
; TELEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-21
Query Match 46.7%; Score 15.4; DB 2; Length 38;
Best Local Similarity 76.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 TACTCACCCTTCGCGAGACCACTAT 30
Db 7 TACTCACCCTTCGCGCGCCGCGACTAT 31
RESULT 39
US-09-039-982A-54

; Sequence 54, Application US/09039982A
; Patent No. 6225042
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Sprrent, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS FOR ACTIVATION OF T-CELLS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6225042th Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,982A
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olson, Arne M.
; REGISTRATION NUMBER: 30,203
; REFERENCE/DOCKET NUMBER: TSRI4710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 580-1180
; TELEFAX: (312) 580-1189
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-039-982A-54
Query Match 46.1%; Score 15.2; DB 3; Length 33;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db 6 TGAGCTCATGATCCCGAGTGCATG 33
RESULT 40
US-09-039-762A-54
; Sequence 54, Application US/09039762A
; Patent No. 6255073
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Sprrent, Jonathan
; APPLICANT: Brunmark, Anders
; APPLICANT: Jackson, Michael
; APPLICANT: Peterson, Per A
; TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Olson & Hierl, Ltd.
; STREET: 20 No. 6255073th Wacker Drive, 36th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

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/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/039,762A
/ FILING DATE: 16-MAR-1998
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OLSON, Arne M.
/ REGISTRATION NUMBER: 30,203
/ REFERENCE/DOCKET NUMBER: TSRI 471.0 DIV.2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 580-1180
/ TELEFAX: (312) 580-1189
/ INFORMATION FOR SEQ ID NO: 54:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/
US-09-039-762A-54
Query Match : 46.1%; Score 15.2; DB 3; Length 33;
Best Local Similarity 71.4%; Pred.No.5.7e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 6 TGAGCTCATGGATCCCCAGTGCCTATG 33

Search completed: November 23, 2004, 22:26:13
Job time : 47.191 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 154.742 Seconds
(without alignments)
1152.370 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33

Sequence: 1 cgggtactacccttcgcagaccatggc 33

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	33	15	US-10-419-022-3
3	31	99.9	31	16	US-10-337-190-1
4	22	66.7	41	17	US-10-451-882-42
5	20	60.6	24	17	US-10-318-416B-34
6	20	60.6	26	17	US-10-318-416B-32
7	20	60.6	32	15	US-10-147-679A-20
8	19.4	58.8	31	9	US-09-782-361-3
9	19	57.6	19	9	US-09-747-419-11
10	19	57.6	19	15	US-10-259-275-11
11	19	57.6	19	18	US-10-667-271-78
12	19	57.6	19	18	US-10-667-271-82
13	19	57.6	19	17	US-10-669-841-2622

13	19	57.6	19	18	US-10-667-271-774	Sequence 774, App
14	19	57.6	19	18	US-10-667-271-778	Sequence 778, App
15	19	57.6	25	17	US-10-471-351-1	Sequence 1, Appli
16	18.4	55.8	24	17	US-10-318-416B-35	Sequence 35, Appl
17	18.4	55.8	26	17	US-10-318-416B-33	Sequence 33, Appl
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19	18	54.5	19	18	US-10-667-271-80	Sequence 80, Appl
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22	18	54.5	19	18	US-10-667-271-777	Sequence 777, App
23	18	54.5	46	15	US-10-240-460-8	Sequence 8, Appli
24	17.4	52.7	19	18	US-10-667-271-76	Sequence 76, Appl
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26	17.4	52.7	23	18	US-10-667-271-1401	Sequence 1401, Ap
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28	17	51.5	17	10	US-09-740-332-4525	Sequence 4525, Ap
29	17	51.5	17	10	US-09-817-879-30	Sequence 30, Appl
30	17	51.5	17	10	US-09-817-879-4525	Sequence 4525, Ap
31	17	51.5	17	17	US-10-669-841-2623	Sequence 2623, Ap
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34	17	51.5	19	18	US-10-667-271-769	Sequence 769, App
35	17	51.5	24	10	US-09-882-945A-237	Sequence 237, App
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37	16.4	49.7	19	18	US-10-667-271-771	Sequence 771, App
38	16	48.5	16	10	US-09-825-805-24	Sequence 24, Appl
39	16	48.5	17	10	US-09-740-332-4526	Sequence 4526, Ap
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41	16	48.5	17	17	US-10-669-841-7119	Sequence 7119, Ap
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49	15.4	46.7	18	10	US-09-882-945A-52	Sequence 52, Appl
50	15.4	46.7	19	18	US-10-667-271-79	Sequence 79, Appl
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52	15.4	46.7	21	18	US-10-667-271-1501	Sequence 1501, Ap
53	15.4	46.7	21	18	US-10-667-271-1513	Sequence 1513, Ap
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58	15.2	46.1	33	14	US-10-105-504A-54	Sequence 54, Appl
59	15.2	46.1	33	14	US-10-105-678A-54	Sequence 54, Appl
60	15.2	46.1	33	15	US-10-266-463A-60	Sequence 60, Appl
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62	15.2	46.1	38	10	US-09-405-032-28	Sequence 28, Appl
63	15.2	46.1	38	10	US-09-405-032-160	Sequence 160, App
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65	15.2	46.1	38	10	US-09-405-032-164	Sequence 164, App
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74	15	45.5	15	9	US-09-274-553D-1562	Sequence 1562, Ap
75	15	45.5	15	9	US-09-274-553D-1563	Sequence 1563, Ap
76	15	45.5	15	9	US-09-274-553D-1599	Sequence 1599, Ap
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78	15	45.5	15	10	US-09-740-332-4749	Sequence 4749, Ap
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86	15	45.5	18	10	US-09-935-338-191	Sequence 191, App	159	14	42.4	15	17	US-10-669-841-7337	Sequence 7337, Ap
87	15	45.5	18	10	US-09-935-338-228	Sequence 228, App	160	14	42.4	15	17	US-10-669-841-7341	Sequence 7341, Ap
88	15	45.5	18	17	US-10-451-882-31	Sequence 31, Appl	c 161	14	42.4	15	17	US-09-740-332-35	Sequence 35, Appl
c 89	15	45.5	19	18	US-10-667-271-77	Sequence 77, Appl	162	14	42.4	17	10	US-09-740-332-4521	Sequence 4521, Ap
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c 91	15	45.5	21	16	US-10-441-830-1	Sequence 1, Appli	164	14	42.4	17	10	US-09-817-879-4521	Sequence 4521, Ap
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c 94	15	45.5	26	15	US-10-309-561-19	Sequence 19, Appl	c 167	14	42.4	19	18	US-10-667-271-32	Sequence 32, Appl
c 95	15	45.5	26	17	US-10-789-355-19	Sequence 19, Appl	c 168	14	42.4	19	18	US-10-667-271-55	Sequence 55, Appl
c 96	15	45.5	26	18	US-10-686-835-19	Sequence 19, Appl	c 169	14	42.4	19	18	US-10-667-271-728	Sequence 728, App
c 97	15	45.5	34	16	US-10-182-936A-162	Sequence 162, App	170	14	42.4	19	18	US-10-667-271-751	Sequence 751, App
c 98	14.8	44.8	19	18	US-10-667-271-53	Sequence 53, Appl	171	14	42.4	19	18	US-10-667-271-780	Sequence 780, App
c 99	14.8	44.8	19	18	US-10-667-271-61	Sequence 61, Appl	172	14	42.4	25	15	US-10-098-263B-109400	Sequence 109400,
100	14.8	44.8	19	18	US-10-667-271-749	Sequence 749, App	c 173	14	42.4	25	15	US-10-098-263B-115307	Sequence 115307,
101	14.8	44.8	19	18	US-10-667-271-757	Sequence 757, App	c 174	14	42.4	26	15	US-10-198-680A-4	Sequence 4, Appli
c 102	14.8	44.8	21	18	US-10-444-853A-146	Sequence 146, App	c 175	14	42.4	26	15	US-10-320-978-3	Sequence 3, Appli
c 103	14.8	44.8	21	18	US-10-444-853A-153	Sequence 153, App	c 176	14	42.4	26	15	US-10-353-563-3	Sequence 3, Appli
c 104	14.8	44.8	21	18	US-10-444-853A-192	Sequence 192, App	c 177	14	42.4	26	15	US-10-353-589-3	Sequence 3, Appli
c 105	14.8	44.8	21	18	US-10-444-853A-193	Sequence 193, App	c 178	14	42.4	26	15	US-10-320-979-3	Sequence 3, Appli
c 106	14.8	44.8	21	18	US-10-444-853A-200	Sequence 200, App	c 179	14	42.4	26	15	US-10-353-894-3	Sequence 4, Appli
c 107	14.8	44.8	21	18	US-10-667-271-1424	Sequence 1424, Ap	c 180	14	42.4	26	15	US-10-198-259A-4	Sequence 4, Appli
c 108	14.8	44.8	21	18	US-10-667-271-1431	Sequence 1431, Ap	c 181	14	42.4	26	16	US-10-198-384A-4	Sequence 4, Appli
c 109	14.8	44.8	21	18	US-10-667-271-1449	Sequence 1449, Ap	c 182	14	42.4	26	16	US-10-791-318-3	Sequence 3, Appli
c 110	14.8	44.8	21	18	US-10-667-271-1450	Sequence 1450, Ap	c 183	14	42.4	26	16	US-10-791-318-3	Sequence 1, Appli
c 111	14.8	44.8	21	18	US-10-667-271-1457	Sequence 1457, Ap	c 184	14	42.4	37	10	US-09-848-754A-6140	Sequence 6140, Ap
c 112	14.8	44.8	23	18	US-10-667-271-1395	Sequence 1395, Ap	c 185	14	42.4	37	15	US-10-230-006-1523	Sequence 1523, Ap
c 113	14.8	44.8	23	18	US-10-667-271-1397	Sequence 1397, Ap	c 186	14	42.4	37	15	US-10-230-006-1523	Sequence 18274, A
c 114	14.8	44.8	25	13	US-10-033-297-121	Sequence 121, App	c 187	14	42.4	37	16	US-10-138-674-18274	Sequence 18274, A
c 115	14.8	44.8	25	15	US-10-290-386-121	Sequence 121, App	c 188	14	42.4	37	17	US-10-287-949A-18274	Sequence 1106, Ap
c 116	14.8	44.8	25	16	US-10-356-861-121	Sequence 121, App	c 189	14	42.4	38	10	US-09-825-805-1106	Sequence 27, Appl
c 117	14.8	44.8	31	14	US-10-225-501-7	Sequence 7, Appli	c 190	14	42.4	47	14	US-10-211-069-27	Sequence 54, Appl
c 118	14.8	44.8	33	10	US-09-882-945A-63	Sequence 63, Appl	c 191	13.8	41.8	19	18	US-10-667-271-54	Sequence 750, App
c 119	14.8	44.8	50	16	US-10-062-188-191	Sequence 191, App	c 192	13.8	41.8	19	18	US-10-667-271-750	Sequence 144, App
c 120	14.6	44.2	34	16	US-10-440-295-5	Sequence 5, Appli	c 193	13.8	41.8	21	18	US-10-444-853A-151	Sequence 151, App
c 121	14.6	44.2	34	17	US-10-204-070A-9	Sequence 9, Appli	194	13.8	41.8	21	18	US-10-444-853A-151	Sequence 199, App
c 122	14.4	43.6	17	10	US-09-740-332-34	Sequence 34, Appl	195	13.8	41.8	21	18	US-10-667-271-1422	Sequence 1422, Ap
c 123	14.4	43.6	17	10	US-09-740-332-4524	Sequence 4524, Ap	c 196	13.8	41.8	21	18	US-10-667-271-1429	Sequence 1429, Ap
c 124	14.4	43.6	17	10	US-09-817-879-34	Sequence 34, Appl	c 197	13.8	41.8	21	18	US-10-667-271-1456	Sequence 1456, Ap
c 125	14.4	43.6	17	10	US-09-817-879-4524	Sequence 4524, Ap	c 198	13.8	41.8	21	18	US-09-866-108-10985	Sequence 10985, A
c 126	14.4	43.6	17	17	US-10-669-841-2627	Sequence 2627, Ap	c 199	13.8	41.8	25	9	US-09-866-108-10985	Sequence 7684, Ap
c 127	14.4	43.6	17	17	US-10-669-841-7117	Sequence 7117, Ap	200	13.8	41.8	25	15	US-10-098-263B-117433	Sequence 117433,
c 128	14.4	43.6	19	18	US-10-667-271-57	Sequence 57, Appl	201	13.8	41.8	25	15	US-10-098-263B-117433	Sequence 117434,
c 129	14.4	43.6	19	18	US-10-667-271-58	Sequence 58, Appl	202	13.8	41.8	25	15	US-10-098-263B-117434	Sequence 10985, A
c 130	14.4	43.6	19	18	US-10-667-271-65	Sequence 65, Appl	c 203	13.8	41.8	28	9	US-09-955-286-3	Sequence 3, Appli
c 131	14.4	43.6	19	18	US-10-667-271-753	Sequence 753, App	c 204	13.8	41.8	31	9	US-09-801-274-816	Sequence 816, App
c 132	14.4	43.6	19	18	US-10-667-271-754	Sequence 754, App	c 205	13.8	41.8	39	17	US-10-318-416B-24	Sequence 24, Appl
c 133	14.4	43.6	19	18	US-10-667-271-761	Sequence 761, App	c 206	13.8	41.8	40	14	US-10-071-485-74	Sequence 74, Appl
c 134	14.4	43.6	22	9	US-09-464-426A-1	Sequence 1, Appli	c 207	13.8	41.8	40	14	US-09-884-465A-177	Sequence 177, App
c 135	14.4	43.6	22	9	US-09-981-215-1	Sequence 1, Appli	c 208	13.8	41.8	45	10	US-09-884-465A-177	Sequence 178, App
c 136	14.4	43.6	25	15	US-10-098-263B-94252	Sequence 94252, A	c 209	13.8	41.8	45	10	US-09-884-465A-178	Sequence 3328, Ap
c 137	14.4	43.6	32	16	US-10-688-272-25	Sequence 25, Appl	c 210	13.8	41.8	50	16	US-10-131-827-3328	Sequence 3827, Ap
c 138	14.4	43.6	41	14	US-10-043-573-79	Sequence 79, Appl	c 211	13.8	41.8	50	16	US-10-131-827-3827	Sequence 64470, A
c 139	14.4	43.6	50	16	US-10-131-827-3821	Sequence 3821, Ap	c 212	13.6	41.2	31	10	US-09-912-263-170	Sequence 170, App
c 140	14.4	43.6	50	16	US-10-131-827-6034	Sequence 6034, Ap	c 213	13.6	41.2	31	10	US-10-156-306-2523	Sequence 2523, Ap
c 141	14.2	43.0	21	15	US-10-168-989-7	Sequence 7, Appli	c 214	13.6	41.2	37	16	US-10-138-674-203280	Sequence 203280, A
c 142	14.2	43.0	33	15	US-10-304-038-7	Sequence 7, Appli	c 215	13.6	41.2	37	16	US-10-138-674-203280	Sequence 20329, A
c 143	14.2	43.0	50	15	US-10-393-815-204	Sequence 204, App	c 216	13.6	41.2	37	16	US-10-138-674-20407	Sequence 20407, A
c 144	14	42.4	15	9	US-09-504-231A-1524	Sequence 1524, App	c 217	13.6	41.2	37	17	US-10-287-949A-20329	Sequence 20329, A
c 145	14	42.4	15	9	US-09-274-553D-1524	Sequence 1524, App	c 218	13.6	41.2	37	17	US-10-287-949A-20329	Sequence 4832, Ap
c 146	14	42.4	15	10	US-09-740-332-4578	Sequence 4578, Ap	c 219	13.6	41.2	37	17	US-10-287-949A-20407	Sequence 20407, A
c 147	14	42.4	15	10	US-09-740-332-4625	Sequence 4625, Ap	c 220	13.6	41.2	38	10	US-09-780-533A-4832	Sequence 4832, Ap
c 148	14	42.4	15	10	US-09-740-332-4627	Sequence 4627, Ap	c 221	13.6	41.2	38	10	US-09-780-164-1920	Sequence 1920, Ap
c 149	14	42.4	15	10	US-09-740-332-4744	Sequence 4744, Ap	c 222	13.6	41.2	47	15	US-10-170-097-708	Sequence 708, App
c 150	14	42.4	15	10	US-09-740-332-4748	Sequence 4748, Ap	c 223	13.6	41.2	50	16	US-10-131-827-3697	Sequence 3697, Ap
c 151	14	42.4	15	10	US-09-817-879-4578	Sequence 4578, Ap	c 224	13.6	41.2	50	16	US-10-131-827-3697	Sequence 1557, Ap
c 152	14	42.4	15	10	US-09-817-879-4625	Sequence 4625, Ap	c 225	13.4	40.6	15	9	US-09-504-231A-1557	Sequence 4727, Ap
c 153	14	42.4	15	10	US-09-817-879-4627	Sequence 4627, Ap	c 226	13.4	40.6	15	10	US-09-740-332-4727	Sequence 4727, Ap
c 154	14	42.4	15	10	US-09-817-879-4744	Sequence 4744, Ap	c 227	13.4	40.6	15	10	US-09-817-879-4727	Sequence 7320, Ap
c 155	14	42.4	15	10	US-09-817-879-4748	Sequence 4748, Ap	c 228	13.4	40.6	15	17	US-10-669-841-7320	Sequence 12, Appl
c 156	14	42.4	15	17	US-10-669-841-7171	Sequence 7171, Ap	c 229	13.4	40.6	18	17	US-10-318-416B-12	Sequence 69, Appl
c 157	14	42.4	15	17	US-10-669-841-7218	Sequence 7218, Ap	c 230	13.4	40.6	18	17	US-10-669-841-7218	Sequence 69, Appl
c 158	14	42.4	15	17	US-10-669-841-7220	Sequence 7220, Ap	c 231	13.4	40.6	19	18	US-10-667-271-69	Sequence 69, Appl

232	13.4	40.6	19	18	US-10-667-271-765	Sequence 765, App.	305	13.	39.4	24	15	US-10-196-232-12	Sequence 12, Appl
233	13.4	40.6	25	15	US-10-098-263B-29535	Sequence 29535, A	306	13	39.4	24	16	US-10-210-281-191	Sequence 191, App
234	13.4	40.6	25	15	US-10-098-263B-99882	Sequence 99882, A	307	13	39.4	25	9	US-09-866-108-10981	Sequence 10981, A
235	13.4	40.6	25	15	US-10-098-263B-100331	Sequence 100331, A	308	13	39.4	25	9	US-09-866-108-10982	Sequence 10982, A
236	13.4	40.6	26	14	US-10-096-718-74	Sequence 74, Appl	309	13	39.4	25	9	US-09-866-108-10983	Sequence 10983, A
237	13.4	40.6	30	15	US-10-212-962-10	Sequence 10, Appl	310	13	39.4	25	9	US-09-866-108-10984	Sequence 10984, A
238	13.4	40.6	33	15	US-10-371-525-104	Sequence 104, App	311	13	39.4	25	9	US-09-866-108-10986	Sequence 10986, A
239	13.4	40.6	33	15	US-10-371-069-104	Sequence 104, App	312	13	39.4	25	9	US-09-866-108-10987	Sequence 10987, A
240	13.4	40.6	33	15	US-10-371-645-104	Sequence 104, App	313	13	39.4	25	9	US-09-866-108-10988	Sequence 10988, A
241	13.4	40.6	33	15	US-10-371-260-104	Sequence 104, App	314	13	39.4	25	9	US-09-866-108-10989	Sequence 10989, A
242	13.4	40.6	40	10	US-09-907-111-154	Sequence 154, App	315	13	39.4	25	15	US-10-098-263B-57742	Sequence 57742, A
243	13.4	40.6	47	16	US-10-349-143-1903	Sequence 1903, App	316	13	39.4	25	15	US-10-098-263B-84574	Sequence 84574, A
244	13.4	40.6	48	10	US-09-468-147-205	Sequence 205, App	317	13	39.4	25	15	US-10-098-263B-88668	Sequence 88668, A
245	13.4	40.6	48	15	US-10-319-745-205	Sequence 205, App	318	13	39.4	25	15	US-10-098-263B-89294	Sequence 89294, A
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248	13.2	40.0	25	15	US-10-098-263B-31785	Sequence 31785, A	321	13	39.4	25	17	US-10-723-361-10982	Sequence 10982, A
249	13.2	40.0	25	15	US-10-098-263B-68842	Sequence 68842, A	322	13	39.4	25	17	US-10-723-361-10983	Sequence 10983, A
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252	13.2	40.0	25	15	US-10-098-263B-95278	Sequence 95278, A	325	13	39.4	25	17	US-10-723-361-10987	Sequence 10987, A
253	13.2	40.0	25	15	US-10-098-263B-104519	Sequence 104519, A	326	13	39.4	25	17	US-10-723-361-10988	Sequence 10988, A
254	13.2	40.0	29	15	US-10-229-346-26	Sequence 26, Appl	327	13	39.4	25	17	US-10-723-361-10989	Sequence 10989, A
255	13.2	40.0	29	18	US-10-487-846-26	Sequence 26, Appl	328	13	39.4	29	10	US-09-770-158-16	Sequence 16, Appl
256	13.2	40.0	31	18	US-10-422-588-4	Sequence 4, Appl	329	13	39.4	32	9	US-09-755-633-13	Sequence 13, Appl
257	13.2	40.0	32	9	US-09-745-605-21	Sequence 21, Appl	330	13	39.4	32	14	US-10-218-654-138	Sequence 138, App
258	13.2	40.0	33	9	US-09-745-605-35	Sequence 35, Appl	331	13	39.4	32	15	US-10-262-439-138	Sequence 138, App
259	13.2	40.0	33	16	US-10-385-662-18	Sequence 18, Appl	332	13	39.4	32	18	US-10-787-382-13	Sequence 13, Appl
260	13.2	40.0	41	16	US-10-035-833A-2069	Sequence 2069, App	333	13	39.4	36	10	US-09-848-754A-9535	Sequence 9535, App
261	13.2	40.0	41	16	US-10-035-833A-7326	Sequence 7326, App	334	13	39.4	37	10	US-09-827-395A-1596	Sequence 1596, App
262	13.2	40.0	47	16	US-10-349-143-3114	Sequence 3114, App	335	13	39.4	37	10	US-09-827-395A-1729	Sequence 1729, App
263	13.2	40.0	50	16	US-10-131-827-7901	Sequence 7901, App	336	13	39.4	37	10	US-09-827-395A-1737	Sequence 1737, App
264	13	39.4	13	10	US-09-740-332-4577	Sequence 4577, App	337	13	39.4	37	15	US-10-156-306-6253	Sequence 6253, App
265	13	39.4	13	10	US-09-740-332-4604	Sequence 4604, App	338	13	39.4	37	15	US-10-430-882-1596	Sequence 1596, App
266	13	39.4	13	10	US-09-740-332-4620	Sequence 4620, App	339	13	39.4	37	15	US-10-430-882-1729	Sequence 1729, App
267	13	39.4	13	10	US-09-740-332-4622	Sequence 4622, App	340	13	39.4	37	15	US-10-430-882-1737	Sequence 1737, App
268	13	39.4	13	10	US-09-740-332-4690	Sequence 4690, App	341	13	39.4	37	16	US-10-138-674-18388	Sequence 18388, A
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270	13	39.4	13	10	US-09-740-332-4736	Sequence 4736, App	343	13	39.4	37	17	US-10-287-949A-18388	Sequence 18388, A
271	13	39.4	13	10	US-09-740-332-4737	Sequence 4737, App	344	13	39.4	37	17	US-10-287-949A-20606	Sequence 20606, A
272	13	39.4	13	10	US-09-817-879-4577	Sequence 4577, App	345	13	39.4	38	10	US-09-825-805-914	Sequence 914, App
273	13	39.4	13	10	US-09-817-879-4604	Sequence 4604, App	346	13	39.4	38	10	US-09-825-805-1159	Sequence 1159, App
274	13	39.4	13	10	US-09-817-879-4620	Sequence 4620, App	347	13	39.4	38	10	US-09-770-158-2	Sequence 2, Appl
275	13	39.4	13	10	US-09-817-879-4622	Sequence 4622, App	348	13	39.4	38	10	US-09-780-533A-4619	Sequence 4619, App
276	13	39.4	13	10	US-09-817-879-4690	Sequence 4690, App	349	13	39.4	38	10	US-09-930-423-3038	Sequence 3038, App
277	13	39.4	13	10	US-09-817-879-4731	Sequence 4731, App	350	13	39.4	38	10	US-09-780-164-1953	Sequence 1953, App
278	13	39.4	13	10	US-09-817-879-4736	Sequence 4736, App	351	13	39.4	38	10	US-09-745-237A-3038	Sequence 3038, App
279	13	39.4	13	10	US-09-817-879-4737	Sequence 4737, App	352	13	39.4	41	15	US-10-005-956-704	Sequence 704, App
280	13	39.4	13	17	US-10-669-841-7170	Sequence 7170, App	353	13	39.4	41	16	US-10-035-833A-526	Sequence 526, App
281	13	39.4	13	17	US-10-669-841-7197	Sequence 7197, App	354	13	39.4	41	16	US-10-035-833A-6079	Sequence 6079, App
282	13	39.4	13	17	US-10-669-841-7213	Sequence 7213, App	355	13	39.4	45	9	US-09-735-363A-77	Sequence 77, Appl
283	13	39.4	13	17	US-10-669-841-7215	Sequence 7215, App	356	13	39.4	47	16	US-10-349-143-3439	Sequence 3439, App
284	13	39.4	13	17	US-10-669-841-7283	Sequence 7283, App	357	13	39.4	50	16	US-10-131-827-953	Sequence 953, App
285	13	39.4	13	17	US-10-669-841-7324	Sequence 7324, App	358	12.8	38.8	16	10	US-09-825-805-7	Sequence 7, Appl
286	13	39.4	13	17	US-10-669-841-7329	Sequence 7329, App	359	12.8	38.8	17	10	US-09-740-332-4522	Sequence 4522, App
287	13	39.4	13	17	US-10-669-841-7330	Sequence 7330, App	360	12.8	38.8	17	10	US-09-817-879-4522	Sequence 4522, App
288	13	39.4	15	9	US-09-504-231A-7	Sequence 5, Appl	361	12.8	38.8	17	17	US-10-669-841-7115	Sequence 7115, App
289	13	39.4	15	9	US-09-504-231A-5	Sequence 7, Appl	362	12.8	38.8	19	9	US-09-969-373-2873	Sequence 2873, App
290	13	39.4	15	9	US-09-504-231A-1564	Sequence 1564, App	363	12.8	38.8	19	18	US-10-667-271-56	Sequence 56, Appl
291	13	39.4	15	9	US-09-274-553D-5	Sequence 5, Appl	364	12.8	38.8	19	18	US-10-667-271-752	Sequence 752, App
292	13	39.4	15	9	US-09-274-553D-7	Sequence 7, Appl	365	12.8	38.8	20	8	US-08-887-505-83	Sequence 83, Appl
293	13	39.4	15	9	US-09-274-553D-1564	Sequence 1564, App	366	12.8	38.8	21	9	US-09-747-419-16	Sequence 16, Appl
294	13	39.4	17	10	US-09-740-332-4520	Sequence 4520, App	367	12.8	38.8	21	15	US-10-259-275-16	Sequence 16, Appl
295	13	39.4	17	10	US-09-740-332-4527	Sequence 4527, App	368	12.8	38.8	21	16	US-10-467-000-13	Sequence 13, Appl
296	13	39.4	17	10	US-09-817-879-4520	Sequence 4520, App	369	12.8	38.8	23	18	US-10-667-271-1402	Sequence 1402, App
297	13	39.4	17	10	US-09-817-879-4527	Sequence 4527, App	370	12.8	38.8	25	14	US-10-060-830-535	Sequence 535, App
298	13	39.4	17	17	US-10-669-841-7113	Sequence 7113, App	371	12.8	38.8	25	14	US-10-060-830-536	Sequence 536, App
299	13	39.4	17	17	US-10-669-841-7120	Sequence 7120, App	372	12.8	38.8	25	14	US-10-215-112-7462	Sequence 7462, App
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302	13	39.4	19	18	US-10-667-271-760	Sequence 760, App	375	12.8	38.8	25	15	US-10-098-263B-11276	Sequence 11276, A
303	13	39.4	19	18	US-10-667-271-768	Sequence 768, App	376	12.8	38.8	25	15	US-10-098-263B-14936	Sequence 14936, A
304	13	39.4	24	9	US-09-835-381-13	Sequence 13, Appl	377	12.8	38.8	25	15	US-10-098-263B-94251	Sequence 94251, A

378	12.8	38.8	25	17	US-10-717-597-450	Sequence 450, App	C 451	12.6	38.2	37	16	US-10-138-674-20666	Sequence 20666, A
379	12.8	38.8	26	15	US-10-171-319-80	Sequence 80, Appl	C 452	12.6	38.2	37	17	US-10-287-949A-20666	Sequence 20666, A
380	12.8	38.8	26	15	US-10-171-319-80	Sequence 84, Appl	C 453	12.6	38.2	38	10	US-09-825-805-1291	Sequence 1291, Ap
381	12.8	38.8	26	15	US-10-093-463-351	Sequence 351, App	C 454	12.6	38.2	38	10	US-09-825-805-1407	Sequence 1407, Ap
382	12.8	38.8	27	8	US-08-832-488-6	Sequence 6, Appl	C 455	12.6	38.2	38	10	US-09-825-805-1473	Sequence 1473, Ap
383	12.8	38.8	27	8	US-08-832-488-10	Sequence 10, Appl	C 456	12.6	38.2	38	10	US-09-848-754A-4752	Sequence 4752, Ap
384	12.8	38.8	30	9	US-09-946-678-19	Sequence 19, Appl	C 457	12.6	38.2	39	9	US-09-747-003-28	Sequence 28, Appl
385	12.8	38.8	31	15	US-10-435-608-18	Sequence 18, Appl	C 458	12.6	38.2	39	16	US-10-665-460A-58	Sequence 58, Appl
386	12.8	38.8	31	16	US-10-606-060A-34	Sequence 34, Appl	C 459	12.6	38.2	39	16	US-10-665-460A-58	Sequence 59, Appl
387	12.8	38.8	31	16	US-10-622-108-18	Sequence 18, Appl	C 460	12.6	38.2	42	9	US-09-388-089B-14	Sequence 14, Appl
388	12.8	38.8	37	9	US-09-425-762-33	Sequence 33, Appl	C 461	12.6	38.2	42	17	US-10-719-580-4	Sequence 4, Appl
389	12.8	38.8	37	15	US-10-238-960-15	Sequence 15, Appl	C 462	12.6	38.2	45	16	US-10-380-533-91	Sequence 91, Appl
390	12.8	38.8	37	15	US-10-238-960-16	Sequence 16, Appl	C 463	12.6	38.2	47	10	US-09-848-616-152	Sequence 152, App
391	12.8	38.8	37	15	US-10-238-960-20	Sequence 20, Appl	C 464	12.6	38.2	47	10	US-09-918-728B-106	Sequence 106, App
392	12.8	38.8	38	9	US-09-814-292-17	Sequence 17, Appl	C 465	12.6	38.2	47	15	US-10-050-892-152	Sequence 152, App
393	12.8	38.8	39	9	US-09-730-893-11	Sequence 11, Appl	C 466	12.6	38.2	47	15	US-10-050-898-152	Sequence 152, App
394	12.8	38.8	39	10	US-09-940-173A-11	Sequence 11, Appl	C 467	12.6	38.2	47	16	US-10-349-143-3558	Sequence 3558, Ap
395	12.8	38.8	40	9	US-09-419-076-1	Sequence 1, Appl	C 468	12.6	38.2	47	16	US-10-289-456-152	Sequence 152, App
396	12.8	38.8	40	10	US-09-003-810-1	Sequence 1, Appl	C 469	12.6	38.2	47	16	US-10-622-124-95	Sequence 95, Appl
397	12.8	38.8	40	15	US-10-433-168-1	Sequence 1, Appl	C 470	12.6	38.2	47	17	US-10-622-087-65	Sequence 65, Appl
398	12.8	38.8	41	14	US-10-043-573-80	Sequence 80, Appl	C 471	12.6	38.2	50	16	US-10-131-827-705	Sequence 705, App
399	12.8	38.8	45	10	US-09-931-375A-85	Sequence 85, Appl	C 472	12.6	38.2	50	16	US-10-131-827-1263	Sequence 1263, Ap
400	12.8	38.8	50	16	US-10-131-827-4773	Sequence 4773, Ap	C 473	12.4	37.6	15	9	US-09-504-231A-1525	Sequence 1525, Ap
401	12.8	38.8	50	16	US-10-131-827-7864	Sequence 7864, Ap	C 474	12.4	37.6	15	9	US-09-504-231A-1525	Sequence 1525, Ap
402	12.6	38.2	20	9	US-09-734-836-16	Sequence 16, Appl	C 475	12.4	37.6	15	9	US-09-274-553D-1525	Sequence 1525, Ap
403	12.6	38.2	20	10	US-09-953-318-111	Sequence 11, App	C 476	12.4	37.6	15	9	US-09-274-553D-1525	Sequence 1525, Ap
404	12.6	38.2	20	15	US-10-446-373-111	Sequence 11, App	C 477	12.4	37.6	16	10	US-09-825-805-6	Sequence 6, Appl
405	12.6	38.2	20	16	US-10-188-470-59	Sequence 59, Appl	C 478	12.4	37.6	19	18	US-10-667-271-66	Sequence 66, Appl
406	12.6	38.2	23	9	US-09-730-983-13	Sequence 13, Appl	C 479	12.4	37.6	19	18	US-10-667-271-762	Sequence 762, App
407	12.6	38.2	24	15	US-10-441-729-2	Sequence 2, Appl	C 480	12.4	37.6	24	10	US-09-940-185-3340	Sequence 3340, App
408	12.6	38.2	25	9	US-09-866-108-10979	Sequence 10979, A	C 481	12.4	37.6	24	15	US-10-236-104-40	Sequence 40, Appl
409	12.6	38.2	25	9	US-09-866-108-10980	Sequence 10980, A	C 482	12.4	37.6	24	15	US-10-236-104-43	Sequence 43, Appl
410	12.6	38.2	25	14	US-10-112-12397	Sequence 12397, A	C 483	12.4	37.6	25	14	US-10-215-112-7969	Sequence 7969, Ap
411	12.6	38.2	25	15	US-10-098-263B-17396	Sequence 17396, A	C 484	12.4	37.6	25	14	US-10-215-112-11761	Sequence 11761, A
412	12.6	38.2	25	15	US-10-098-263B-47874	Sequence 47874, A	C 485	12.4	37.6	25	14	US-10-215-112-12046	Sequence 12046, A
413	12.6	38.2	25	15	US-10-098-263B-105657	Sequence 105657, A	C 486	12.4	37.6	25	15	US-10-098-263B-3124	Sequence 3124, Ap
414	12.6	38.2	25	15	US-10-098-263B-107763	Sequence 107763, A	C 487	12.4	37.6	25	15	US-10-098-263B-20225	Sequence 20225, A
415	12.6	38.2	25	15	US-10-098-263B-108994	Sequence 108994, A	C 488	12.4	37.6	25	15	US-10-098-263B-22372	Sequence 22372, A
416	12.6	38.2	25	15	US-10-098-263B-117940	Sequence 117940, A	C 489	12.4	37.6	25	15	US-10-098-263B-36916	Sequence 36916, A
417	12.6	38.2	25	17	US-10-717-597-716	Sequence 716, App	C 490	12.4	37.6	25	15	US-10-098-263B-43276	Sequence 43276, A
418	12.6	38.2	25	17	US-10-723-361-10979	Sequence 10979, A	C 491	12.4	37.6	25	15	US-10-098-263B-47999	Sequence 47999, A
419	12.6	38.2	25	17	US-10-723-361-10980	Sequence 10980, A	C 492	12.4	37.6	25	15	US-10-098-263B-50338	Sequence 50338, A
420	12.6	38.2	26	15	US-10-378-168-56	Sequence 56, Appl	C 493	12.4	37.6	25	15	US-10-098-263B-52446	Sequence 52446, A
421	12.6	38.2	26	14	US-10-150-262-10	Sequence 10, Appl	C 494	12.4	37.6	25	15	US-10-098-263B-60640	Sequence 60640, A
422	12.6	38.2	28	9	US-09-927-767-1	Sequence 1, Appl	C 495	12.4	37.6	25	15	US-10-098-263B-65249	Sequence 65249, A
423	12.6	38.2	28	9	US-09-927-885-1	Sequence 1, Appl	C 496	12.4	37.6	25	15	US-10-098-263B-65249	Sequence 65249, A
424	12.6	38.2	28	9	US-09-927-788-1	Sequence 1, Appl	C 497	12.4	37.6	25	15	US-10-098-263B-65250	Sequence 65250, A
425	12.6	38.2	28	9	US-09-927-898-1	Sequence 1, Appl	C 498	12.4	37.6	25	15	US-10-098-263B-84123	Sequence 84123, A
426	12.6	38.2	28	9	US-09-928-227-1	Sequence 1, Appl	C 499	12.4	37.6	25	15	US-10-098-263B-88883	Sequence 88883, A
427	12.6	38.2	29	15	US-10-336-638-329	Sequence 329, App	C 500	12.4	37.6	25	15	US-10-098-263B-109399	Sequence 109399, A
428	12.6	38.2	29	15	US-10-336-638-856	Sequence 856, App	C 501	12.4	37.6	25	15	US-10-098-263B-115308	Sequence 115308, A
429	12.6	38.2	34	10	US-09-920-000-5	Sequence 5, Appl	C 502	12.4	37.6	25	15	US-10-098-263B-126787	Sequence 126787, A
430	12.6	38.2	35	9	US-09-790-398-15	Sequence 15, Appl	C 503	12.4	37.6	26	8	US-08-911-824-19	Sequence 19, Appl
431	12.6	38.2	35	10	US-09-825-805-303	Sequence 303, App	C 504	12.4	37.6	26	14	US-10-096-718-67	Sequence 67, Appl
432	12.6	38.2	35	17	US-10-441-925A-12	Sequence 12, Appl	C 505	12.4	37.6	27	9	US-09-898-883-11	Sequence 11, Appl
433	12.6	38.2	36	10	US-09-848-754A-9510	Sequence 9510, Ap	C 506	12.4	37.6	27	10	US-09-151-376-49	Sequence 49, Appl
434	12.6	38.2	36	10	US-09-261-329-25	Sequence 25, Appl	C 507	12.4	37.6	27	15	US-10-226-820-17	Sequence 17, Appl
435	12.6	38.2	37	10	US-09-825-805-304	Sequence 304, App	C 508	12.4	37.6	27	15	US-10-139-089-49	Sequence 49, Appl
436	12.6	38.2	37	10	US-09-848-616-150	Sequence 150, App	C 509	12.4	37.6	30	16	US-10-321-039-235	Sequence 235, App
437	12.6	38.2	37	10	US-09-927-046-3759	Sequence 3759, App	C 510	12.4	37.6	31	10	US-09-740-332-9320	Sequence 9320, Ap
438	12.6	38.2	37	10	US-09-848-754A-5925	Sequence 5925, Ap	C 511	12.4	37.6	31	10	US-09-817-879-9320	Sequence 9320, Ap
439	12.6	38.2	37	10	US-09-848-754A-6240	Sequence 6240, Ap	C 512	12.4	37.6	31	17	US-10-669-841-15865	Sequence 15865, A
440	12.6	38.2	37	10	US-09-848-754A-6262	Sequence 6262, Ap	C 513	12.4	37.6	32	10	US-09-887-194A-20	Sequence 20, Appl
441	12.6	38.2	37	10	US-09-827-395A-1670	Sequence 1670, Ap	C 514	12.4	37.6	33	8	US-08-736-019-105	Sequence 105, App
442	12.6	38.2	37	15	US-10-289-454-371	Sequence 371, App	C 515	12.4	37.6	37	9	US-09-864-785-1810	Sequence 1810, Ap
443	12.6	38.2	37	15	US-10-050-902-150	Sequence 150, App	C 516	12.4	37.6	37	9	US-09-864-785-1924	Sequence 1924, Ap
444	12.6	38.2	37	15	US-10-050-898-150	Sequence 150, App	C 517	12.4	37.6	37	9	US-09-864-785-2004	Sequence 2004, Ap
445	12.6	38.2	37	15	US-10-430-006-1464	Sequence 1464, Ap	C 518	12.4	37.6	37	10	US-09-927-046-3653	Sequence 3653, Ap
446	12.6	38.2	37	15	US-10-430-006-1670	Sequence 1670, Ap	C 519	12.4	37.6	37	10	US-09-927-046-3873	Sequence 3873, Ap
447	12.6	38.2	37	15	US-10-430-882-1670	Sequence 1670, Ap	C 520	12.4	37.6	37	10	US-09-927-046-3901	Sequence 3901, Ap
448	12.6	38.2	37	15	US-10-430-882-1693	Sequence 1693, Ap	C 521	12.4	37.6	37	10	US-09-848-754A-5921	Sequence 5921, Ap
449	12.6	38.2	37	15	US-10-346-390-151	Sequence 151, App	C 522	12.4	37.6	37	10	US-09-848-754A-6012	Sequence 6012, Ap
450	12.6	38.2	37	16	US-10-289-456-150	Sequence 150, App	C 523	12.4	37.6	37	10	US-09-848-754A-6075	Sequence 6075, Ap

C 524	12.4	37.6	37	10	US-09-848-754A-6142	Sequence 6142, Ap	C 597	12.4	37.6	38	17	US-10-669-841-9232	Sequence 9232, Ap
C 525	12.4	37.6	37	10	US-09-848-754A-6407	Sequence 6407, Ap	C 598	12.4	37.6	38	17	US-10-669-841-9309	Sequence 9309, Ap
C 526	12.4	37.6	37	10	US-09-827-395A-1572	Sequence 1572, Ap	C 599	12.4	37.6	41	15	US-10-408-930-31	Sequence 31, Appl
C 527	12.4	37.6	37	10	US-09-827-395A-1789	Sequence 1789, Ap	C 600	12.4	37.6	41	16	US-10-035-833A-4120	Sequence 4120, Ap
C 528	12.4	37.6	37	15	US-10-156-306-2526	Sequence 2526, Ap	C 601	12.4	37.6	44	11	US-09-837-306-329	Sequence 329, Appl
C 529	12.4	37.6	37	15	US-10-156-306-6114	Sequence 6114, Ap	C 602	12.4	37.6	44	15	US-10-045-674-412	Sequence 412, Appl
C 530	12.4	37.6	37	15	US-10-156-306-6254	Sequence 6254, Ap	C 603	12.4	37.6	46	9	US-09-423-800-19	Sequence 19, Appl
C 531	12.4	37.6	37	15	US-10-230-006-1525	Sequence 1525, Ap	C 604	12.4	37.6	46	14	US-10-182-018-19	Sequence 19, Appl
C 532	12.4	37.6	37	15	US-10-230-006-1614	Sequence 1614, Ap	C 605	12.4	37.6	46	15	US-10-169-003-19	Sequence 19, Appl
C 533	12.4	37.6	37	15	US-10-230-006-1631	Sequence 1631, Ap	C 606	12.4	37.6	46	15	US-10-337-981-19	Sequence 19, Appl
C 534	12.4	37.6	37	15	US-10-430-882-1572	Sequence 1572, Ap	C 607	12.4	37.6	46	15	US-10-191-540-136	Sequence 136, Appl
C 535	12.4	37.6	37	15	US-10-430-882-1789	Sequence 1789, Ap	C 608	12.4	37.6	46	16	US-10-453-483-115	Sequence 115, Appl
C 536	12.4	37.6	37	16	US-10-138-674-18255	Sequence 18255, A	C 609	12.4	37.6	48	16	US-10-344-733-19	Sequence 19, Appl
C 537	12.4	37.6	37	16	US-10-138-674-18279	Sequence 18279, A	C 610	12.4	37.6	47	16	US-10-349-143-930	Sequence 930, Appl
C 538	12.4	37.6	37	16	US-10-138-674-18313	Sequence 18313, A	C 611	12.4	37.6	47	16	US-10-349-143-2410	Sequence 2410, Ap
C 539	12.4	37.6	37	16	US-10-138-674-18377	Sequence 18377, A	C 612	12.4	37.6	47	16	US-10-294-934-822	Sequence 822, Appl
C 540	12.4	37.6	37	16	US-10-138-674-18556	Sequence 18556, A	C 613	12.4	37.6	50	10	US-09-920-394-6	Sequence 6, Appl
C 541	12.4	37.6	37	16	US-10-138-674-18603	Sequence 18603, A	C 614	12.4	37.6	50	16	US-10-131-827-161	Sequence 161, Appl
C 542	12.4	37.6	37	16	US-10-138-674-18707	Sequence 18707, A	C 615	12.4	37.6	50	16	US-10-131-827-4631	Sequence 4631, Ap
C 543	12.4	37.6	37	16	US-10-138-674-18714	Sequence 18714, A	C 616	12.4	37.6	50	18	US-10-431-627-4	Sequence 4, Appl
C 544	12.4	37.6	37	16	US-10-138-674-18728	Sequence 18728, A	C 617	12.2	37.0	17	9	US-09-866-108-6089	Sequence 6089, Ap
C 545	12.4	37.6	37	16	US-10-138-674-18772	Sequence 18772, A	C 618	12.2	37.0	17	9	US-09-908-130-2	Sequence 2, Appl
C 546	12.4	37.6	37	16	US-10-138-674-20303	Sequence 20303, A	C 619	12.2	37.0	17	9	US-09-908-131-2	Sequence 2, Appl
C 547	12.4	37.6	37	16	US-10-138-674-20573	Sequence 20573, A	C 620	12.2	37.0	17	9	US-09-907-795-2	Sequence 2, Appl
C 548	12.4	37.6	37	16	US-10-138-674-20636	Sequence 20636, A	C 621	12.2	37.0	17	10	US-09-930-423-1581	Sequence 1581, Ap
C 549	12.4	37.6	37	17	US-10-287-949A-18255	Sequence 18255, A	C 622	12.2	37.0	17	10	US-09-745-237A-1581	Sequence 1581, Ap
C 550	12.4	37.6	37	17	US-10-287-949A-18279	Sequence 18279, A	C 623	12.2	37.0	17	13	US-10-041-856-81	Sequence 81, Appl
C 551	12.4	37.6	37	17	US-10-287-949A-18313	Sequence 18313, A	C 624	12.2	37.0	17	14	US-10-124-884-2	Sequence 2, Appl
C 552	12.4	37.6	37	17	US-10-287-949A-18377	Sequence 18377, A	C 625	12.2	37.0	17	15	US-10-230-006-45	Sequence 45, Appl
C 553	12.4	37.6	37	17	US-10-287-949A-18556	Sequence 18556, A	C 626	12.2	37.0	17	17	US-10-723-361-6089	Sequence 6089, Ap
C 554	12.4	37.6	37	17	US-10-287-949A-18603	Sequence 18603, A	C 627	12.2	37.0	18	17	US-10-250-997-1	Sequence 1, Appl
C 555	12.4	37.6	37	17	US-10-287-949A-18707	Sequence 18707, A	C 628	12.2	37.0	19	16	US-10-412-382-43	Sequence 43, Appl
C 556	12.4	37.6	37	17	US-10-287-949A-18714	Sequence 18714, A	C 629	12.2	37.0	20	9	US-09-816-079-7	Sequence 7, Appl
C 557	12.4	37.6	37	17	US-10-287-949A-18728	Sequence 18728, A	C 630	12.2	37.0	20	15	US-10-301-661A-21	Sequence 21, Appl
C 558	12.4	37.6	37	17	US-10-287-949A-18772	Sequence 18772, A	C 631	12.2	37.0	20	15	US-10-301-661A-88	Sequence 88, Appl
C 559	12.4	37.6	37	17	US-10-287-949A-20303	Sequence 20303, A	C 632	12.2	37.0	20	15	US-10-109-349A-245	Sequence 245, Appl
C 560	12.4	37.6	37	17	US-10-287-949A-20636	Sequence 20636, A	C 633	12.2	37.0	20	17	US-10-619-739-310	Sequence 310, Appl
C 561	12.4	37.6	37	17	US-09-825-805-919	Sequence 919, Appl	C 634	12.2	37.0	20	18	US-10-660-122-21	Sequence 21, Appl
C 562	12.4	37.6	38	10	US-09-825-805-938	Sequence 938, Ap	C 635	12.2	37.0	21	18	US-10-786-720-13148	Sequence 13148, A
C 563	12.4	37.6	38	10	US-09-825-805-954	Sequence 954, Appl	C 636	12.2	37.0	24	10	US-09-940-185-2746	Sequence 2746, Ap
C 564	12.4	37.6	38	10	US-09-825-805-979	Sequence 979, Appl	C 637	12.2	37.0	25	9	US-09-866-108-14601	Sequence 14601, A
C 565	12.4	37.6	38	10	US-09-825-805-1006	Sequence 1006, Ap	C 638	12.2	37.0	25	9	US-09-866-108-14602	Sequence 14602, A
C 566	12.4	37.6	38	10	US-09-825-805-1085	Sequence 1085, Ap	C 639	12.2	37.0	25	9	US-09-925-796-18	Sequence 18, Appl
C 567	12.4	37.6	38	10	US-09-825-805-1098	Sequence 1098, Ap	C 640	12.2	37.0	25	9	US-09-941-450-18	Sequence 18, Appl
C 568	12.4	37.6	38	10	US-09-825-805-1236	Sequence 1236, Ap	C 641	12.2	37.0	25	9	US-09-942-090-18	Sequence 18, Appl
C 569	12.4	37.6	38	10	US-09-825-805-1255	Sequence 1255, Ap	C 642	12.2	37.0	25	14	US-10-060-830-534	Sequence 534, Appl
C 570	12.4	37.6	38	10	US-09-825-805-1403	Sequence 1403, Ap	C 643	12.2	37.0	25	14	US-10-215-112-5708	Sequence 5708, Ap
C 571	12.4	37.6	38	10	US-09-877-478-4281	Sequence 4281, Ap	C 644	12.2	37.0	25	14	US-10-215-112-13906	Sequence 13906, A
C 572	12.4	37.6	38	10	US-09-877-478-4341	Sequence 4341, Ap	C 645	12.2	37.0	25	15	US-10-098-263B-5769	Sequence 5769, Ap
C 573	12.4	37.6	38	10	US-09-877-478-4418	Sequence 4418, Ap	C 646	12.2	37.0	25	15	US-10-098-263B-7683	Sequence 7683, Ap
C 574	12.4	37.6	38	10	US-09-776-474-2073	Sequence 2073, Ap	C 647	12.2	37.0	25	15	US-10-098-263B-35813	Sequence 35813, A
C 575	12.4	37.6	38	10	US-09-776-474-2143	Sequence 2143, Ap	C 648	12.2	37.0	25	15	US-10-098-263B-64615	Sequence 64615, A
C 576	12.4	37.6	38	10	US-09-930-423-2939	Sequence 2939, Ap	C 649	12.2	37.0	25	15	US-10-098-263B-66594	Sequence 66594, A
C 577	12.4	37.6	38	10	US-09-930-423-2991	Sequence 2991, Ap	C 650	12.2	37.0	25	15	US-10-098-263B-67026	Sequence 67026, A
C 578	12.4	37.6	38	10	US-09-930-423-2998	Sequence 2998, Ap	C 651	12.2	37.0	25	15	US-10-098-263B-67338	Sequence 67338, A
C 579	12.4	37.6	38	10	US-09-930-423-3000	Sequence 3000, Ap	C 652	12.2	37.0	25	15	US-10-098-263B-78907	Sequence 78907, A
C 580	12.4	37.6	38	10	US-09-930-423-3171	Sequence 3171, Ap	C 653	12.2	37.0	25	15	US-10-098-263B-86270	Sequence 86270, A
C 581	12.4	37.6	38	10	US-09-930-423-3171	Sequence 3171, Ap	C 654	12.2	37.0	25	15	US-10-098-263B-87898	Sequence 87898, A
C 582	12.4	37.6	38	10	US-09-745-237A-1841	Sequence 1841, Ap	C 655	12.2	37.0	25	15	US-10-098-263B-92652	Sequence 92652, A
C 583	12.4	37.6	38	10	US-09-745-237A-2939	Sequence 2939, Ap	C 656	12.2	37.0	25	15	US-10-098-263B-13184	Sequence 13184, A
C 584	12.4	37.6	38	10	US-09-745-237A-2991	Sequence 2991, Ap	C 657	12.2	37.0	25	15	US-10-098-263B-130640	Sequence 130640, A
C 585	12.4	37.6	38	10	US-09-745-237A-2997	Sequence 2997, Ap	C 658	12.2	37.0	25	15	US-10-060-998-1585	Sequence 1585, Ap
C 586	12.4	37.6	38	10	US-09-745-237A-2991	Sequence 2991, Ap	C 659	12.2	37.0	25	17	US-10-723-361-14601	Sequence 14601, A
C 587	12.4	37.6	38	10	US-09-745-237A-2998	Sequence 2998, Ap	C 660	12.2	37.0	25	17	US-10-723-361-14602	Sequence 14602, A
C 588	12.4	37.6	38	10	US-09-745-237A-3000	Sequence 3000, Ap	C 661	12.2	37.0	25	18	US-10-843-944-18	Sequence 18, Appl
C 589	12.4	37.6	38	10	US-10-191-540-137	Sequence 137, Appl	C 662	12.2	37.0	26	9	US-09-732-618-35	Sequence 35, Appl
C 590	12.4	37.6	38	15	US-10-453-483-116	Sequence 116, Appl	C 663	12.2	37.0	26	15	US-10-218-567-12	Sequence 12, Appl
C 591	12.4	37.6	38	16	US-10-342-902-4281	Sequence 4281, Ap	C 664	12.2	37.0	27	9	US-09-770-967-8	Sequence 8, Appl
C 592	12.4	37.6	38	16	US-10-342-902-4341	Sequence 4341, Ap	C 665	12.2	37.0	27	9	US-09-858-369-8	Sequence 8, Appl
C 593	12.4	37.6	38	16	US-10-342-902-4418	Sequence 4418, Ap	C 666	12.2	37.0	27	9	US-09-819-522-8	Sequence 8, Appl
C 594	12.4	37.6	38	16	US-10-469-304-13	Sequence 13, Appl	C 667	12.2	37.0	27	9	US-09-828-061A-9	Sequence 9, Appl
C 595	12.4	37.6	38	17	US-10-669-841-9172	Sequence 9172, Ap	C 668	12.2	37.0	27	9	US-09-757-251-9	Sequence 9, Appl
C 596	12.4	37.6	38	17			C 669	12.2	37.0	27	9	US-09-784-897A-8	Sequence 8, Appl

c 670	12.2	37.0	27	9	US-09-770-983-8	Sequence 8, Appli	c 743	12	36.4	22	16	US-10-461-790-119	Sequence 119, App
c 671	12.2	37.0	27	9	US-09-828-325A-9	Sequence 9, Appli	744	12	36.4	22	18	US-10-660-122-19	Sequence 19, Appl
c 672	12.2	37.0	27	9	US-09-757-217A-9	Sequence 9, Appli	745	12	36.4	24	9	US-09-973-451-18	Sequence 18, Appl
c 673	12.2	37.0	27	9	US-09-828-255A-9	Sequence 9, Appli	746	12	36.4	24	10	US-09-940-185-2633	Sequence 2633, Ap
c 674	12.2	37.0	27	9	US-09-784-818-8	Sequence 8, Appli	c 747	12	36.4	25	9	US-09-866-108-10990	Sequence 10990, A
c 675	12.2	37.0	27	10	US-09-756-248-8	Sequence 8, Appli	c 748	12	36.4	25	14	US-10-215-112-12413	Sequence 12413, A
c 676	12.2	37.0	27	11	US-09-828-317A-9	Sequence 9, Appli	c 749	12	36.4	25	15	US-10-098-263B-47198	Sequence 47198, A
c 677	12.2	37.0	27	15	US-10-244-215-74	Sequence 74, Appli	c 750	12	36.4	25	15	US-10-098-263B-50355	Sequence 50355, A
c 678	12.2	37.0	28	9	US-09-779-881-2	Sequence 2, Appli	c 751	12	36.4	25	15	US-10-098-263B-54146	Sequence 54146, A
c 679	12.2	37.0	28	18	US-10-687-402-16	Sequence 16, Appli	752	12	36.4	25	15	US-10-098-263B-55238	Sequence 55238, A
c 680	12.2	37.0	30	16	US-10-412-382-54	Sequence 54, Appli	753	12	36.4	25	15	US-10-098-263B-57444	Sequence 57444, A
c 681	12.2	37.0	32	9	US-09-837-644-4	Sequence 4, Appli	754	12	36.4	25	15	US-10-098-263B-64469	Sequence 64469, A
c 682	12.2	37.0	32	14	US-10-027-760-4	Sequence 4, Appli	755	12	36.4	25	15	US-10-098-263B-84004	Sequence 84004, A
c 683	12.2	37.0	32	16	US-10-622-108-36	Sequence 36, Appli	c 756	12	36.4	25	15	US-10-098-263B-95095	Sequence 95095, A
c 684	12.2	37.0	33	10	US-09-981-002-22	Sequence 22, Appli	c 757	12	36.4	25	15	US-10-098-263B-95096	Sequence 95096, A
c 685	12.2	37.0	36	16	US-10-682-595-8	Sequence 8, Appli	c 758	12	36.4	25	15	US-10-098-263B-96197	Sequence 96197, A
c 686	12.2	37.0	37	10	US-09-405-032-36	Sequence 36, Appli	759	12	36.4	25	15	US-10-098-263B-99822	Sequence 99822, A
c 687	12.2	37.0	37	10	US-09-405-032-38	Sequence 38, Appli	760	12	36.4	25	15	US-10-098-263B-100302	Sequence 100302, A
c 688	12.2	37.0	39	14	US-10-086-156-41	Sequence 41, Appli	761	12	36.4	25	15	US-10-098-263B-103785	Sequence 103785, A
c 689	12.2	37.0	39	18	US-10-031-123B-28	Sequence 28, Appli	762	12	36.4	25	15	US-10-098-263B-111921	Sequence 111921, A
c 690	12.2	37.0	40	9	US-09-245-802-54	Sequence 54, Appli	c 763	12	36.4	25	15	US-10-098-263B-117644	Sequence 117644, A
c 691	12.2	37.0	40	9	US-09-780-923-67	Sequence 67, Appli	c 764	12	36.4	25	15	US-10-278-455-33	Sequence 33, Appl
c 692	12.2	37.0	40	9	US-09-780-923-72	Sequence 72, Appli	c 765	12	36.4	25	15	US-10-278-437-33	Sequence 33, Appl
c 693	12.2	37.0	40	9	US-09-780-923-78	Sequence 78, Appli	c 766	12	36.4	25	17	US-10-723-361-10990	Sequence 10990, A
c 694	12.2	37.0	40	9	US-09-780-923-81	Sequence 81, Appli	767	12	36.4	26	9	US-09-784-911-21	Sequence 21, Appl
c 695	12.2	37.0	40	9	US-09-780-923-82	Sequence 82, Appli	768	12	36.4	27	17	US-09-716-359-29	Sequence 29, Appl
c 696	12.2	37.0	40	9	US-09-759-508B-4	Sequence 4, Appli	769	12	36.4	29	9	US-09-982-308-14	Sequence 14, Appl
c 697	12.2	37.0	40	9	US-09-759-508B-9	Sequence 9, Appli	770	12	36.4	29	13	US-10-145-014-14	Sequence 14, Appl
c 698	12.2	37.0	40	10	US-09-963-847B-54	Sequence 54, Appli	771	12	36.4	29	13	US-10-336-638-748	Sequence 748, App
c 699	12.2	37.0	40	15	US-10-230-576-3	Sequence 3, Appli	772	12	36.4	29	15	US-10-235-079B-11	Sequence 11, Appl
c 700	12.2	37.0	41	16	US-10-035-833A-6184	Sequence 6184, Ap	773	12	36.4	30	15	US-10-772-656-69	Sequence 69, Appl
c 701	12.2	37.0	42	14	US-10-181-836-14	Sequence 14, Appli	774	12	36.4	31	17	US-10-314-861-20	Sequence 20, Appl
c 702	12.2	37.0	45	18	US-10-031-123B-10	Sequence 10, Appli	775	12	36.4	32	15	US-10-706-466-9	Sequence 9, Appli
c 703	12.2	37.0	46	16	US-10-406-027-131	Sequence 131, App	776	12	36.4	32	16	US-09-894-839-42	Sequence 42, Appl
c 704	12.2	37.0	47	16	US-10-349-143-519	Sequence 519, App	c 777	12	36.4	33	15	US-10-176-255-18	Sequence 18, Appl
c 705	12.2	37.0	47	16	US-10-349-143-3353	Sequence 3353, Ap	778	12	36.4	33	15	US-10-176-255-19	Sequence 19, Appl
c 706	12.2	37.0	47	16	US-10-294-934-776	Sequence 776, App	c 779	12	36.4	33	15	US-10-055-555-18	Sequence 18, Appl
c 707	12.2	37.0	47	16	US-10-333-429-109	Sequence 109, App	780	12	36.4	33	15	US-10-055-555-19	Sequence 19, Appl
c 708	12.2	37.0	48	15	US-10-230-006-2248	Sequence 2248, Ap	c 781	12	36.4	33	16	US-10-392-837A-49	Sequence 49, Appl
c 709	12.2	37.0	49	16	US-10-380-705-37	Sequence 27, Appli	782	12	36.4	33	18	US-10-815-495-10	Sequence 10, Appl
c 710	12.2	37.0	50	16	US-10-131-827-3371	Sequence 3371, Ap	783	12	36.4	35	9	US-09-982-308-11	Sequence 11, Appl
c 711	12	36.4	12	8	US-08-887-505-98	Sequence 98, Appli	c 784	12	36.4	35	10	US-09-825-805-207	Sequence 207, App
c 712	12	36.4	13	10	US-09-740-332-4720	Sequence 4720, Ap	785	12	36.4	35	13	US-10-145-014-11	Sequence 11, Appl
c 713	12	36.4	13	10	US-09-817-879-4720	Sequence 4720, Ap	786	12	36.4	36	9	US-09-504-231A-2882	Sequence 2882, Ap
c 714	12	36.4	13	17	US-10-669-841-7313	Sequence 7313, Ap	787	12	36.4	36	9	US-09-274-553D-2882	Sequence 2882, Ap
c 715	12	36.4	14	16	US-10-461-790-122	Sequence 122, App	c 788	12	36.4	36	10	US-09-848-754A-9561	Sequence 9561, Ap
c 716	12	36.4	15	9	US-09-504-231A-1526	Sequence 1526, Ap	c 789	12	36.4	37	9	US-09-864-785-1748	Sequence 1748, Ap
c 717	12	36.4	15	9	US-09-274-553D-1526	Sequence 1526, Ap	c 790	12	36.4	37	9	US-09-864-785-1798	Sequence 1798, Ap
c 718	12	36.4	15	10	US-09-740-332-4707	Sequence 4707, Ap	c 791	12	36.4	37	10	US-09-825-805-208	Sequence 208, App
c 719	12	36.4	15	10	US-09-740-332-4708	Sequence 4708, Ap	c 792	12	36.4	37	10	US-09-848-616-149	Sequence 149, App
c 720	12	36.4	15	10	US-09-740-332-4723	Sequence 4723, Ap	c 793	12	36.4	37	10	US-09-927-046-3796	Sequence 3796, Ap
c 721	12	36.4	15	10	US-09-817-879-4707	Sequence 4707, Ap	c 794	12	36.4	37	10	US-09-848-754A-6001	Sequence 6001, Ap
c 722	12	36.4	15	10	US-09-817-879-4708	Sequence 4708, Ap	c 795	12	36.4	37	10	US-09-848-754A-6301	Sequence 6301, Ap
c 723	12	36.4	15	10	US-09-817-879-4723	Sequence 4723, Ap	c 796	12	36.4	37	10	US-09-848-754A-6328	Sequence 6328, Ap
c 724	12	36.4	15	17	US-10-669-841-7300	Sequence 7300, Ap	c 797	12	36.4	37	10	US-09-848-754A-6345	Sequence 6345, Ap
c 725	12	36.4	15	17	US-10-669-841-7301	Sequence 7301, Ap	c 798	12	36.4	37	10	US-09-848-754A-6398	Sequence 6398, Ap
c 726	12	36.4	15	17	US-10-669-841-7316	Sequence 7316, Ap	c 799	12	36.4	37	10	US-09-827-395A-1780	Sequence 1780, Ap
c 727	12	36.4	17	10	US-09-740-332-38	Sequence 28, Appli	c 800	12	36.4	37	15	US-10-156-306-2576	Sequence 2576, Ap
c 728	12	36.4	17	10	US-09-740-332-36	Sequence 36, Appli	c 801	12	36.4	37	15	US-10-156-306-2638	Sequence 2638, Ap
c 729	12	36.4	17	10	US-09-817-879-28	Sequence 28, Appli	c 802	12	36.4	37	15	US-10-156-306-6076	Sequence 6076, Ap
c 730	12	36.4	17	10	US-09-817-879-36	Sequence 36, Appli	c 803	12	36.4	37	15	US-10-156-306-6120	Sequence 6120, Ap
c 731	12	36.4	17	17	US-10-669-841-2621	Sequence 2621, Ap	c 804	12	36.4	37	15	US-10-156-306-6122	Sequence 6122, Ap
c 732	12	36.4	17	17	US-10-669-841-2621	Sequence 2621, Ap	c 805	12	36.4	37	15	US-10-156-306-6178	Sequence 6178, Ap
c 733	12	36.4	19	18	US-10-667-271-67	Sequence 67, Appli	c 806	12	36.4	37	15	US-10-156-306-6308	Sequence 6308, Ap
c 734	12	36.4	19	18	US-10-667-271-70	Sequence 70, Appli	c 807	12	36.4	37	15	US-10-289-454-370	Sequence 370, App
c 735	12	36.4	19	18	US-10-667-271-763	Sequence 763, App	c 808	12	36.4	37	15	US-10-050-902-149	Sequence 149, App
c 736	12	36.4	19	18	US-10-667-271-766	Sequence 766, App	c 809	12	36.4	37	15	US-10-050-988-149	Sequence 149, App
c 737	12	36.4	20	8	US-08-887-505-84	Sequence 84, Appli	c 810	12	36.4	37	15	US-10-230-006-1453	Sequence 1453, Ap
c 738	12	36.4	20	10	US-08-944-410-9	Sequence 9, Appli	c 811	12	36.4	37	15	US-10-430-882-1780	Sequence 1780, Ap
c 739	12	36.4	20	10	US-09-882-945A-60	Sequence 60, Appli	c 812	12	36.4	37	15	US-10-346-190-150	Sequence 150, App
c 740	12	36.4	20	16	US-10-300-288-42	Sequence 42, Appli	c 813	12	36.4	37	16	US-10-289-456-149	Sequence 149, App
c 741	12	36.4	21	15	US-10-258-746-4	Sequence 4, Appli	c 814	12	36.4	37	16	US-10-289-456-149	Sequence 92, Appl
c 742	12	36.4	22	15	US-10-136-728-126	Sequence 126, App	815	12	36.4	37	16	US-10-622-124-93	Sequence 93, Appl

C 816	12	36.4	37	16	US-10-138-674-18155	Sequence 18165, A	889	12	36.4	38	17	US-10-287-949A-15929	Sequence 15929, A
C 817	12	36.4	37	16	US-10-138-674-18153	Sequence 18193, A	890	12	36.4	38	17	US-10-669-841-8115	Sequence 8115, Ap
C 818	12	36.4	37	16	US-10-138-674-18339	Sequence 18339, A	891	12	36.4	38	17	US-10-669-841-8389	Sequence 8389, Ap
C 819	12	36.4	37	16	US-10-138-674-18339	Sequence 18389, A	892	12	36.4	38	17	US-10-669-841-8732	Sequence 8732, Ap
C 820	12	36.4	37	16	US-10-138-674-18408	Sequence 18408, A	C 893	12	36.4	38	17	US-10-669-841-9372	Sequence 9372, Ap
C 821	12	36.4	37	16	US-10-138-674-18453	Sequence 18453, A	C 894	12	36.4	39	15	US-10-323-069A-83	Sequence 83, Appl
C 822	12	36.4	37	16	US-10-138-674-18473	Sequence 18453, A	C 895	12	36.4	40	9	US-09-245-802-13	Sequence 13, Appl
C 823	12	36.4	37	16	US-10-138-674-18486	Sequence 18486, A	C 896	12	36.4	40	10	US-09-963-827B-144	Sequence 144, App
C 824	12	36.4	37	16	US-10-138-674-20261	Sequence 20261, A	C 897	12	36.4	40	18	US-10-469-851-230	Sequence 230, Appl
C 825	12	36.4	37	16	US-10-138-674-20387	Sequence 20387, A	C 898	12	36.4	41	15	US-10-296-616-13	Sequence 13, Appl
C 826	12	36.4	37	16	US-10-138-674-20431	Sequence 20431, A	C 899	12	36.4	41	15	US-10-296-616-14	Sequence 14, Appl
C 827	12	36.4	37	16	US-10-138-674-20473	Sequence 20473, A	C 900	12	36.4	41	16	US-10-035-833A-941	Sequence 941, App
C 828	12	36.4	37	16	US-10-138-674-20512	Sequence 20512, A	C 901	12	36.4	41	16	US-10-035-833A-2057	Sequence 2057, App
C 829	12	36.4	37	16	US-10-138-674-20516	Sequence 20516, A	C 902	12	36.4	41	16	US-10-035-833A-6951	Sequence 6951, Ap
C 830	12	36.4	37	16	US-10-138-674-20627	Sequence 20627, A	C 903	12	36.4	41	16	US-10-035-833A-7314	Sequence 7314, Ap
C 831	12	36.4	37	17	US-10-287-949A-18165	Sequence 18165, A	C 904	12	36.4	42	9	US-09-101-807-5	Sequence 5, Appl
C 832	12	36.4	37	17	US-10-287-949A-18193	Sequence 18193, A	C 905	12	36.4	44	15	US-10-270-071-3	Sequence 3, Appl
C 833	12	36.4	37	17	US-10-287-949A-18339	Sequence 18339, A	C 906	12	36.4	44	15	US-10-251-215-29	Sequence 29, Appl
C 834	12	36.4	37	17	US-10-287-949A-18389	Sequence 18389, A	C 907	12	36.4	45	14	US-10-146-835-18	Sequence 18, Appl
C 835	12	36.4	37	17	US-10-287-949A-18408	Sequence 18408, A	C 908	12	36.4	47	16	US-10-294-934-712	Sequence 712, App
C 836	12	36.4	37	17	US-10-287-949A-18453	Sequence 18453, A	C 909	12	36.4	48	14	US-10-165-857-4	Sequence 4, Appl
C 837	12	36.4	37	17	US-10-287-949A-18473	Sequence 18473, A	C 910	12	36.4	48	15	US-10-295-798-16	Sequence 16, Appl
C 838	12	36.4	37	17	US-10-287-949A-18486	Sequence 18486, A	C 911	12	36.4	48	15	US-10-244-142A-18	Sequence 18, Appl
C 839	12	36.4	37	17	US-10-287-949A-20261	Sequence 20261, A	C 912	12	36.4	48	15	US-10-165-856A-4	Sequence 4, Appl
C 840	12	36.4	37	17	US-10-287-949A-20387	Sequence 20387, A	C 913	12	36.4	48	17	US-10-165-856A-4	Sequence 4, Appl
C 841	12	36.4	37	17	US-10-287-949A-20431	Sequence 20431, A	C 914	12	36.4	50	16	US-10-131-827-1356	Sequence 1356, Ap
C 842	12	36.4	37	17	US-10-287-949A-20473	Sequence 20473, A	C 915	11.8	35.8	15	9	US-09-504-231A-1558	Sequence 1558, Ap
C 843	12	36.4	37	17	US-10-287-949A-20512	Sequence 20512, A	C 916	11.8	35.8	15	9	US-09-274-553D-1558	Sequence 1558, Ap
C 844	12	36.4	37	17	US-10-287-949A-20516	Sequence 20516, A	C 917	11.8	35.8	17	9	US-09-866-108-6087	Sequence 6087, Ap
C 845	12	36.4	37	17	US-10-287-949A-20627	Sequence 20627, A	C 918	11.8	35.8	17	9	US-09-866-108-6088	Sequence 6088, Ap
C 846	12	36.4	37	17	US-10-622-087-62	Sequence 62, Appl	C 919	11.8	35.8	17	10	US-09-818-875-3194	Sequence 3194, Ap
C 847	12	36.4	37	17	US-09-825-805-936	Sequence 936, Appl	C 920	11.8	35.8	17	10	US-09-818-875-3195	Sequence 3195, Ap
C 848	12	36.4	38	10	US-09-825-805-987	Sequence 987, App	C 921	11.8	35.8	17	10	US-09-940-925A-152	Sequence 152, App
C 849	12	36.4	38	10	US-09-825-805-1332	Sequence 1332, Ap	C 922	11.8	35.8	17	10	US-09-941-193A-152	Sequence 152, App
C 850	12	36.4	38	10	US-09-825-805-1361	Sequence 1361, Ap	C 923	11.8	35.8	17	10	US-09-740-332-33	Sequence 33, Appl
C 851	12	36.4	38	10	US-09-825-805-1362	Sequence 1362, Ap	C 924	11.8	35.8	17	10	US-09-817-879-33	Sequence 33, Appl
C 852	12	36.4	38	10	US-09-730-289B-2596	Sequence 2596, Ap	C 925	11.8	35.8	17	15	US-10-230-006-535	Sequence 535, App
C 853	12	36.4	38	10	US-09-730-289B-2803	Sequence 2803, Ap	C 926	11.8	35.8	17	15	US-10-230-006-536	Sequence 536, App
C 854	12	36.4	38	10	US-09-780-533A-3211	Sequence 3211, Ap	C 927	11.8	35.8	17	15	US-10-209-787-3194	Sequence 3194, Ap
C 855	12	36.4	38	10	US-09-780-533A-4514	Sequence 4514, Ap	C 928	11.8	35.8	17	15	US-10-209-787-3195	Sequence 3195, Ap
C 856	12	36.4	38	10	US-09-780-533A-4514	Sequence 4514, Ap	C 929	11.8	35.8	17	16	US-10-261-185-3194	Sequence 3194, Ap
C 857	12	36.4	38	10	US-09-877-478-3498	Sequence 3498, Ap	C 930	11.8	35.8	17	16	US-10-261-185-3195	Sequence 3195, Ap
C 858	12	36.4	38	10	US-09-877-478-3498	Sequence 3498, Ap	C 931	11.8	35.8	17	17	US-10-669-841-2626	Sequence 2626, Ap
C 859	12	36.4	38	10	US-09-877-478-3498	Sequence 3498, Ap	C 932	11.8	35.8	17	17	US-10-723-361-6087	Sequence 6087, Ap
C 860	12	36.4	38	10	US-09-776-474-2132	Sequence 2132, Ap	C 933	11.8	35.8	17	17	US-10-723-361-6088	Sequence 6088, Ap
C 861	12	36.4	38	10	US-09-930-423-2567	Sequence 2567, Ap	C 934	11.8	35.8	17	17	US-10-681-074-3194	Sequence 3194, Ap
C 862	12	36.4	38	10	US-09-930-423-2719	Sequence 2719, Ap	C 935	11.8	35.8	17	17	US-10-681-074-3195	Sequence 3195, Ap
C 863	12	36.4	38	10	US-09-930-423-3050	Sequence 3050, Ap	C 936	11.8	35.8	17	18	US-10-660-122-23	Sequence 23, Appl
C 864	12	36.4	38	10	US-09-930-423-3089	Sequence 3089, Ap	C 937	11.8	35.8	19	18	US-10-667-271-62	Sequence 62, Appl
C 865	12	36.4	38	10	US-09-930-423-3194	Sequence 3194, Ap	C 938	11.8	35.8	19	18	US-10-667-271-758	Sequence 758, App
C 866	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 939	11.8	35.8	20	9	US-09-855-797A-36	Sequence 36, Appl
C 867	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 940	11.8	35.8	20	9	US-09-981-621-11	Sequence 11, Appl
C 868	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 941	11.8	35.8	20	9	US-09-728-574-43	Sequence 43, Appl
C 869	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 942	11.8	35.8	20	9	US-09-907-900-36	Sequence 36, Appl
C 870	12	36.4	38	10	US-09-780-164-1243	Sequence 1243, Ap	C 943	11.8	35.8	20	9	US-09-907-900-36	Sequence 36, Appl
C 871	12	36.4	38	10	US-09-745-237A-2567	Sequence 2567, Ap	C 944	11.8	35.8	20	10	US-09-909-595-36	Sequence 36, Appl
C 872	12	36.4	38	10	US-09-745-237A-2719	Sequence 2719, Ap	C 945	11.8	35.8	20	10	US-09-985-448-36	Sequence 36, Appl
C 873	12	36.4	38	10	US-09-745-237A-3050	Sequence 3050, Ap	C 946	11.8	35.8	20	15	US-10-196-842-9	Sequence 9, Appl
C 874	12	36.4	38	10	US-09-745-237A-3089	Sequence 3089, Ap	C 947	11.8	35.8	20	15	US-10-197-026A-18	Sequence 18, Appl
C 875	12	36.4	38	10	US-09-745-237A-3194	Sequence 3194, Ap	C 948	11.8	35.8	20	15	US-10-300-892-36	Sequence 36, Appl
C 876	12	36.4	38	15	US-10-156-306-1802	Sequence 1802, Ap	C 949	11.8	35.8	20	15	US-10-331-109-1	Sequence 1, Appl
C 877	12	36.4	38	15	US-10-230-006-842	Sequence 842, App	C 950	11.8	35.8	20	15	US-10-331-109-2	Sequence 2, Appl
C 878	12	36.4	38	16	US-10-342-902-3224	Sequence 3224, Ap	C 951	11.8	35.8	20	15	US-10-159-834-33	Sequence 33, Appl
C 879	12	36.4	38	16	US-10-342-902-3498	Sequence 3498, Ap	C 952	11.8	35.8	20	16	US-10-159-834-101	Sequence 101, App
C 880	12	36.4	38	16	US-10-342-902-3841	Sequence 3841, Ap	C 953	11.8	35.8	20	16	US-10-289-762-5638	Sequence 5638, Ap
C 881	12	36.4	38	16	US-10-342-902-4481	Sequence 4481, Ap	C 954	11.8	35.8	20	16	US-10-303-199A-3	Sequence 3, Appl
C 882	12	36.4	38	16	US-10-138-674-13539	Sequence 13539, A	C 955	11.8	35.8	20	16	US-10-680-316-36	Sequence 36, Appl
C 883	12	36.4	38	16	US-10-138-674-13697	Sequence 13697, A	C 956	11.8	35.8	20	17	US-10-815-730-36	Sequence 36, Appl
C 884	12	36.4	38	16	US-10-138-674-13836	Sequence 13836, A	C 957	11.8	35.8	20	17	US-10-820-133-36	Sequence 36, Appl
C 885	12	36.4	38	16	US-10-138-674-15929	Sequence 15929, A	C 958	11.8	35.8	22	15	US-10-419-034-5	Sequence 5, Appl
C 886	12	36.4	38	17	US-10-287-949A-13539	Sequence 13539, A	C 959	11.8	35.8	24	10	US-09-827-737-90	Sequence 90, Appl
C 887	12	36.4	38	17	US-10-287-949A-13697	Sequence 13697, A	C 960	11.8	35.8	25	9	US-09-829-066B-10	Sequence 10, Appl
C 888	12	36.4	38	17	US-10-287-949A-13836	Sequence 13836, A	C 961	11.8	35.8	25	14	US-10-060-830-537	Sequence 537, App

Sequence 14238, A
Sequence 1847, Ap
Sequence 4640, Ap
Sequence 4533, Ap
Sequence 6720, Ap
Sequence 17151, A
Sequence 29536, A
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Sequence 104724, A
Sequence 112256, A
Sequence 114794, A
Sequence 118102, A
Sequence 128255, A
Sequence 128409, A
Sequence 130429, A
Sequence 1828, Ap
Sequence 47, Appl
Sequence 34, Appl
Sequence 5, Appl

11.8 35.8 25 14 US-10-215-112-14238
11.8 35.8 25 15 US-10-098-263B-1847
11.8 35.8 25 15 US-10-098-263B-4640
11.8 35.8 25 15 US-10-098-263B-4953
11.8 35.8 25 15 US-10-098-263B-6720
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11.8 35.8 25 15 US-10-098-263B-29536
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11.8 35.8 25 15 US-10-098-263B-36188
11.8 35.8 25 15 US-10-098-263B-38311
11.8 35.8 25 15 US-10-098-263B-41441
11.8 35.8 25 15 US-10-098-263B-43815
11.8 35.8 25 15 US-10-098-263B-47317
11.8 35.8 25 15 US-10-098-263B-48106
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11.8 35.8 25 15 US-10-098-263B-128409
11.8 35.8 25 15 US-10-098-263B-130429
11.8 35.8 25 17 US-10-775-169-1828
11.8 35.8 26 9 US-09-117-860-47
11.8 35.8 26 9 US-09-732-618-34
11.8 35.8 29 9 US-09-884-566-5

ALIGNMENTS

RESULT 1
US-10-087-631B-3
; Sequence 3, Application US/10087631B
; Publication No. US20030054372A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/087,631B
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST650 HCV specific probe
US-10-087-631B-3

Query Match 100.0%; Score 33; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33

RESULT 2
US-10-419-022-3
; Sequence 3, Application US/10419022
; Publication No. US20030165982A1
; GENERAL INFORMATION:
; APPLICANT: JAEGER, STEPHAN
; TITLE OF INVENTION: A METHOD FOR THE DETERMINATION OF A NUCLEIC ACID USING A
; FILE REFERENCE: 1803-335-999
; CURRENT APPLICATION NUMBER: US/10/419,022
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/10/087,631B
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ST650 HCV specific probe
US-10-419-022-3

Query Match 100.0%; Score 33; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATGCG 33

RESULT 3
US-10-337-190-1
; Sequence 1, Application US/10337190
; Publication No. US20040014070A1
; GENERAL INFORMATION:
; APPLICANT: Pinsl, Judith
; APPLICANT: Wenzig, Peter
; APPLICANT: Schoenbrunner, Ralf
; APPLICANT: O'Donnell, Patrick
; APPLICANT: Kyger, Erich
; APPLICANT: Malhotra, Kushbeer
; APPLICANT: Weindel, Kurt
; APPLICANT: Bartl, Knut
; TITLE OF INVENTION: Use of Silica Material in an Amplification Reaction
; FILE REFERENCE: 21255-US
; CURRENT APPLICATION NUMBER: US/10/337,190
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: 60/347,3237
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: HCV specific probe
US-10-337-190-1

Query Match 93.9%; Score 31; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31
Db 1 CGGTGTACTACCGTTCGCGAGACCACCTATG 31

RESULT 4
US-10-451-882-42
; Sequence 42, Application US/10451882
; Publication No. US20040185455A1
; GENERAL INFORMATION:
; APPLICANT: Takara Shuzo Co., Ltd.
; TITLE OF INVENTION: Method for detection of virulent organisms
; FILE REFERENCE: 662981
; CURRENT APPLICATION NUMBER: US/10/451,882
; PRIOR FILING DATE: 2004-01-05
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2000-396321
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2000-396222
; PRIOR FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: JP 2001-199552
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: JP 2001-278920
; PRIOR FILING DATE: 2001-09-13
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 42
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer area to amplify a portion of HCV.
US-10-451-882-42

Query Match 66.7%; Score 22; DB 17; Length 41;
Best Local Similarity 97.1%; Pred. No. 6.6;
Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGGTGTACTCACC-GTTCGCGAGACCACTATGGC 33
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DB 5 CGGTGTACTCACC GTTCGCGAGACCACTATGGC 38
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RESULT 5
US-10-318-416B-34/c
; Sequence 34, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; FILE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-34

Query Match 60.6%; Score 20; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGGC 33
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DB 24 GTTCGCGAGACCACTATGGC 5
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RESULT 6
US-10-318-416B-32
; Sequence 32, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:

; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; FILE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-32

Query Match 60.6%; Score 20; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCGCGAGACCACTATGGC 33
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DB 1 GTTCGCGAGACCACTATGGC 20
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RESULT 7
US-10-147-679A-20
; Sequence 20, Application US/10147679A
; Publication No. US20030224366A1
; GENERAL INFORMATION:
; APPLICANT: Weindel, Kurt
; APPLICANT: Riedling, Michael
; APPLICANT: Geiger, Albert
; TITLE OF INVENTION: Magnetic glass particles, method for their preparation
; TITLE OF INVENTION: and uses thereof
; FILE REFERENCE: 1803-344-999
; CURRENT APPLICATION NUMBER: US/10/147,679A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: EP99122853.7
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide probe (HCV)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: derivatisation with a
; OTHER INFORMATION: Pentamethine-di-indocarbocyanine via a
; OTHER INFORMATION: alkylphosphatidyl-linker (Pharmacia Biotech
; OTHER INFORMATION: Cy5-N-ethyl-phosphoramidite)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: N represents a
; OTHER INFORMATION: 2-(amino-cyclohexyl)-propane-1,3-diol-linker
; OTHER INFORMATION: derivatised with 6-carboxy-fluorescein (Biogenex
; OTHER INFORMATION: CX-FAM-phosphoramidite)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (31)
; OTHER INFORMATION: derivatisation with a 3'-terminal phosphate group
US-10-147-679A-20

Query Match 60.6%; Score 20; DB 15; Length 32;
Best Local Similarity 96.9%; Pred. No. 51;

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Matches 31; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 CGGTGTACTCAGC-TTCCGCGAGACCACTATG 31
Db 1 CGGTGTACTCAGCGTTCCGCGAGACCACTATG 32

RESULT 8
US-09-782-361-3/c
; Sequence 3, Application US/09782361
; Patent No. US20020064778A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yu-Wen
; TITLE OF INVENTION: PRIMER-SPECIFIC AND MISPAIR EXTENSION ASSAY FOR IDENTIFYING GEN
; FILE REFERENCE: 2883-4757US
; CURRENT APPLICATION NUMBER: US/09/782,361
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: sense universal primer for PCR (second round)
US-09-782-361-3

Query Match 58.8%; Score 19.4; DB 9; Length 31;
Best Local Similarity 95.2%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CGGTTCGCGAGACCACTATGG 32
Db 21 CGGTTCGCGAGACCACTATGG 1

RESULT 9
US-09-747-419-11
; Sequence 11, Application US/09747419
; Patent No. US20020155582A1
; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0101
; CURRENT APPLICATION NUMBER: US/09/747,419
; CURRENT FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-747-419-11

Query Match 57.6%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTCCGCGAGACCACTATGG 32
Db 1 GTTCCGCGAGACCACTATGG 19

RESULT 10
US-10-259-275-11
; Sequence 11, Application US/10259275
; Publication No. US20030125541A1
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; GENERAL INFORMATION:
; APPLICANT: Lemon, Stanley M.
; APPLICANT: Yi, Minkyung
; TITLE OF INVENTION: REPLICATION COMPETENT HEPATITIS C VIRUS AND METHODS OF USE
; FILE REFERENCE: 265.0007 0120
; CURRENT APPLICATION NUMBER: US/10/259,275
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/171,909
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 09/747,419
; PRIOR FILING DATE: 2000-12-23
; PRIOR APPLICATION NUMBER: US 60/325,236
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/338,123
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-10-259-275-11

Query Match 57.6%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 GTTCCGCGAGACCACTATGG 32
Db 1 GTTCCGCGAGACCACTATGG 19

RESULT 11
US-10-667-271-78/c
; Sequence 78, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-7638)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-78

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
      |||||
Db 19 TTCCGCAGACCACTATGGC 1

RESULT 12
US-10-667-271-82/c
; Sequence 82, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-667-271-82

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGG 32
      |||||
Db 19 GTTCCGCAGACCACTATGG 1

RESULT 13
US-10-667-271-774
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; Sequence 774, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 774
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-774

Query Match      57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
      :|||||:|:|:|
Db 1  UUCGCGACCAUUGGC 19

RESULT 14
US-10-667-271-778
; Sequence 778, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
```

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; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 778
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:  s1NA antisense region
US-10-667-271-778

Query Match          57.6%; Score 19; DB 18; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGG 32
Db 1 GUUCCGCAGACCACTATGG 19

RESULT 15
US-10-471-351-1/c
; Sequence 1, Application US/10471351
; Publication No. US20040115685A1
; GENERAL INFORMATION:
; APPLICANT: Tercero, Juan Carlos
; APPLICANT: Garcia, Lucia
; APPLICANT: Guisan, Jose Manuel
; APPLICANT: Fernandez, Roberto
; APPLICANT: Fuentes, Manuel
; TITLE OF INVENTION: IMMOBILISATION OF LIGANDS
; FILE REFERENCE: 14620-025U1
; CURRENT APPLICATION NUMBER: US/10/471,351
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/GB02/01059
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: GB 0105745.4
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: this sequence has an aminated 3'-terminus
; FEATURE:
; OTHER INFORMATION: Probe sequence
US-10-471-351-1

Query Match          57.6%; Score 19; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCAGACCACTATGGC 33
Db 25 TTCCGCAGACCACTATGGC 7

US-10-087-631b-3.max.rnpb
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US-10-318-416B-35/c
; Sequence 35, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-35

Query Match          55.8%; Score 18.4; DB 17; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGGC 33
Db 24 GTTCCGCAGACCACTATGGC 5

RESULT 17
US-10-318-416B-33
; Sequence 33, Application US/10318416B
; Publication No. US20040115643A1
; GENERAL INFORMATION:
; APPLICANT: Lizardi, Paul M.
; APPLICANT: Gribanov, Oleg G.
; TITLE OF INVENTION: THERMODYNAMIC EQUILIBRIUM EXTENSION OF
; TITLE OF INVENTION: PRIMERS
; FILE REFERENCE: 25006.0012U1
; CURRENT APPLICATION NUMBER: US/10/318,416B
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-10-318-416B-33

Query Match          55.8%; Score 18.4; DB 17; Length 26;
Best Local Similarity 95.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTTCCGCAGACCACTATGGC 33
Db 1 GTTCCGCAGACCACTATGGC 20

RESULT 18
US-10-008-140B-11
; Sequence 11, Application US/10008140B
; Publication No. US20030124512A1
; GENERAL INFORMATION:
; APPLICANT: Pharmasset, Ltd.
; APPLICANT: Stuyver, Lieven
```

; TITLE OF INVENTION: Simultaneous Quantification of Nucleic Acids in Diseased Cells
; FILE REFERENCE: 08841.105021
; CURRENT APPLICATION NUMBER: US/10/008,140B
; CURRENT FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotides used to amplify HCV (primers) antisense
US-10-008-140B-11

Query Match 54.5%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCGACCACTATGG 32
Db 1 TTCGCGACCACTATGG 18

RESULT 19
US-10-667-271-80/c
; Sequence 80, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

US-10-667-271-80

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCGACCACTATGG 32
Db 1 TTCGCGACCACTATGG 18

RESULT 21
US-10-667-271-776
; Sequence 776, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

US-10-667-271-80

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCGACCACTATGG 32
Db 1 TTCGCGACCACTATGG 18

Qy 14 GTTCCGACCACTATG 31
Db 18 GTTCCGACCACTATG 1

RESULT 20
US-10-667-271-81/c
; Sequence 81, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

US-10-667-271-81

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TCCGCGACCACTATGGC 33
Db 19 TCCGCGACCACTATGGC 2

RESULT 21
US-10-667-271-776
; Sequence 776, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

US-10-667-271-81

Query Match 54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TCCGCGACCACTATGGC 33
Db 19 TCCGCGACCACTATGGC 2

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; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 776
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: s1NA antisense region
US-10-667-271-776

Query Match          54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 77.8%; Pred. No. 3.9e+02;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 14 GTTCCGCAGACCACCTATG 31
Db 2 GUUCCGCAGACCACCUAUG 19

RESULT 22
US-10-667-271-777
; Sequence 777, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB03-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
```

```
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 777
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: s1NA antisense region
US-10-667-271-777

Query Match          54.5%; Score 18; DB 18; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 16 TCCGCAGACCACCTATGGC 33
Db 1 UCCGCAGACCACCUAUGGC 18

RESULT 23
US-10-240-460-8/c
; Sequence 8, Application US/10240460
; Publication No. US20030207292A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030207292A1omi, Tsugunori
; APPLICANT: Nagamine, Kentaro
; TITLE OF INVENTION: METHOD FOR AMPLIFYING NUCLEIC ACID BY USING
; FILE REFERENCE: 201487/1110
; CURRENT APPLICATION NUMBER: US/10/240,460
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/JF01/02771
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-111939
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificially
; OTHER INFORMATION: synthesized primer sequence
US-10-240-460-8

Query Match          54.5%; Score 18; DB 15; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 TCCGCAGACCACCTATGGC 33
Db 46 TCCGCAGACCACCTATGGC 29

RESULT 24
US-10-667-271-76/c
; Sequence 76, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MBHB02-763B)
```

; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-10-667-271-772

Query Match 52.7%; Score 17.4; DB 18; Length 19;
Best Local Similarity 94.7%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCACTAT 30
|:|||||
Db 19 CCGTTCGCGAGACCACTAT 1

RESULT 25
US-10-667-271-772
; Sequence 772, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence
US-10-667-271-772

; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 772
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-667-271-772

Query Match 52.7%; Score 17.4; DB 18; Length 19;
Best Local Similarity 73.7%; Pred. No. 7.2e+02;
Matches 14; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGAGACCACTAT 30
|:|||||
Db 1 CCGUUCGCGAGACCAUAU 19

RESULT 26
US-10-667-271-1401/c
; Sequence 1401, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/129 (MBH02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1705
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1401
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense region
US-10-667-271-1401

Query Match 52.7%; Score 17.4; DB 18; Length 23;
Best Local Similarity 94.7%; Pred. No. 7.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 12 CCGTTCGCGAGACCACTAT 30
Db 19 CCGTTCGCGAGACCACTAT 1

RESULT 27
US-09-740-332-30/c
; Sequence 30, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-30

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCGAGACCACTATGG 32
Db 17 TCCGCGAGACCACTATGG 1

RESULT 28
US-09-740-332-4525
; Sequence 4525, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-4525

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCACTATG 31
Db 1 UUCCGCGAGACCAUAUG 17

RESULT 29
US-09-817-879-30/c
; Sequence 30, Application US/09817879
```

```
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-30

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TCCGCGAGACCACTATGG 32
Db 17 TCCGCGAGACCACTATGG 1

RESULT 30
US-09-817-879-4525
; Sequence 4525, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MH800-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4525
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4525

Query Match 51.5%; Score 17; DB 10; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTCCGCGAGACCACTATG 31
Db 1 UUCCGCGAGACCAUAUG 17

RESULT 31
US-10-669-841-2623/c
; Sequence 2623, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, McSwiggen
; APPLICANT: James, Morrissey
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patrice, Lee
```



```
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; FILE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; PRIOR FILING DATE: 2000-02-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2623
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-2623
```

```
Query Match 51.5%; Score 17; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TCCGCAGACCACTATGG 32
Db 17 TCCGCAGACCACTATGG 1

RESULT 32
US-10-669-841-7118
; Sequence 7118, Application US/10669841
; Publication No. US20040127446A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Lawrence, Blatt
; APPLICANT: Dennis, Macejak
; APPLICANT: James, McSwiggen
; APPLICANT: David, Morrissey
; APPLICANT: Pamela, Pavco
; APPLICANT: Patricia, Lee
; APPLICANT: Kenneth, Draper
; APPLICANT: Elisabeth, Roberts
; TITLE OF INVENTION: OLIGONUCLEOTIDE MEDIATED INHIBITION OF HEPATITIS B VIRUS AND HEPA
; FILE OF INVENTION: VIRUS REPLICATION
; FILE REFERENCE: 400/042US (MEHB02-249-E)
; CURRENT APPLICATION NUMBER: US/10/669,841
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/296,876
```

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; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/335,059
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 60/337,055
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 09/817,879
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/740,332
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 09/611,931
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 09/504,321
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 16207
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7118
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-10-669-841-7118

Query Match 51.5%; Score 17; DB 17; Length 17;
Best Local Similarity 76.5%; Pred. No. 1.1e+03;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCAGACCACTATG 31
Db 1 UCCGCAGACCACTAUG 17

RESULT 33
US-10-667-271-73/c
; Sequence 73, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129 (MEHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
```

17 CCGCAGACCACTATGCC 33
|||||:|:|
Db 1 CCGCAGACCACTATGCC 17

RESULT 35
US-09-882-945A-237/c
; Sequence 237, Application US/09882945A
; Publication No. US20030143535A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Allawi, Hatim
; APPLICANT: Dong, Fang
; APPLICANT: Neri, Bruce
; APPLICANT: Vener, Tatiana
; TITLE OF INVENTION: Nucleic Acid Accessible Hybridization Sites
; FILE REFERENCE: FORS-04586
; CURRENT APPLICATION NUMBER: US/09/882,945A
; CURRENT FILING DATE: 2001-06-15
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 237
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-882-945A-237

Query Match 51.5%; Score 17; DB 10; Length 24;
Best Local Similarity 100.0%; Pred.No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CCGCAGACCACTATGCC 33
|||||:|:|
Db 24 CCGCAGACCACTATGCC 8

RESULT 36
US-10-667-271-75/c
; Sequence 75, Application US/10667271
; Publication No. US20040209831A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics
; APPLICANT: McSwiggen, James
; APPLICANT: Macejak, Dennis
; APPLICANT: Beigelman, Leonid
; APPLICANT: Morrissey, David
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Hepatitis C Virus (HCV)
; FILE REFERENCE: 400/129. (MHB02-763B)
; CURRENT APPLICATION NUMBER: US/10/667,271
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: PCT / US03/05043
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT / US02/09187
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: USSN 60/401,104
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: USSN 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: USSN 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: USSN 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: USSN 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: USSN 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: USSN 60/409,293
; PRIOR FILING DATE: 2002-09-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1705
SOFTWARE: PatentIn version 3.2

SEQ ID NO 75
LENGTH: 19

TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re

US-10-667-271-75

Query Match 49.7%; Score 16.4; DB 18; Length 19;

Best Local Similarity 94.4%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTA 29

Db 18 CGGTTCGCGACCACTA 1

RESULT 37

US-10-667-271-771

Sequence 771, Application US/10667271

Publication No. US20040209831A1

GENERAL INFORMATION:

APPLICANT: Sirna Therapeutics

APPLICANT: McSwiggen, James

APPLICANT: Macejak, Dennis

APPLICANT: Beigelman, Leonid

APPLICANT: Morrissey, David

TITLE OF INVENTION: RNA interference Mediated Inhibition of Hepatitis C Virus (HCV)

TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)

FILE REFERENCE: 400/129 (MBHB02-763B)

CURRENT APPLICATION NUMBER: US/10/667,271

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: US 10/444,853

PRIOR FILING DATE: 2003-05-23

PRIOR APPLICATION NUMBER: PCT / US03/05043

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: PCT / US02/09187

PRIOR FILING DATE: 2002-03-26

PRIOR APPLICATION NUMBER: USSN 60/401,104

PRIOR FILING DATE: 2002-08-05

PRIOR APPLICATION NUMBER: USSN 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: USSN 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: USSN 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: USSN 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: USSN 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: USSN 60/409,293

PRIOR FILING DATE: 2002-09-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1705

SOFTWARE: PatentIn version 3.2

SEQ ID NO 771

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region

US-10-667-271-771

Query Match 49.7%; Score 16.4; DB 18; Length 19;

Best Local Similarity 77.8%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;

Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCGTTCGCGACCACTA 29

Db 2 CGGUUCCGACCACTA 19

RESULT 38

US-09-825-805-24/c

Sequence 24, Application US/09825805

Publication No. US20030004122A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpeisky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Zinnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

FILE REFERENCE: MBH00-831-F (400/009)

CURRENT APPLICATION NUMBER: US/09/825,805

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: 09/578,223

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 09/476,387

PRIOR FILING DATE: 1999-12-30

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1558

SOFTWARE: PatentIn version 3.0

SEQ ID NO 24

LENGTH: 16

TYPE: RNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Hepatitis C Virus

US-09-825-805-24

Query Match 48.5%; Score 16; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 3e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TTCGCGACCACTAT 30

Db 16 TTCGCGACCACTAT 1

RESULT 39

US-09-740-332-4526

Sequence 4526, Application US/09740332

Publication No. US20030125270A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related

FILE REFERENCE: REI 400/003

CURRENT APPLICATION NUMBER: US/09/740,332

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9704

SOFTWARE: PatentIn version 3.0

SEQ ID NO 4526

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-740-332-4526

Query Match 48.5%; Score 16; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03; 0; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
|||||:|:|:
Db 1 CGCAGACCACTATGGC 16

RESULT 40

US-09-817-879-4526
; Sequence 4526, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection
; FILE REFERENCE: MBH00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-4526

Query Match 48.5%; Score 16; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 3e+03; 0; Indels 0; Gaps 0;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 18 CGCAGACCACTATGGC 33
|||||:|:|:
Db 1 CGCAGACCACTATGGC 16

Search completed: November 24, 2004, 03:42:14
Job time : 164.842 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1582.15 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-3

Perfect score: 33
Sequence: 1 cgggtactacacgttcgcagaccattatggc 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	15.2	46.1	47	8	BH848576
C 3	14.4	43.6	37	7	H03404 Y148c01.81
C 4	14.2	43.0	50	1	AU106643 AU106643
C 5	14	42.4	46	7	T56929 Y83f08.12
C 6	14	42.4	50	1	AU102254 AU102254
C 7	13.8	41.8	32	8	BH861153 SALK 0345
C 8	13.8	41.8	45	8	AZ331523 1M0059F01
C 9	13.6	41.2	41	9	CR403035 Arabidops
C 10	13.6	41.2	43	9	CR403034 Arabidops
C 11	13.6	41.2	45	2	BE251857 601115885
C 12	13.6	41.2	47	8	BZ763121 SALK 1135
C 13	13.4	40.6	28	9	CG719689 11190580
C 14	13.4	40.6	36	8	AZ498025 1M0335B09
C 15	13.4	40.6	39	9	TA3H02P
C 16	13.4	40.6	44	8	BH620252 1007061G0
C 17	13.2	40.0	41	8	AZ785555 2M0029G04
C 18	13.2	40.0	42	8	AZ812045 2M0078A04
C 19	13.2	40.0	45	8	B1102544 602889548
C 20	13.2	40.0	45	8	BZ660777 SALK 0242
C 21	13.2	40.0	50	1	AU102740 AU102740
C 22	13.2	40.0	50	1	AU105906 AU105906
C 23	13	39.4	38	8	AZ786726 2M0032H20
C 24	13	39.4	42	9	AL765117 Arabidops

c 98	11.8	35.8	46	9	TA68B01Q	AL465151 T. brucei	c 171	11.4	34.5	50	1	AU105781	AU105781
c 99	11.8	35.8	47	9	CL423878	CL423878 01S0750-0	c 172	11.4	34.5	50	1	AU105838	AU105838
c 100	11.8	35.8	49	1	AI527771	AI527771 u128001.Y	c 173	11.4	34.5	50	1	AU107272	AU107272
c 101	11.8	35.8	49	7	CF642375	CF642375 D50.H06.F	c 174	11.4	34.5	50	1	AU107274	AU107274
c 102	11.8	35.8	49	9	AL771898	AL771898 Arabidops	c 175	11.4	34.5	50	1	AU107281	AU107281
c 103	11.8	35.8	50	1	AU102330	AU102330 1M0306K11	c 176	11.4	34.5	50	1	AU107284	AU107284
c 104	11.6	35.2	31	8	AZ481726	AZ481726 1M0306K11	c 177	11.4	34.5	50	1	AU107285	AU107285
c 105	11.6	35.2	34	1	AA889919	AA889919 aJ87007.s	c 178	11.4	34.5	50	1	AU107287	AU107287
c 106	11.6	35.2	34	1	AI051365	AI051365 0w25110.X	c 179	11.4	34.5	50	1	AU107288	AU107288
c 107	11.6	35.2	36	2	BE255223	BE255223 601115777	c 180	11.4	34.5	50	1	AU107290	AU107290
c 108	11.6	35.2	37	1	AV833600	AV833600 AV833600	c 181	11.4	34.5	50	1	AU107291	AU107291
c 109	11.6	35.2	37	2	AW250626	AW250626 2822256.S	c 182	11.4	34.5	50	1	AU107293	AU107293
c 110	11.6	35.2	37	8	AZ827785	AZ827785 2M0104J23	c 183	11.4	34.5	50	1	AU107294	AU107294
c 111	11.6	35.2	40	1	AA903929	AA903929 0e7302.s	c 184	11.4	34.5	50	1	AU107295	AU107295
c 112	11.6	35.2	40	1	AA928240	AA928240 0n87c07.s	c 185	11.4	34.5	50	1	AU107400	AU107400
c 113	11.6	35.2	40	1	AV842793	AV842793 AV842793	c 186	11.4	34.5	50	1	AU108027	AU108027
c 114	11.6	35.2	40	8	BH900992	BH900992 KG08154-S	c 187	11.4	34.5	50	2	AW689452	AW689452
c 115	11.6	35.2	43	8	BH853202	BH853202 SALK_0761	c 188	11.4	34.5	50	2	AW6843903	AW6843903
c 116	11.6	35.2	43	8	BZ762248	BZ762248 SALK_0925	c 189	11.4	34.5	50	8	AZ787909	AZ787909
c 117	11.6	35.2	44	8	BH805848	BH805848 1008062F0	c 190	11.2	33.9	19	6	CF298891	CF298891
c 118	11.6	35.2	46	1	AA828900	AA828900 0d75h11.s	c 191	11.2	33.9	25	1	AA948130	AA948130
c 119	11.6	35.2	46	2	BE612731	BE612731 601452593	c 192	11.2	33.9	26	8	AZ445551	AZ445551
c 120	11.6	35.2	46	8	CC326487	CC326487 XN729.B8y	c 193	11.2	33.9	27	1	AL045548	AL045548
c 121	11.6	35.2	47	8	AZ766816	AZ766816 1M0564E10	c 194	11.2	33.9	29	7	HI5932	HI5932
c 122	11.6	35.2	49	1	AI424311	AI424311 1e90505.X	c 195	11.2	33.9	30	4	BI915618	BI915618
c 123	11.6	35.2	50	1	AU104929	AU104929 AU104929	c 196	11.2	33.9	31	4	BI915569	BI915569
c 124	11.6	35.2	50	1	AU107670	AU107670 AU107670	c 197	11.2	33.9	32	9	CL300541	CL300541
c 125	11.6	35.2	50	1	AU108094	AU108094 AU108094	c 198	11.2	33.9	33	8	AZ379585	AZ379585
c 126	11.6	35.2	50	2	AW18967	AW18967 un10504.Y	c 199	11.2	33.9	34	7	N57329	N57329
c 127	11.6	35.2	50	6	CB192172	CB192172 PY25904.Y	c 200	11.2	33.9	37	8	AZ960486	AZ960486
c 128	11.6	35.2	50	9	TA284A04P	TA284A04P T. brucei	c 201	11.2	33.9	39	9	CG722883	CG722883
c 129	11.4	34.5	25	9	TA296B02Q	TA296B02Q T. brucei	c 202	11.2	33.9	41	9	CL437876	CL437876
c 130	11.4	34.5	26	8	AZ386054	AZ386054 1M0145A05	c 203	11.2	33.9	42	8	AZ939796	AZ939796
c 131	11.4	34.5	28	1	AA713615	AA713615 nv70h08.s	c 204	11.2	33.9	42	9	DR26M14S	DR26M14S
c 132	11.4	34.5	28	1	AI354551	AI354551 qc98g05.X	c 205	11.2	33.9	43	9	TA119G10P	TA119G10P
c 133	11.4	34.5	32	9	CG733270	CG733270 1119155C0	c 206	11.2	33.9	43	1	AA894519	AA894519
c 134	11.4	34.5	32	9	AJ622328	AJ622328 Drosophil	c 207	11.2	33.9	45	6	CA968495	CA968495
c 135	11.4	34.5	34	1	AA176515	AA176515 2p37a12.r	c 208	11.2	33.9	45	9	CG728115	CG728115
c 136	11.4	34.5	34	8	AZ482003	AZ482003 1M0306D16	c 209	11.2	33.9	47	8	AZ775202	AZ775202
c 137	11.4	34.5	34	8	AZ941539	AZ941539 2M0201N13	c 210	11.2	33.9	47	9	AG189046	AG189046
c 138	11.4	34.5	37	1	AL043032	AL043032 DXFp434P	c 211	11.2	33.9	48	1	AJ646947	AJ646947
c 139	11.4	34.5	37	8	AZ374579	AZ374579 1M0127M20	c 212	11.2	33.9	48	8	AZ462540	AZ462540
c 140	11.4	34.5	37	8	AZ596892	AZ596892 1M0410M24	c 213	11.2	33.9	48	8	BH253038	BH253038
c 141	11.4	34.5	38	9	AX002721	AX002721 Arabidops	c 214	11.2	33.9	48	8	BH740754	BH740754
c 142	11.4	34.5	38	9	CL310548	CL310548 03S4741-0	c 215	11.2	33.9	48	9	CG719583	CG719583
c 143	11.4	34.5	38	9	AZ825899	AZ825899 2M0101P13	c 216	11.2	33.9	49	1	AA738220	AA738220
c 144	11.4	34.5	39	8	AZ825899	AZ825899 2M0101P13	c 217	11.2	33.9	49	1	AA605689	AA605689
c 145	11.4	34.5	41	8	AZ606010	AZ606010 1M0427K11	c 218	11.2	33.9	49	7	CN752134	CN752134
c 146	11.4	34.5	42	8	AZ344983	AZ344983 1M0079M14	c 219	11.2	33.9	49	8	AZ601892	AZ601892
c 147	11.4	34.5	42	8	AZ816309	AZ816309 2M0085D01	c 220	11.2	33.9	49	9	BX660891	BX660891
c 148	11.4	34.5	43	7	R07765	R07765 YF15907.s1	c 221	11.2	33.9	50	1	AU102811	AU102811
c 149	11.4	34.5	43	8	AZ875350	AZ875350 2M0189M19	c 222	11.2	33.9	50	1	AU103483	AU103483
c 150	11.4	34.5	43	9	CL436351	CL436351 FST2795-N	c 223	11.2	33.9	50	1	AU103978	AU103978
c 151	11.4	34.5	44	1	AV833798	AV833798 AV833798	c 224	11.2	33.9	50	1	AU104105	AU104105
c 152	11.4	34.5	44	8	AQ025716	AQ025716 1(2)K0280	c 225	11.2	33.9	50	1	AU104116	AU104116
c 153	11.4	34.5	46	1	AA814610	AA814610 0b97d06.s	c 226	11.2	33.9	50	1	AU104118	AU104118
c 154	11.4	34.5	46	1	AA485011	AA485011 aa39e10.r	c 227	11.2	33.9	50	1	AU104128	AU104128
c 155	11.4	34.5	46	1	AA591686	AA591686 v113g08.r	c 228	11.2	33.9	50	1	AU104131	AU104131
c 156	11.4	34.5	46	2	BE336269	BE336269 601062658	c 229	11.2	33.9	50	1	AU104203	AU104203
c 157	11.4	34.5	47	9	CL309626	CL309626 03S2012-0	c 230	11.2	33.9	50	1	AU104204	AU104204
c 158	11.4	34.5	49	1	AA871018	AA871018 vq29c04.r	c 231	11.2	33.9	50	1	AU104237	AU104237
c 159	11.4	34.5	49	5	BQ585216	BQ585216 S011421-0	c 232	11.2	33.9	50	1	AU104238	AU104238
c 160	11.4	34.5	49	7	H92807	H92807 YF90a12.r1	c 233	11.2	33.9	50	1	AU105452	AU105452
c 161	11.4	34.5	49	8	BH608645	BH608645 611.LL18N	c 234	11.2	33.9	50	1	AU107600	AU107600
c 162	11.4	34.5	49	8	BH902910	BH902910 SALK_1015	c 235	11.2	33.9	50	6	CB064335	CB064335
c 163	11.4	34.5	49	9	AL757297	AL757297 Arabidops	c 236	11.2	33.9	50	6	CB191277	CB191277
c 164	11.4	34.5	50	1	AU102594	AU102594 AU102594	c 237	11.2	33.9	50	6	CB191839	CB191839
c 165	11.4	34.5	50	1	AU103659	AU103659 AU103659	c 238	11.2	33.9	50	8	AZ597958	AZ597958
c 166	11.4	34.5	50	1	AU103666	AU103666 AU103666	c 239	11.2	33.9	50	9	AL765665	AL765665
c 167	11.4	34.5	50	1	AU104973	AU104973 AU104973	c 240	11.2	33.9	50	9	DMES46715	DMES46715
c 168	11.4	34.5	50	1	AU105080	AU105080 AU105080	c 241	11.2	33.9	50	9	CL685441	CL685441
c 169	11.4	34.5	50	1	AU105723	AU105723 AU105723	c 242	11	33.3	19	8	AZ626779	AZ626779
c 170	11.4	34.5	50	1	AU105774	AU105774 AU105774	c 243	11	33.3	22	8	AZ603594	AZ603594

C 244	11	33.3	23	9	TAL20H10P	AL462505	T. brucei	C 317	10.8	32.7	34	7	T90379	T90379 yd43e08.s1
C 245	11	33.3	25	1	A1000229	AI000229	OC40b07.s	C 318	10.8	32.7	36	1	A1223280	A1223280 gg53f04.x
C 246	11	33.3	25	8	A2871659	ZM0184G07.s		C 319	10.8	32.7	36	8	A2331632	A2331632 1M0059N10
C 247	11	33.3	29	8	A2961088	ZM0229G21		C 320	10.8	32.7	36	9	TA345F06Q	TA345F06Q T. brucei
C 248	11	33.3	29	9	AG192228	Pan trogl		C 321	10.8	32.7	37	9	DR18M6T	DR18M6T Danio rer
C 249	11	33.3	31	9	AL757862	AL757862	Arabidops	C 322	10.8	32.7	38	1	AJ652144	AJ652144 AJ652144
C 250	11	33.3	31	9	BX532709	BX532709	Arabidops	C 323	10.8	32.7	39	2	BF339449	BF339449 602039103
C 251	11	33.3	33	8	BZ661231	SALK_0246		C 324	10.8	32.7	39	2	BF342092	BF342092 602012848
C 252	11	33.3	33	8	BZ767418	SALK_1388		C 325	10.8	32.7	39	8	AZ595333	AZ595333 1M0407F23
C 253	11	33.3	33	8	BZ767420	SALK_1388		C 326	10.8	32.7	40	1	AI003400	AI003400 am78h01.s
C 254	11	33.3	33	9	DME545177	DME545177	Drosophil	C 327	10.8	32.7	40	1	AA589938	AA589938 v181f04.r
C 255	11	33.3	34	9	CLY03538-3	CLY03538-3		C 328	10.8	32.7	40	8	AZ453043	AZ453043 1M0254A13
C 256	11	33.3	36	8	BH846810	BH846810	SALK_0105	C 329	10.8	32.7	41	8	AZ765994	AZ765994 1M0563D16
C 257	11	33.3	36	9	CG728704	CG728704	1115T02F0	C 330	10.8	32.7	41	9	CL439311	CL439311 PST902-3
C 258	11	33.3	37	1	AA873944	AA873944	vm86a07.r	C 331	10.8	32.7	42	6	CF032091	CF032091 QCE13h07
C 259	11	33.3	37	1	AA974682	op29b04.s		C 332	10.8	32.7	42	6	CF281741	CF281741 14ETL--08
C 260	11	33.3	37	8	BH847357	BH847357	SALK_0528	C 333	10.8	32.7	42	6	CF281741	CF281741 14ETL--08
C 261	11	33.3	38	9	AG213121	Oryza sat		C 334	10.8	32.7	42	9	AJ594706	AJ594706 Arabidops
C 262	11	33.3	39	7	CF642114	D47_H04_F		C 335	10.8	32.7	42	9	AI696963	AI696963 wc76c08.x
C 263	11	33.3	39	8	AZ793656	AZ793656	2M0047J04	C 336	10.8	32.7	43	1	AA621647	AA621647 af54a06.s
C 264	11	33.3	39	9	CG894914	CG894914	03S4734-0	C 337	10.8	32.7	43	8	AZ778700	AZ778700 2M0014F03
C 265	11	33.3	39	9	CL234238	CL234238	02S0288-0	C 338	10.8	32.7	44	1	AJ680183	AJ680183 AJ680183
C 266	11	33.3	39	9	CL234495	02S0422-0		C 339	10.8	32.7	44	4	BI829988	BI829988 603080234
C 267	11	33.3	40	8	AZ486679	AZ486679	1M0314B23	C 340	10.8	32.7	44	9	DME546976	DME546976 Drosophil
C 268	11	33.3	40	8	CC043523	3591_1_15		C 341	10.8	32.7	45	8	AZ773590	AZ773590 2M0001C07
C 269	11	33.3	41	8	AZ475800	AZ475800	1M0294G10	C 342	10.8	32.7	45	8	CC455309	CC455309 SALK_0805
C 270	11	33.3	41	8	BH626346	1007112H0		C 343	10.8	32.7	46	7	W89234	W89234 mf39c11.r1
C 271	11	33.3	42	1	AA553224	vk89c09.s		C 344	10.8	32.7	46	7	W91341	W91341 mg17d01.r1
C 272	11	33.3	42	8	AQ025866	1(2)K0870		C 345	10.8	32.7	46	8	B2355101	B2355101 SALK_1263
C 273	11	33.3	42	9	CG716838	CG716838	1119046D0	C 346	10.8	32.7	46	9	CC941127	CC941127 01S0649-0
C 274	11	33.3	42	9	AG227149	Lotus cor		C 347	10.8	32.7	47	6	CF339432	CF339432 BCL1--04-
C 275	11	33.3	43	1	AI445286	18h03.x		C 348	10.8	32.7	47	6	CO780863	CO780863 RLO10D_D0
C 276	11	33.3	43	4	BH397324	5009-0-31		C 349	10.8	32.7	47	8	BH846659	BH846659 SALK_0095
C 277	11	33.3	43	8	BH902203	SALK_0914		C 350	10.8	32.7	47	9	CL303536	CL303536 M041A07_G
C 278	11	33.3	43	9	CL309631	03S2012-0		C 351	10.8	32.7	47	9	T93941	T93941 ye06f04.r1
C 279	11	33.3	44	1	AU014001	AU014001		C 352	10.8	32.7	48	9	AL763935	AL763935 Arabidops
C 280	11	33.3	44	6	CB275423	WLR151-15		C 353	10.8	32.7	48	9	CL234325	CL234325 02S0422-0
C 281	11	33.3	44	8	BH626498	1007091C0		C 354	10.8	32.7	48	9	CL844507	CL844507 EY12526-5
C 282	11	33.3	44	9	CL569510	AN0535_Sa		C 355	10.8	32.7	49	1	AI188903	AI188903 Qd36C11.x
C 283	11	33.3	45	8	AZ640312	1M0502G18		C 356	10.8	32.7	49	7	H28255	H28255 y160e03.r1
C 284	11	33.3	46	1	AA790759	vm18g12.r		C 357	10.8	32.7	49	9	DME546181	DME546181 Drosophil
C 285	11	33.3	47	1	AV855281	AV855281		C 358	10.8	32.7	49	9	CC886568	CC886568 SALK_1487
C 286	11	33.3	47	4	BM046304	603626308		C 359	10.8	32.7	50	1	AA907197	AA907197 0103e04.s
C 287	11	33.3	47	4	BM047185	603627544		C 360	10.8	32.7	50	1	AU102575	AU102575 AU102575
C 288	11	33.3	47	8	AZ997109	2M0283H01		C 361	10.8	32.7	50	1	AU102576	AU102576 AU102576
C 289	11	33.3	47	8	BH813635	BH813635	SALK_0645	C 362	10.8	32.7	50	1	AU102741	AU102741 AU102741
C 290	11	33.3	48	2	AW247978	2819657.5		C 363	10.8	32.7	50	1	AU103004	AU103004 AU103004
C 291	11	33.3	48	8	AZ916239	PstI_4_b1		C 364	10.8	32.7	50	1	AU103644	AU103644 AU103644
C 292	11	33.3	48	8	BH851849	BH851849	SALK_0736	C 365	10.8	32.7	50	1	AU103647	AU103647 AU103647
C 293	11	33.3	49	8	AZ470342	AZ470342	1M0284E22	C 366	10.8	32.7	50	1	AU103703	AU103703 AU103703
C 294	11	33.3	49	8	CC178559	NPX468_Ba		C 367	10.8	32.7	50	1	AU104156	AU104156 AU104156
C 295	11	33.3	50	1	AU102580	AU102580		C 368	10.8	32.7	50	1	AU104947	AU104947 AU104947
C 296	11	33.3	50	1	AU102242	AU102242		C 369	10.8	32.7	50	1	AU105919	AU105919 AU105919
C 297	11	33.3	50	1	AU102580	AU102580		C 370	10.8	32.7	50	1	AU105921	AU105921 AU105921
C 298	11	33.3	50	1	AU102994	AU102994		C 371	10.8	32.7	50	1	AU106375	AU106375 AU106375
C 299	11	33.3	50	1	AU104458	AU104458		C 372	10.8	32.7	50	1	AU106379	AU106379 AU106379
C 300	11	33.3	50	1	AU105285	AU105285		C 373	10.8	32.7	50	1	AU106383	AU106383 AU106383
C 301	11	33.3	50	1	AU105578	AU105578		C 374	10.8	32.7	50	1	AU106949	AU106949 AU106949
C 302	11	33.3	50	1	AU106968	AU106968		C 375	10.8	32.7	50	1	AU107469	AU107469 AU107469
C 303	11	33.3	50	1	AU107280	AU107280		C 376	10.8	32.7	50	5	EX734506	EX734506 BX734506
C 304	11	33.3	50	1	AU107282	AU107282		C 377	10.8	32.7	50	8	BZ769278	BZ769278 SALK_1419
C 305	11	33.3	50	9	TA101G05P	TA101G05P		C 378	10.8	32.7	50	9	DR1211T	DR1211T Danio rer
C 306	11	33.3	50	9	CL309184	CL309184	03S2010-0	C 379	10.8	32.7	50	9	DR1211T	DR1211T Danio rer
C 307	10.8	32.7	19	8	AZ804253	AZ804253	2M0065008	C 380	10.6	32.1	24	8	AZ314869	AZ314869 1M0031D19
C 308	10.8	32.7	24	8	AZ804253	AZ804253	2M0065008	C 381	10.6	32.1	25	1	AA565870	AA565870 nj32f03.s
C 309	10.8	32.7	25	1	AL039948	AL039948	DKZp434J	C 382	10.6	32.1	25	4	BM398821	BM398821 5009-0-5-
C 310	10.8	32.7	25	8	AZ507387	AZ507387	1M0349D04	C 383	10.6	32.1	28	8	BH861193	BH861193 SALK_0347
C 311	10.8	32.7	26	8	AZ507387	AZ507387	1M0349D04	C 384	10.6	32.1	28	8	BH906920	BH906920 SALK_0366
C 312	10.8	32.7	26	9	TA199A09P	TA199A09P		C 385	10.6	32.1	28	9	TA216E09Q	TA216E09Q T. brucei
C 313	10.8	32.7	29	8	AZ799919	AZ799919	2M0057J08	C 386	10.6	32.1	30	7	T94314	T94314 Ye37g03.s1
C 314	10.8	32.7	30	8	AZ582016	AZ582016	1M0374C01	C 387	10.6	32.1	30	8	AZ326805	AZ326805 1M0049820
C 315	10.8	32.7	30	8	AZ602767	AZ602767	1M0421M07	C 388	10.6	32.1	31	1	AV848542	AV848542 AV848542
C 316	10.8	32.7	34	1	AV833590	AV833590		C 389	10.6	32.1	31	1	AV848542	AV848542 AV848542

C 390	10.6	32.1	31	8	AZ380740	1M0136N14	AZ380740	1M0136N14	C 463	10.6	32.1	50	1	AUI04890	AUI04890
C 391	10.6	32.1	32	1	AV962980	AV962980	AV962980	AV962980	C 464	10.6	32.1	50	1	AUI04926	AUI04926
C 392	10.6	32.1	32	1	BX895415	ArabiDops	BX895415	ArabiDops	C 465	10.6	32.1	50	1	AUI05181	AUI05181
C 393	10.6	32.1	33	4	BI593580	603341963	BI593580	603341963	C 466	10.6	32.1	50	1	AUI06313	AUI06313
C 394	10.6	32.1	33	8	BH256406	KG00828-5	BH256406	KG00828-5	C 467	10.6	32.1	50	1	AUI06314	AUI06314
C 395	10.6	32.1	33	8	HA256406	KG00828-5	HA256406	KG00828-5	C 468	10.6	32.1	50	1	AUI06316	AUI06316
C 396	10.6	32.1	34	1	AA934127	on95d08.s	AA934127	on95d08.s	C 469	10.6	32.1	50	1	AUI06870	AUI06870
C 397	10.6	32.1	34	1	AA934127	on95d08.s	AA934127	on95d08.s	C 470	10.6	32.1	50	1	AUI06878	AUI06878
C 398	10.6	32.1	36	8	BH848296	SALK_0677	BH848296	SALK_0677	C 471	10.6	32.1	50	1	AUI06952	AUI06952
C 399	10.6	32.1	36	8	BZ597107	SALK_0994	BZ597107	SALK_0994	C 472	10.6	32.1	50	1	AUI06957	AUI06957
C 400	10.6	32.1	37	1	AA972482	Op4d03.s	AA972482	Op4d03.s	C 473	10.6	32.1	50	1	AUI07027	AUI07027
C 401	10.6	32.1	37	1	AA972482	Op4d03.s	AA972482	Op4d03.s	C 474	10.6	32.1	50	1	AUI07275	AUI07275
C 402	10.6	32.1	38	9	AG216229	Drosophi1	AG216229	Drosophi1	C 475	10.6	32.1	50	1	AUI08025	AUI08025
C 403	10.6	32.1	38	9	AG216229	Drosophi1	AG216229	Drosophi1	C 476	10.6	32.1	50	1	AUI08028	AUI08028
C 404	10.6	32.1	39	1	AUI08671	AUI08671	AUI08671	AUI08671	C 477	10.6	32.1	50	1	AUI08029	AUI08029
C 405	10.6	32.1	39	8	BZ291057	SALK_1123	BZ291057	SALK_1123	C 478	10.6	32.1	50	2	BZ368091	601221989
C 406	10.6	32.1	39	9	CL661999	PRIO140b	CL661999	PRIO140b	C 479	10.6	32.1	50	8	BZ763937	SALK_1228
C 407	10.6	32.1	40	1	AA961031	Op08g11.s	AA961031	Op08g11.s	C 480	10.6	32.1	50	9	CNS07FCJ	AL608293 Anopheles
C 408	10.6	32.1	40	1	AI337481	AI337481	AI337481	AI337481	C 481	10.6	32.1	50	9	HSMC39C08	AL74070 T. brucei
C 409	10.6	32.1	40	7	T49499	Ya76a12.r1	T49499	Ya76a12.r1	C 482	10.6	32.1	50	9	TA215A01P	AL479508 T. brucei
C 410	10.6	32.1	42	2	AW455805	2DZ Neuro	AW455805	2DZ Neuro	C 483	10.6	32.1	50	9	CG799492	1118002G1
C 411	10.6	32.1	42	6	CF299124	7LEAF-02	CF299124	7LEAF-02	C 484	10.4	31.5	19	6	CF298023	7LEAF-01
C 412	10.6	32.1	42	8	AZ768020	1M0567G18	AZ768020	1M0567G18	C 485	10.4	31.5	21	1	AJ648125	AJ648125
C 413	10.6	32.1	42	9	CC799365	01S0473-0	CC799365	01S0473-0	C 486	10.4	31.5	21	6	CF315101	HD--03-00
C 414	10.6	32.1	43	2	BF161778	601770701	BF161778	601770701	C 487	10.4	31.5	21	9	TA185E09P	AL474070 T. brucei
C 415	10.6	32.1	43	4	BJ076110	EJ076110	BJ076110	EJ076110	C 488	10.4	31.5	23	8	AZ806411	2M0068L22
C 416	10.6	32.1	43	4	AJ773579	2M0001006	AJ773579	2M0001006	C 489	10.4	31.5	25	9	AG204424	Pan trogl
C 417	10.6	32.1	43	8	AZ809933	2M0074K07	AZ809933	2M0074K07	C 490	10.4	31.5	26	9	AG203073	AG203073
C 418	10.6	32.1	43	9	AL762950	ArabiDops	AL762950	ArabiDops	C 491	10.4	31.5	31	1	AA968474	AA968474
C 419	10.6	32.1	44	8	BH000259	2M0288A03	BH000259	2M0288A03	C 492	10.4	31.5	31	1	AA968474	AA968474
C 420	10.6	32.1	44	8	BH000259	2M0288A03	BH000259	2M0288A03	C 493	10.4	31.5	31	7	H30580	AL174157 vz84e01.r
C 421	10.6	32.1	44	8	BH857536	SALK_0473	BH857536	SALK_0473	C 494	10.4	31.5	32	8	AZ513928	1M0360G15
C 422	10.6	32.1	44	8	BZ382740	SALK_1187	BZ382740	SALK_1187	C 495	10.4	31.5	33	8	AZ513928	1M0360G15
C 423	10.6	32.1	45	1	AV962808	AV962808	AV962808	AV962808	C 496	10.4	31.5	33	9	AL759548	AL759548
C 424	10.6	32.1	45	8	AZ460870	1M0266M23	AZ460870	1M0266M23	C 497	10.4	31.5	34	1	AA906611	ok79h09.s
C 425	10.6	32.1	45	8	AZ796865	2M0052117	AZ796865	2M0052117	C 498	10.4	31.5	34	1	AV832421	AV832421
C 426	10.6	32.1	45	9	AJ622613	Drosophi1	AJ622613	Drosophi1	C 499	10.4	31.5	34	2	BF301588	BF301588
C 427	10.6	32.1	45	9	AX943362	ArabiDops	AX943362	ArabiDops	C 500	10.4	31.5	34	6	CF302742	7LEAF--08
C 428	10.6	32.1	45	9	TA126F09P	TA126F09P	TA126F09P	TA126F09P	C 501	10.4	31.5	34	7	N63645	N63645
C 429	10.6	32.1	46	1	AA674366	vp99a11.r	AA674366	vp99a11.r	C 502	10.4	31.5	34	8	AZ820869	2M0093E20
C 430	10.6	32.1	46	8	AZ802993	2M0063E08	AZ802993	2M0063E08	C 503	10.4	31.5	34	8	BZ357538	SALK_1308
C 431	10.6	32.1	46	8	BZ382796	SALK_1188	BZ382796	SALK_1188	C 504	10.4	31.5	34	9	RA7898	RA7898
C 432	10.6	32.1	46	9	AX948932	ArabiDops	AX948932	ArabiDops	C 505	10.4	31.5	35	9	TA348007Q	TA348007Q
C 433	10.6	32.1	47	1	AV672363	ArabiDops	AV672363	ArabiDops	C 506	10.4	31.5	35	8	AZ666583	AZ666583
C 434	10.6	32.1	47	1	AV962403	AV962403	AV962403	AV962403	C 507	10.4	31.5	37	1	AUI051308	cx24d05.x
C 435	10.6	32.1	47	8	AZ767816	1M0567H24	AZ767816	1M0567H24	C 508	10.4	31.5	37	1	AJ746682	AJ746682
C 436	10.6	32.1	47	8	AZ785454	2M0029A21	AZ785454	2M0029A21	C 509	10.4	31.5	37	8	AZ796238	2M0051E23
C 437	10.6	32.1	47	9	TA448H10Q	TA448H10Q	TA448H10Q	TA448H10Q	C 510	10.4	31.5	37	8	BH789296	SALK_0016
C 438	10.6	32.1	48	2	BF507294	8184P-15	BF507294	8184P-15	C 511	10.4	31.5	37	9	AL953736	ArabiDops
C 439	10.6	32.1	48	8	BZ762247	SALK_0925	BZ762247	SALK_0925	C 512	10.4	31.5	38	1	AUI051308	cx24d05.x
C 440	10.6	32.1	48	8	CC026876	3591_1.55	CC026876	3591_1.55	C 513	10.4	31.5	38	4	BG256610	602370273
C 441	10.6	32.1	48	9	AL944927	ArabiDops	AL944927	ArabiDops	C 514	10.4	31.5	39	1	AV834039	AV834039
C 442	10.6	32.1	48	9	AB082911	Drosophi1	AB082911	Drosophi1	C 515	10.4	31.5	39	7	D74282	CELK079A5F
C 443	10.6	32.1	49	1	AA691190	vt34c05.r	AA691190	vt34c05.r	C 516	10.4	31.5	39	8	AZ586761	1M03920A4
C 444	10.6	32.1	49	1	AA920052	vy63h11.r	AA920052	vy63h11.r	C 517	10.4	31.5	39	9	AL754052	ArabiDops
C 445	10.6	32.1	49	1	AI093925	ga27e01.s	AI093925	ga27e01.s	C 518	10.4	31.5	40	1	AA972484	op42602.s
C 446	10.6	32.1	49	1	AI444379	fb26f01.x	AI444379	fb26f01.x	C 519	10.4	31.5	40	1	AI180630	uc67f04.r
C 447	10.6	32.1	49	1	AA576898	nm78g10.s	AA576898	nm78g10.s	C 520	10.4	31.5	40	7	H87885	H87885
C 448	10.6	32.1	49	2	AW733869	sk78e03.y	AW733869	sk78e03.y	C 521	10.4	31.5	40	8	BZ290948	SALK_0932
C 449	10.6	32.1	49	8	BH213269	SALK_0089	BH213269	SALK_0089	C 522	10.4	31.5	41	7	H58496	yr21f01.s1
C 450	10.6	32.1	49	8	BH213269	SALK_0089	BH213269	SALK_0089	C 523	10.4	31.5	41	8	AZ442277	1M0234P50
C 451	10.6	32.1	49	8	CC040332	3591_1.13	CC040332	3591_1.13	C 524	10.4	31.5	42	8	CN750518	ApDt-XV1-
C 452	10.6	32.1	49	9	AL755450	ArabiDops	AL755450	ArabiDops	C 525	10.4	31.5	42	8	AZ803563	2M0064I03
C 453	10.6	32.1	50	1	AI000832	oe56d03.s	AI000832	oe56d03.s	C 526	10.4	31.5	42	8	AZ810624	2M0076H13
C 454	10.6	32.1	50	1	AI000832	oe56d03.s	AI000832	oe56d03.s	C 527	10.4	31.5	42	8	BH913376	BH913376
C 455	10.6	32.1	50	1	AUI02318	AUI02318	AUI02318	AUI02318	C 528	10.4	31.5	43	1	AA724794	AA724794
C 456	10.6	32.1	50	1	AUI02357	AUI02357	AUI02357	AUI02357	C 529	10.4	31.5	43	1	AA780094	af36d09.s
C 457	10.6	32.1	50	1	AUI02545	AUI02545	AUI02545	AUI02545	C 530	10.4	31.5	43	1	AA926972	om26a12.s
C 458	10.6	32.1	50	1	AUI02574	AUI02574	AUI02574	AUI02574	C 531	10.4	31.5	43	1	AI496775	AI496775
C 459	10.6	32.1	50	1	AUI02574	AUI02574	AUI02574	AUI02574	C 532	10.4	31.5	43	7	D19179	D19179
C 460	10.6	32.1	50	1	AUI02576	AUI02576	AUI02576	AUI02576	C 533	10.4	31.5	43	8	AZ760136	1M0553P02
C 461	10.6	32.1	50	1	AUI03363	AUI03363	AUI03363	AUI03363	C 534	10.4	31.5	43	8	BZ583819	3590_1.46
C 462	10.6	32.1	50	1	AUI03654	AUI03654	AUI03654	AUI03654	C 535	10.4	31.5	44	8	BZ382706	SALK_1187

536	10.4	31.5	44	8	BZ766131	SALK_1368	BZ766131	SALK_1368	C 609	10.4	31.5	50	8	BH792388	SALK_0641
537	10.4	31.5	45	6	CA501308	WHE4032.A	CA501308	WHE4032.A	C 610	10.4	31.5	50	9	CR086715	Reverse s
538	10.4	31.5	45	8	AZ388589	1M0148K11	AZ388589	1M0148K11	C 611	10.4	31.5	50	9	CR209947	Forward s
539	10.4	31.5	45	8	AZ836121	2M013OH14	AZ836121	2M013OH14	C 612	10.4	31.5	50	9	CR258485	Forward s
540	10.4	31.5	45	8	CA459052	SALK_1238	CA459052	SALK_1238	C 613	10.4	31.5	50	9	CG722042	1119070B0
541	10.4	31.5	45	1	AA033181	mi39C04.r	AA033181	mi39C04.r	C 614	10.4	31.5	50	9	CL294055	03F3660-0
542	10.4	31.5	46	1	AA033181	mi39C04.r	AA033181	mi39C04.r	C 615	10.2	30.9	18	9	CL438119	PS16842-N
543	10.4	31.5	46	1	AA764234	vv45h05.r	AA764234	vv45h05.r	C 616	10.2	30.9	21	7	D20707	HUMGSO1683
544	10.4	31.5	46	1	AA905936	oJ83b02.s	AA905936	oJ83b02.s	C 617	10.2	30.9	21	8	AZ410517	1M0183M02
545	10.4	31.5	46	1	AI033350	ox02e11.s	AI033350	ox02e11.s	C 618	10.2	30.9	23	8	AZ340024	1M0071G15
546	10.4	31.5	46	1	AI074797	oy03a11.s	AI074797	oy03a11.s	C 619	10.2	30.9	23	8	AZ345482	1M0080B01
547	10.4	31.5	46	1	AI243457	tf72e12.x	AI243457	tf72e12.x	C 620	10.2	30.9	24	8	AZ776777	2M0010C10
548	10.4	31.5	46	1	AA530925	nj47a12.s	AA530925	nj47a12.s	C 621	10.2	30.9	25	8	BZ595389	SALK_0869
549	10.4	31.5	46	7	N77017	Y283B09.r1	N77017	Y283B09.r1	C 622	10.2	30.9	26	8	AZ448691	1M0246H04
550	10.4	31.5	46	8	AZ595176	1M0407D12	AZ595176	1M0407D12	C 623	10.2	30.9	27	8	AZ778941	1M0014E09
551	10.4	31.5	46	8	AZ759592	1M0552D23	AZ759592	1M0552D23	C 624	10.2	30.9	28	8	BZ379973	SALK_1144
552	10.4	31.5	46	8	CC019509	3591_1_15	CC019509	3591_1_15	C 625	10.2	30.9	29	9	CC794002	SALK_0400
553	10.4	31.5	46	8	CC024979	3591_1_41	CC024979	3591_1_41	C 626	10.2	30.9	30	9	TA287B04Q	T_brucei
554	10.4	31.5	46	8	CC025399	3591_1_45	CC025399	3591_1_45	C 627	10.2	30.9	30	9	CG716166	1119044G1
555	10.4	31.5	46	8	CC035175	3591_1_73	CC035175	3591_1_73	C 628	10.2	30.9	31	1	AA962313	oos3e01.s
556	10.4	31.5	46	8	CC035185	3591_1_73	CC035185	3591_1_73	C 629	10.2	30.9	31	1	AI431100	sa22c11.x
557	10.4	31.5	46	9	AL766407	Arabidops	AL766407	Arabidops	C 630	10.2	30.9	31	9	AL761056	Arabidops
558	10.4	31.5	46	9	AG234855	Lotus cor	AG234855	Lotus cor	C 631	10.2	30.9	31	9	TA106A06P	AL459090 T_brucei
559	10.4	31.5	47	7	H57037	Y709402.r1	H57037	Y709402.r1	C 632	10.2	30.9	31	9	CG847269	01S0642-0
560	10.4	31.5	47	8	BZ594927	SALK_0854	BZ594927	SALK_0854	C 633	10.2	30.9	32	9	TA167E01P	T_brucei
561	10.4	31.5	47	8	BZ597017	SALK_0992	BZ597017	SALK_0992	C 634	10.2	30.9	32	9	TA65C12Q	AL458671 T_brucei
562	10.4	31.5	47	9	CL214568	W245A05 G	CL214568	W245A05 G	C 635	10.2	30.9	33	2	AW720395	LjNEST22C
563	10.4	31.5	48	1	AU258691	AU258691	AU258691	AU258691	C 636	10.2	30.9	33	8	BZ763071	SALK_1118
564	10.4	31.5	48	1	AA599637	ag10a11.s	AA599637	ag10a11.s	C 637	10.2	30.9	33	9	DR2B14S	AL742422 Dario rer
565	10.4	31.5	48	6	CF319341	HD--09-M2	CF319341	HD--09-M2	C 638	10.2	30.9	33	9	CG711782	1119022G0
566	10.4	31.5	48	8	AZ794791	2M0048B13	AZ794791	2M0048B13	C 639	10.2	30.9	33	9	CL246799	02S0715-0
567	10.4	31.5	48	9	BX243182	Dario rer	BX243182	Dario rer	C 640	10.2	30.9	33	9	CL246831	02S0715-0
568	10.4	31.5	48	9	TA11D09Q	T_brucei	TA11D09Q	T_brucei	C 641	10.2	30.9	33	9	CL309674	03S2012-0
569	10.4	31.5	49	1	AA947544	od87b10.s	AA947544	od87b10.s	C 642	10.2	30.9	34	1	AA932589	oos1e02.s
570	10.4	31.5	49	1	AI154153	ud78g01.r	AI154153	ud78g01.r	C 643	10.2	30.9	34	1	AA230484	mv73h07.r
571	10.4	31.5	49	1	AV832413	AV832413	AV832413	AV832413	C 644	10.2	30.9	34	8	AZ307617	1M0009H18
572	10.4	31.5	49	4	B1518984	603062281	B1518984	603062281	C 645	10.2	30.9	34	8	AZ665048	1M0545H18
573	10.4	31.5	49	8	BH903414	SALK_1025	BH903414	SALK_1025	C 646	10.2	30.9	35	8	AQ025554	EP(X)1632
574	10.4	31.5	49	8	BH909013	SALK_0517	BH909013	SALK_0517	C 647	10.2	30.9	36	5	BQ035387	SK2-0117
575	10.4	31.5	49	8	BZ382279	SALK_1180	BZ382279	SALK_1180	C 648	10.2	30.9	36	8	CA457010	SALK_1050
576	10.4	31.5	49	8	BZ582697	3590_1_47	BZ582697	3590_1_47	C 649	10.2	30.9	36	9	AG190718	Pan trogl
577	10.4	31.5	50	1	AU102411	AU102411	AU102411	AU102411	C 650	10.2	30.9	37	1	AI446533	tj05b05.x
578	10.4	31.5	50	1	AU102424	AU102424	AU102424	AU102424	C 651	10.2	30.9	37	8	BH790191	SALK_0565
579	10.4	31.5	50	1	AU102425	AU102425	AU102425	AU102425	C 652	10.2	30.9	37	9	CC799910	01S0783-0
580	10.4	31.5	50	1	AU102702	AU102702	AU102702	AU102702	C 653	10.2	30.9	38	8	AZ500985	1M0339F07
581	10.4	31.5	50	1	AU103362	AU103362	AU103362	AU103362	C 654	10.2	30.9	38	8	BH904654	SALK_1048
582	10.4	31.5	50	1	AU103709	AU103709	AU103709	AU103709	C 655	10.2	30.9	38	8	AJ594660	Arabidops
583	10.4	31.5	50	1	AU104074	AU104074	AU104074	AU104074	C 656	10.2	30.9	38	9	AJ594660	Arabidops
584	10.4	31.5	50	1	AU104287	AU104287	AU104287	AU104287	C 657	10.2	30.9	38	9	TA117B04P	AL464666 T_brucei
585	10.4	31.5	50	1	AU104321	AU104321	AU104321	AU104321	C 658	10.2	30.9	38	9	TA117B04P	AL464666 T_brucei
586	10.4	31.5	50	1	AU104757	AU104757	AU104757	AU104757	C 659	10.2	30.9	39	4	BI225668	602949042
587	10.4	31.5	50	1	AU104827	AU104827	AU104827	AU104827	C 660	10.2	30.9	39	8	AZ408167	1M0179C14
588	10.4	31.5	50	1	AU104870	AU104870	AU104870	AU104870	C 661	10.2	30.9	39	8	CC060550	EY04745-5
589	10.4	31.5	50	1	AU105167	AU105167	AU105167	AU105167	C 662	10.2	30.9	39	9	TA306D11P	T_brucei
590	10.4	31.5	50	1	AU105222	AU105222	AU105222	AU105222	C 663	10.2	30.9	40	1	AI118560	ue23b06.x
591	10.4	31.5	50	1	AU105909	AU105909	AU105909	AU105909	C 664	10.2	30.9	40	1	AI538827	tp61b08.x
592	10.4	31.5	50	1	AU105910	AU105910	AU105910	AU105910	C 665	10.2	30.9	40	1	AI747109	ul09f07.x
593	10.4	31.5	50	1	AU105913	AU105913	AU105913	AU105913	C 666	10.2	30.9	40	1	AA258320	zr59f02.s
594	10.4	31.5	50	1	AU106034	AU106034	AU106034	AU106034	C 667	10.2	30.9	40	1	AA437989	vd21b08.s
595	10.4	31.5	50	1	AU106054	AU106054	AU106054	AU106054	C 668	10.2	30.9	40	9	AJ587421	Arabidops
596	10.4	31.5	50	1	AU106605	AU106605	AU106605	AU106605	C 669	10.2	30.9	40	9	CG705667	01S0583-0
597	10.4	31.5	50	1	AU106752	AU106752	AU106752	AU106752	C 670	10.2	30.9	41	1	AG255638	Lotus cor
598	10.4	31.5	50	1	AU106754	AU106754	AU106754	AU106754	C 671	10.2	30.9	41	1	AV967266	AV967266
599	10.4	31.5	50	1	AU106756	AU106756	AU106756	AU106756	C 672	10.2	30.9	41	4	AJ055018	BJ055018
600	10.4	31.5	50	1	AU106757	AU106757	AU106757	AU106757	C 673	10.2	30.9	41	8	AF039768	AF039768
601	10.4	31.5	50	1	AU106761	AU106761	AU106761	AU106761	C 674	10.2	30.9	41	8	AZ308318	1M0011M07
602	10.4	31.5	50	1	AU106902	AU106902	AU106902	AU106902	C 675	10.2	30.9	41	8	BZ353318	SALK_1201
603	10.4	31.5	50	1	AU107323	AU107323	AU107323	AU107323	C 676	10.2	30.9	41	9	DR4311S	AL976347 Dario rer
604	10.4	31.5	50	1	AU107939	AU107939	AU107939	AU107939	C 677	10.2	30.9	41	9	CC940900	01S0615-0
605	10.4	31.5	50	1	AU108026	AU108026	AU108026	AU108026	C 678	10.2	30.9	41	9	CG893475	03G3041-0
606	10.4	31.5	50	2	BE368091	601221989	BE368091	601221989	C 679	10.2	30.9	42	1	AA778293	zf35a01.s
607	10.4	31.5	50	4	B1853636	603380763	B1853636	603380763	C 680	10.2	30.9	42	1	AJ651067	AJ651067
608	10.4	31.5	50	6	CB191985	py23d01.y	CB191985	py23d01.y	C 681	10.2	30.9	42	6	CD743540	IRB14_B02

682	10.2	30.9	42	8	BH799740	1008109H1	755	10.2	30.9	50	1	AU104073	AU104073
683	10.2	30.9	42	9	AL936639	Arabidops	c 756	10.2	30.9	50	1	AU104084	AU104084
684	10.2	30.9	42	9	BX35511	Arabidops	c 757	10.2	30.9	50	1	AU104152	AU104152
685	10.2	30.9	43	1	AX902242	Arabidops	c 758	10.2	30.9	50	1	AU104242	AU104242
686	10.2	30.9	43	1	BG915507	602815734	c 759	10.2	30.9	50	1	AU104293	AU104293
687	10.2	30.9	43	8	BH903344	SALK 1024	760	10.2	30.9	50	1	AU104594	AU104594
688	10.2	30.9	43	8	CL520077	DAH8G05 F	761	10.2	30.9	50	1	AU104617	AU104617
689	10.2	30.9	44	6	CD747102	S202 G02	762	10.2	30.9	50	1	AU104620	AU104620
690	10.2	30.9	44	8	AZ340483	1M0072N19	763	10.2	30.9	50	1	AU104631	AU104631
691	10.2	30.9	44	8	AZ514943	1M0361024	764	10.2	30.9	50	1	AU104683	AU104683
692	10.2	30.9	44	8	CC458522	SALK 1194	c 765	10.2	30.9	50	1	AU104964	AU104964
693	10.2	30.9	44	8	AL758939	Arabidops	c 766	10.2	30.9	50	1	AU105688	AU105688
694	10.2	30.9	44	9	BX285481	Arabidops	c 767	10.2	30.9	50	1	AU105697	AU105697
695	10.2	30.9	45	7	TC9111	TC911109.r1	c 768	10.2	30.9	50	1	AU106367	AU106367
696	10.2	30.9	45	8	AZ2885975	2M0268F01	c 769	10.2	30.9	50	1	AU106372	AU106372
697	10.2	30.9	45	8	BH850110	SALK 0708	c 770	10.2	30.9	50	1	AU106745	AU106745
698	10.2	30.9	45	8	BZ353391	SALK 1202	c 771	10.2	30.9	50	1	AU106746	AU106746
699	10.2	30.9	45	9	CL246803	0250715-0	c 772	10.2	30.9	50	1	AU106802	AU106802
700	10.2	30.9	45	9	CL528502	ASV17E02	c 773	10.2	30.9	50	1	AU107130	AU107130
701	10.2	30.9	46	1	AA681479	vr37h02.r	c 774	10.2	30.9	50	1	AU107136	AU107136
702	10.2	30.9	46	1	AI185186	qe35f12.s	c 775	10.2	30.9	50	1	AU107137	AU107137
703	10.2	30.9	46	1	AI612864	tz57h05.x	c 776	10.2	30.9	50	1	AU107139	AU107139
704	10.2	30.9	46	1	AA511536	vj24e05.r	c 777	10.2	30.9	50	1	AU107140	AU107140
705	10.2	30.9	46	8	AZ503840	1M0343H16	c 778	10.2	30.9	50	1	AU107141	AU107141
706	10.2	30.9	46	8	BH909511	SALK 0541	c 779	10.2	30.9	50	1	AU107142	AU107142
707	10.2	30.9	46	8	AJ588695	Arabidops	c 780	10.2	30.9	50	1	AU107329	AU107329
708	10.2	30.9	46	9	AJ588695	Arabidops	c 781	10.2	30.9	50	1	AU108040	AU108040
709	10.2	30.9	47	6	CF337893	JMT--08-I	c 782	10.2	30.9	50	4	BG554327	dag72a10
710	10.2	30.9	47	8	BH752651	SALK 0189	c 783	10.2	30.9	50	6	CA355903	NISC 1u05
711	10.2	30.9	47	8	BH792501	SALK 0646	c 784	10.2	30.9	50	6	CA586369	LBC01975
712	10.2	30.9	47	8	BH849777	SALK 0702	c 785	10.2	30.9	50	8	AF149676	AF149676
713	10.2	30.9	47	8	BH851581	SALK 0732	c 786	10.2	30.9	50	8	AZ307590	1M0009N10
714	10.2	30.9	47	8	BH901058	KG08639-3	c 787	10.2	30.9	50	8	AZ817068	2M0086C07
715	10.2	30.9	47	9	BX130256	Danio rer	c 788	10.2	30.9	50	8	BH747393	SALK 1041
716	10.2	30.9	47	9	BX130256	Danio rer	c 789	10.2	30.9	50	8	BH904193	SALK 1041
717	10.2	30.9	47	9	CNS07FA0	Arabidops	c 790	10.2	30.9	50	8	BH904193	SALK 1041
718	10.2	30.9	47	9	CL310999	03S4743-0	c 791	10.2	30.9	50	9	DR23F2S	Arabidops
719	10.2	30.9	47	9	AB081891	Drosophila	c 792	10.2	30.9	50	9	CG732627	Danio rer
720	10.2	30.9	48	1	AU256785	AU256785	c 793	10.2	30.9	50	9	CG732627	Danio rer
721	10.2	30.9	48	1	AA399365	zt50d07.s	c 794	10.2	30.9	50	9	CL233835	01S0638-0
722	10.2	30.9	48	1	AA501194	vh75d02.r	c 795	10.2	30.9	50	9	AG216296	Drosophila
723	10.2	30.9	48	1	BJ048095	Arabidops	c 796	10.2	30.9	50	9	AG216296	Drosophila
724	10.2	30.9	48	6	CF298019	7LEAF--01	c 797	10.2	30.9	50	9	AG216296	Drosophila
725	10.2	30.9	48	8	BZ290243	SALK 0236	c 798	10.2	30.9	50	9	AG216296	Drosophila
726	10.2	30.9	48	8	BZ355275	SALK 1265	c 799	10.2	30.9	50	9	AG216296	Drosophila
727	10.2	30.9	48	8	BZ762165	SALK 0918	c 800	10.2	30.9	50	9	AG216296	Drosophila
728	10.2	30.9	48	8	BZ765295	SALK 1297	c 801	10.2	30.9	50	9	AG216296	Drosophila
729	10.2	30.9	48	9	BX945139	Arabidops	c 802	10.2	30.9	50	9	AG216296	Drosophila
730	10.2	30.9	48	9	TA207C01Q	Arabidops	c 803	10.2	30.9	50	9	AG216296	Drosophila
731	10.2	30.9	49	1	AA333611	Oh87e12.s	c 804	10.2	30.9	50	9	AG216296	Drosophila
732	10.2	30.9	49	1	AI096140	SWOVL3CAN	c 805	10.2	30.9	50	9	AG216296	Drosophila
733	10.2	30.9	49	1	AI198147	qi51b10.x	c 806	10.2	30.9	50	9	AG216296	Drosophila
734	10.2	30.9	49	1	AI198147	qi51b10.x	c 807	10.2	30.9	50	9	AG216296	Drosophila
735	10.2	30.9	49	1	AA478678	Arabidops	c 808	10.2	30.9	50	9	AG216296	Drosophila
736	10.2	30.9	49	7	H02223	Yj38e10.s1	c 809	10.2	30.9	50	9	AG216296	Drosophila
737	10.2	30.9	49	7	H02223	Yj38e10.s1	c 810	10.2	30.9	50	9	AG216296	Drosophila
738	10.2	30.9	49	7	W39290	zc76g04.r1	c 811	10.2	30.9	50	9	AG216296	Drosophila
739	10.2	30.9	49	7	W39290	zc76g04.r1	c 812	10.2	30.9	50	9	AG216296	Drosophila
740	10.2	30.9	49	7	W39290	zc76g04.r1	c 813	10.2	30.9	50	9	AG216296	Drosophila
741	10.2	30.9	49	8	AZ783979	2M0026K08	c 814	10.2	30.9	50	9	AG216296	Drosophila
742	10.2	30.9	49	8	BH791118	SALK 0587	c 815	10.2	30.9	50	9	AG216296	Drosophila
743	10.2	30.9	49	8	BH809509	KG06021-3	c 816	10.2	30.9	50	9	AG216296	Drosophila
744	10.2	30.9	49	8	BH907122	SALK 0383	c 817	10.2	30.9	50	9	AG216296	Drosophila
745	10.2	30.9	49	9	CG715750	1119043C0	c 818	10.2	30.9	50	9	AG216296	Drosophila
746	10.2	30.9	49	9	AG190566	Pan trogl	c 819	10.2	30.9	50	9	AG216296	Drosophila
747	10.2	30.9	50	1	AU102366	AU102366	c 820	10.2	30.9	50	9	AG216296	Drosophila
748	10.2	30.9	50	1	AU102572	AU102572	c 821	10.2	30.9	50	9	AG216296	Drosophila
749	10.2	30.9	50	1	AU102572	AU102572	c 822	10.2	30.9	50	9	AG216296	Drosophila
750	10.2	30.9	50	1	AU103250	AU103250	c 823	10.2	30.9	50	9	AG216296	Drosophila
751	10.2	30.9	50	1	AU104034	AU104034	c 824	10.2	30.9	50	9	AG216296	Drosophila
752	10.2	30.9	50	1	AU104050	AU104050	c 825	10.2	30.9	50	9	AG216296	Drosophila
753	10.2	30.9	50	1	AU104054	AU104054	c 826	10.2	30.9	50	9	AG216296	Drosophila
754	10.2	30.9	50	1	AU104055	AU104055	c 827	10.2	30.9	50	9	AG216296	Drosophila

C 828	10	30.3	34	8	BH907784	BH907784 SALK_0440	901	10	30.3	47	8	AZ835122	AZ835122	2M0129M08
829	10	30.3	35	1	AU237255	AU237255	902	10	30.3	47	8	BH856671	BH856671	BH856671 SALK_0793
C 830	10	30.3	35	2	AU245489	AU245489 2822716.5	C 903	10	30.3	47	8	CG326500	CG326500	CG326500 XN701 Bay
C 831	10	30.3	35	7	N70888	N70888 za89f11.81	904	10	30.3	47	9	BX285002	BX285002	Arabidops
C 832	10	30.3	35	8	AZ594762	AZ594762 1M0406M23	C 905	10	30.3	47	9	CL519316	CL519316	DAgIH09 F
C 833	10	30.3	35	8	AZ788299	AZ788299 2M0035U17	C 906	10	30.3	48	1	AA930605	AA930605	YV63e08.r
C 834	10	30.3	35	8	CG060475	CG060475 EY02581-3	C 907	10	30.3	48	1	AV840907	AV840907	AV840907
C 835	10	30.3	36	1	AA706884	AA706884 2j26H10.8	C 908	10	30.3	48	1	AA402658	AA402658	zu49e08.s
C 836	10	30.3	36	8	AZ581836	AZ581836 1M0370013	C 909	10	30.3	48	4	BI459090	BI459090	603199445
C 837	10	30.3	37	1	AA9334082	AA9334082 0n27G11.8	C 910	10	30.3	48	4	AZ772295	AZ772295	1M0583M04
C 838	10	30.3	37	1	AI198787	AI198787 qf79C02.x	C 911	10	30.3	48	8	AZ991463	AZ991463	2M0275X10
C 839	10	30.3	37	1	AI208266	AI208266 GY59e08.x	C 912	10	30.3	48	9	CR397288	CR397288	Arabidops
C 840	10	30.3	37	4	BG722105	BG722105 602698519	C 913	10	30.3	49	1	AA715207	AA715207	nu63g10.s
C 841	10	30.3	37	7	H43693	H43693 Y080B05.81	C 914	10	30.3	49	1	AA813480	AA813480	ai67a09.s
C 842	10	30.3	37	8	BZ383683	BZ383683 SALK_1342	C 915	10	30.3	49	1	AI208610	AI208610	QG45h02.x
C 843	10	30.3	37	8	BZ597109	BZ597109 SALK_0994	C 916	10	30.3	49	1	AI244893	AI244893	QJ98f06.x
C 844	10	30.3	37	9	AJ597362	AJ597362 Arabidops	C 917	10	30.3	49	1	AA154290	AA154290	ms01g03.x
C 845	10	30.3	37	9	CG724253	CG724253 1119080D0	C 918	10	30.3	49	1	AA232796	AA232796	zr47a03.r
C 846	10	30.3	37	9	AG201808	AG201808 Pan trogl	C 919	10	30.3	49	1	AV966624	AV966624	AV966624
C 847	10	30.3	38	4	BI547045	BI547045 603190269	C 920	10	30.3	49	4	BG250805	BG250805	602363222
C 848	10	30.3	38	8	AZ429651	AZ429651 1M0213P09	C 921	10	30.3	49	8	AZ345664	AZ345664	1M0080M23
C 849	10	30.3	38	8	AZ492391	AZ492391 1M0326D04	C 922	10	30.3	49	8	BH862617	BH862617	SALK_0902
C 850	10	30.3	38	8	AZ863007	AZ863007 2M0170N23	C 923	10	30.3	49	8	BH916381	BH916381	3526_1.52
C 851	10	30.3	38	9	AL942234	AL942234 Arabidops	C 924	10	30.3	49	9	TA58C07Q	TA58C07Q	T. brucei
C 852	10	30.3	38	9	TH292F07P	TH292F07P	C 925	10	30.3	50	1	AU102409	AU102409	AU102409
C 853	10	30.3	39	8	BH855773	BH855773 SALK_0846	C 926	10	30.3	50	1	AU102616	AU102616	AU102616
C 854	10	30.3	39	9	AL937027	AL937027 Arabidops	C 927	10	30.3	50	1	AU102658	AU102658	AU102658
C 855	10	30.3	40	1	AA726265	AA726265 vu89c01.r	C 928	10	30.3	50	1	AU102723	AU102723	AU102723
C 856	10	30.3	40	1	AI098410	AI098410 uc05e09.r	C 929	10	30.3	50	1	AU103202	AU103202	AU103202
C 857	10	30.3	40	1	AI157055	AI157055 udl1d02.r	C 930	10	30.3	50	1	AU103205	AU103205	AU103205
C 858	10	30.3	40	1	AJ239967	AJ239967 AJ239967	C 931	10	30.3	50	1	AU103661	AU103661	AU103661
C 859	10	30.3	40	1	AJ683751	AJ683751 AJ683751	C 932	10	30.3	50	1	AU103688	AU103688	AU103688
C 860	10	30.3	40	1	AA164815	AA164815 zo99g09.s	C 933	10	30.3	50	1	AU103691	AU103691	AU103691
C 861	10	30.3	40	1	AA437731	AA437731 vd68a09.r	C 934	10	30.3	50	1	AU103698	AU103698	AU103698
C 862	10	30.3	40	2	BE900485	BE900485 601673731	C 935	10	30.3	50	1	AU103788	AU103788	AU103788
C 863	10	30.3	40	7	H97838	H97838 YW09C01.81	C 936	10	30.3	50	1	AU104168	AU104168	AU104168
C 864	10	30.3	40	9	CG846786	CG846786 CMHD-GT.7	C 937	10	30.3	50	1	AU104205	AU104205	AU104205
C 865	10	30.3	41	8	AZ842109	AZ842109 2M0140M22	C 938	10	30.3	50	1	AU104262	AU104262	AU104262
C 866	10	30.3	41	8	BH611871	BH611871 SALK_0318	C 939	10	30.3	50	1	AU104715	AU104715	AU104715
C 867	10	30.3	41	9	CG781503	CG781503 1123045E0	C 940	10	30.3	50	1	AU104866	AU104866	AU104866
C 868	10	30.3	42	4	BG113593	BG113593 602284072	C 941	10	30.3	50	1	AU105411	AU105411	AU105411
C 869	10	30.3	42	4	BI553162	BI553162 603197760	C 942	10	30.3	50	1	AU105690	AU105690	AU105690
C 870	10	30.3	42	4	BI562641	BI562641 603256577	C 943	10	30.3	50	1	AU105770	AU105770	AU105770
C 871	10	30.3	42	9	BX141156	BX141156 Danilo rer	C 944	10	30.3	50	1	AU105771	AU105771	AU105771
C 872	10	30.3	43	1	AA877060	AA877060 nz43g09.s	C 945	10	30.3	50	1	AU105775	AU105775	AU105775
C 873	10	30.3	43	1	AI786712	AI786712 vj56b03.x	C 946	10	30.3	50	1	AU105780	AU105780	AU105780
C 874	10	30.3	43	1	AA549203	AA549203 vk85d08.s	C 947	10	30.3	50	1	AU105781	AU105781	AU105781
C 875	10	30.3	43	7	R71759	R71759 YJ85g09.81	C 948	10	30.3	50	1	AU105782	AU105782	AU105782
C 876	10	30.3	43	8	AZ639598	AZ639598 1M0501L07	C 949	10	30.3	50	1	AU105905	AU105905	AU105905
C 877	10	30.3	43	9	AL944631	AL944631 Arabidops	C 950	10	30.3	50	1	AU106028	AU106028	AU106028
C 878	10	30.3	43	9	AL947531	AL947531 Arabidops	C 951	10	30.3	50	1	AU106303	AU106303	AU106303
C 879	10	30.3	44	4	BG928099	BG928099 HNC46-1-B	C 952	10	30.3	50	1	AU106345	AU106345	AU106345
C 880	10	30.3	44	5	BQ588161	BQ588161 E012337-0	C 953	10	30.3	50	1	AU106346	AU106346	AU106346
C 881	10	30.3	44	8	AZ778327	AZ778327 2M0013016	C 954	10	30.3	50	1	AU106406	AU106406	AU106406
C 882	10	30.3	44	8	BH847111	BH847111 SALK_0132	C 955	10	30.3	50	1	AU106424	AU106424	AU106424
C 883	10	30.3	44	8	BH850740	BH850740 SALK_0717	C 956	10	30.3	50	1	AU106529	AU106529	AU106529
C 884	10	30.3	44	8	BH913151	BH913151 3526_1.38	C 957	10	30.3	50	1	AU106614	AU106614	AU106614
C 885	10	30.3	44	8	BZ591723	BZ591723 3590_1.64	C 958	10	30.3	50	1	AU106648	AU106648	AU106648
C 886	10	30.3	44	8	BZ595035	BZ595035 SALK_0855	C 959	10	30.3	50	1	AU106965	AU106965	AU106965
C 887	10	30.3	44	9	CR399731	CR399731 Arabidops	C 960	10	30.3	50	1	AU107197	AU107197	AU107197
C 888	10	30.3	45	4	BI158736	BI158736 602921522	C 961	10	30.3	50	1	AU107216	AU107216	AU107216
C 889	10	30.3	45	4	BI218941	BI218941 602938541	C 962	10	30.3	50	1	AU107233	AU107233	AU107233
C 890	10	30.3	45	8	BH913356	BH913356 3526_1.39	C 963	10	30.3	50	1	AU107574	AU107574	AU107574
C 891	10	30.3	45	9	CG712338	CG712338 111902F60	C 964	10	30.3	50	1	AU107587	AU107587	AU107587
C 892	10	30.3	45	9	AG195118	AG195118 Pan trogl	C 965	10	30.3	50	1	AU107588	AU107588	AU107588
C 893	10	30.3	46	1	AA954628	AA954628 o83e04.s	C 966	10	30.3	50	1	AU107673	AU107673	AU107673
C 894	10	30.3	46	1	AI000080	AI000080 o850e04.s	C 967	10	30.3	50	1	AU108020	AU108020	AU108020
C 895	10	30.3	46	1	AI284041	AI284041 qt72d04.x	C 968	10	30.3	50	1	AU108091	AU108091	AU108091
C 896	10	30.3	46	1	AV954130	AV954130 AV954130	C 969	10	30.3	50	1	AV952032	AV952032	AV952032
C 897	10	30.3	46	7	R94481	R94481 YG40G11.81	C 970	10	30.3	50	4	BG113114	BG113114	602283773
C 898	10	30.3	46	8	BH170395	BH170395 SALK_0028	C 971	10	30.3	50	6	CD486104	CD486104	CFU56.LH0
C 899	10	30.3	46	9	DME545047	DME545047 Drosophil	C 972	10	30.3	50	8	AZ416047	AZ416047	1M0191E11
C 900	10	30.3	47	7	H55083	H55083 CHR220022 C	C 973	10	30.3	50	8	BH847539	BH847539	SALK_0547

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c 974 10 30.3 50 9 CR267426 Forward s
975 10 30.3 50 9 CG721449
976 10 30.3 50 9 CG729623
c 977 9.8 29.7 20 8 AZ788491
c 978 9.8 29.7 21 8 AZ777774
979 9.8 29.7 22 9 CL670003
980 9.8 29.7 22 9 CL682717
981 9.8 29.7 23 8 BH848405
c 982 9.8 29.7 25 8 AZ644875
983 9.8 29.7 26 1 AJ684340
c 984 9.8 29.7 26 8 AZ486575
c 985 9.8 29.7 26 8 AZ957576
986 9.8 29.7 26 8 AZ969979
c 987 9.8 29.7 26 8 BH902249
c 988 9.8 29.7 26 9 AG202142
989 9.8 29.7 27 7 H77342
990 9.8 29.7 28 1 AI461340
991 9.8 29.7 28 1 AJ686029
992 9.8 29.7 28 5 BQ589286
993 9.8 29.7 28 8 AZ834553
c 994 9.8 29.7 28 9 AJ595741
995 9.8 29.7 29 8 AZ623273
c 996 9.8 29.7 29 8 AZ766277
997 9.8 29.7 29 8 AZ777646
c 998 9.8 29.7 30 1 AV857379
c 999 9.8 29.7 30 4 BI838550
c1000 9.8 29.7 30 8 AZ319785

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ALIGNMENTS

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RESULT 1
AZ759762/c 47 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
IM0552A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0552A19 R, genomic survey sequence.
ACCESSION
AZ759762 GI:12866879
VERSION
GSS.
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
REFERENCE
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: A column: 19
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 47.
FEATURES
source
Location/Qualifiers
1..47
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552A19"
/sex="Male"

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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ORIGIN

```

Query Match 47.9%; Score 15.8; DB 8; Length 47;
Best Local Similarity 74.1%; Pred. No. 3.6e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 6 TACTCACCCTTCCGACGACCACTATGG 32
|||||
DB 28 TACTCTGTTTCCCCGAGACTACTATGG 2
|||||

```

RESULT 2

```

BH848576/c 47 bp DNA linear GSS 13-JUN-2002
LOCUS
DEFINITION
SALK_068548.14.75.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_068548.14.75.x, genomic
survey sequence.
ACCESSION
BH848576
VERSION
BH848576.1 GI:21419447
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 47)
REFERENCE
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single-pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="Genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_068548.14.75.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion

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elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN

Query Match 46.1%; Score 15.2; DB 8; Length 47;
Best Local Similarity 71.4%; Pred. No. 6.5e+04;
Matches 20; Conservative 0; Mismatches 8; Indels - 0; Gaps 0;

RESULT	3
H03404/c	
LOCUS	
DEFINITION	H03404_37 bp mRNA linear EST 20-JUN-1995 YJ48C04.s1 Soares placenta Nd2HP Homo sapiens cDNA clone IMAGE:151974 3' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN cDNA sequence.

ORGANISM

homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

ORIGIN
Query Match 43.8%; Score 14.4; DB 7; Length 37;
Best Local Similarity 65.8%; Pred. No. 1.4e+05;
Matches 21; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 2 GGTGTA CTACCGTTC CGCAGACCA CTATGGC 33
Db 34 GCTATCATCAAGTTTC CGGTGACCA CTGAGTC 3

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RESULT 4	50 bp	linear	EST 28-JAN-2004
REUSE106643			
LOCUS	50 bp	linear	EST 28-JAN-2004
DEFINITION	Sugano Homo sapiens cDNA library	Homo sapiens cDNA clone	
	KAT05346, mRNA sequence.		

KEYWORDS	EST.	ORGANISM
SOURCE	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 50)	

TITLE
Diverse transcriptional initiation revealed by fine, large-scale
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Naka, N., Ueda, I., Iwoga, T., Yamada, I., Morishima, S.,
Okubo, A.,

BOOKING MEDLINE PUBMED	COMMENT
21270072	ando, K. P. 2 (37), 368-393 (2001).
21270072	Contact: Yutaka Suzuki
11375929	Institute of Medical Science, University of Tokyo
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
	Email: ysuzuki@ims.u-tokyo.ac.jp
	Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
	Sugano, S. Construction and characterization of a full
	length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
	149-156 (1997).

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="KAT05346"
/clone_lib="Sugano Homo sapiens cDNA library"

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Query Match      43.0%; Score 14.2; DB 1; Length 50;
Best Local Similarity 70.4%; Pred. No. 1.8e+05;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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RESULT 5	
T56929	
LOCUS	T56929 46 bp mRNA linear EST 07-FEB-1995
DEFINITION	ya83f08.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68295', similar to contains L1 repetitive element, mRNA sequence.
ACCESSION	T56929
VERSION	T56929.1 GI:658790
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 46)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favallo, A., Gish, W., Hawkins, E., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J., Trevaskis, B., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL

Genome Res. 6 (9), 807-828 (1996)

MEDLINE

97044478

PUBMED

8889549

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 360
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality

Insert length: 360 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 1.

FEATURES

source

1. .46

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:68295"

/tissue type="fetal spleen"

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/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Stratagene fetal spleen (#937205)"

/note="Organ: spleen; Vector: Bluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Pooled spleens. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

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3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

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3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ms.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

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ORIGIN

Query Match 42.4%; Score 14; DB 1; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Department of Virology

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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ms.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. .50

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="ADSE01101"

/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 42.4%; Score 14; DB 1; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ms.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and

Sugano, S. Construction and characterization of a full length-enriched and a 5'-end

```

Best Local Similarity 72.0%; Pred. No. 2.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TACTCACCCTTCGCGACCACTAT 30
   ||||| ||| ||| |||
Db 5 TACTCACCATTACCAATGCAATAT 29
   ||||| ||| ||| |||

RESULT 8
AZ331523
LOCUS 45 bp DNA linear GSS 29-SEP-2000
DEFINITION clone UUGCLM0059F01 R, genomic survey sequence.
ACCESSION AZ331523
VERSION AZ331523.1 GI:10394300
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 45)
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhauser, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: F column: 01
Seq primer: CACACAGGAACAGTATGACC
Class: plasmid ends
High quality sequence stop: 45.

FEATURES
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0059F01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 41.8%; Score 13.8; DB 8; Length 45;

Best Local Similarity 72.0%; Pred. No. 2.6e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5 GTACTCACCCTTCGCGACCACTA 29
   ||||| ||| ||| |||
Db 1 GTACTCACCCTACCTCTCTCCACA 25
   ||||| ||| ||| |||

RESULT 9
CR403035
LOCUS 41 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-860A07-025973,
genomic survey sequence.
ACCESSION CR403035
VERSION CR403035.1 GI:46943763
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse Genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and
Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE 14682050
PUBMED
REFERENCE 4 (bases 1 to 41)
Rosso, M.G., Strizhov, N., Li, Y. and Weishaar, B.
AUTHORS Direct Submission
TITLE Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
JOURNAL This sequence has been recovered from the left border of the T-DNA.
COMMENT It indicates an insertion within the locus defined by BAC clone
T15D22. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-860A07-025973"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

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```

ORIGIN
Query Match          41.2%; Score 13.6; DB 9; Length 41;
Best Local Similarity 67.9%; Pred. No. 3.2e+05;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 6 TACTACCGTTCCGACGACCATATGGC 33
    ||||| ||||| ||||| ||||| |||||
Db 5 TGCTCTCTTCTCCCTAAACCAAAATGGC 32

RESULT 10
CR403034          43 bp DNA linear GSS 02-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-860A07-025972,
genomic survey sequence.
CR403034
ACCESSION CR403034.1 GI:46943762
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS Li,Y.,Rosso,M.G., Strizhov,N., Viehoveer,P. and Weissshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weissshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weissshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE
AUTHORS Li,Y., Strizhov,N., Rosso,M.G. and Weissshaar,B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T15022. Details on the protocols used for generation of the
sequences are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
1..43
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-860A07-025972"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

ORIGIN
Query Match          41.2%; Score 13.6; DB 9; Length 43;
Best Local Similarity 67.9%; Pred. No. 3.2e+05;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 6 TACTACCGTTCCGACGACCATATGGC 33
    ||||| ||||| ||||| ||||| |||||
Db 6 TGCTCTCTTCTCCCAATACCAAAATGGC 33

RESULT 11
BE251857/c
LOCUS BE251857
DEFINITION BE251857 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356276 5',
mRNA sequence.
ACCESSION BE251857
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW161 row: j column: 21
High quality sequence stop: 41.
Location/Qualifiers
1..45
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3356276"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_16"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match          41.2%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 CTCACCGTTCCGACGACCAAC 27
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Db 23 CTCCTCGTTCCGACATCTC 4

RESULT 12
BZ763121/c
LOCUS BZ763121
DEFINITION BZ763121 47 bp DNA linear GSS 13-MAR-2003
SALK_113559.16.10.x Arabidopsis thaliana T-DNA insertion lines
Arabidopsis thaliana genomic clone SALK_113559.16.10.x, genomic

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survey sequence.
BZ763121
VERSION BZ763121.1 GI:28935674
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 47)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A sequence-indexed library of insertion mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of Atig07240.
Class: TDNA tagged.
FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="Col-0"
/ecotype="3702"
/clone_lib="SALK_113559.16.10.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 41.2%; Score 13.6; DB 8; Length 47;
Best Local Similarity 80.0%; Pred. NO. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 7 ACTACCGTTCGCAGACCA 26
Db 47 ACACAGTTCGCGGCCA 28
RESULT 13
CG719689/c
LOCUS CG719689 28 bp DNA linear GSS 20-OCT-2003
DEFINITION 119058G03.2EL_y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.
ACCESSION CG719689
VERSION CG719689.1 GI:37751846
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 28)
Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119058 row: G column: 03
Class: transposon-tagged.
FEATURES
source
Location/Qualifiers
1..28
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmldb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."
ORIGIN
Query Match 40.6%; Score 13.4; DB 9; Length 28;
Best Local Similarity 73.9%; Pred. NO. 3.8e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 8 CTCACCGTTCGCAGACCATAT 30
Db 25 CTCACCGTTCGGAATCATCAT 3
RESULT 14
AZ498025
LOCUS AZ498025 36 bp DNA linear GSS 05-OCT-2000
DEFINITION IM0335B09F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0335B09 F, genomic survey sequence.
ACCESSION AZ498025
VERSION AZ498025.1 GI:10675499
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 36)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0335 row: B column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 36.
FEATURES
Location/Qualifiers

```

```

source
1..36
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGC1M0335B09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
Query Match 40.6%; Score 13.4; DB 8; Length 36;
Best Local Similarity 73.9%; Pred. No. 3.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 TCACGTTCCGACCACTATG 31
Db 12 TCAGTGTCTGGGACCAATAG 34

RESULT 15
TA3H02P
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 3h02, forward sequence, genomic survey sequence.
ACCESSION AL451569
VERSION AL451569.1 GI:11854297
KEYWORDS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 39)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREP927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nleay@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

```

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source
1..39
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="3h02"

ORIGIN
Query Match 40.6%; Score 13.4; DB 9; Length 39;
Best Local Similarity 73.9%; Pred. No. 3.9e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 10 CACGTTCCGACCACTATGG 32
Db 2 CAACGCTCGAATACCACTGG 24

RESULT 16
BH620252
LOCUS
DEFINITION
1007061G07.2EL y1 1007 - RescueMu Grid H Zea mays genomic, genomic survey sequence.
ACCESSION BH620252
VERSION BH620252.1 GI:18431908
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 44)
AUTHORS Walbot, V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001).
COMMENT Contact: Walbot, V.
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.
Plate: 1007061 column: 18
Class: transposon-tagged.
Location/Qualifiers
1..44
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1007 - RescueMu Grid H"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmldb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN
Query Match 40.6%; Score 13.4; DB 8; Length 44;
Best Local Similarity 64.5%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

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QY 2 GGTGTAATCAGCGTTCGCGAGACCACTATGG 32
DB 1 GTTGTCTTTCGTCCTCCGCGCTCAAAGG 31

RESULT 17
A2785555/c
LOCUS A2785555 41 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0029G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0029G04 R, genomic survey sequence.
ACCESSION A2785555
VERSION A2785555.1 GI:12922431
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 41)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: G column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 41.
Location/Qualifiers
1. 41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0029G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES
source
1. 41
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0029G04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 41;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTCACCGTTCGCGAGACCACTATGCG 33
DB 34 CCCACCGTGATGTCACAGCAGTGTGCG 9

RESULT 18
A2812045/c
LOCUS A2812045 42 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0078A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0078A04 R, genomic survey sequence.
ACCESSION A2812045
VERSION A2812045.1 GI:12980903
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: A column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 42.
Location/Qualifiers
1. 42
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0078A04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 42;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 4 TGTACTCACGTTCCGACGACCACTA 29
  ||||| ||||| ||||| |||||
Db 29 TTTCCCACTGTTGAGCATATCACTA 4

RESULT 19
B1102544
LOCUS
DEFINITION B1102544 45 bp mRNA linear EST 26-JUN-2001
5' mRNA sequence.
ACCESSION B1102544
VERSION B1102544
KEYWORDS B1102544.1 GI:14553437
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 45)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabsr@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1122 row: p column: 12
High quality sequence stop: 45.
Location/Qualifiers
1..45
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5044859"
/lab_host="PH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library. |"

ORIGIN
Query Match 40.0%; Score 13.2; DB 4; Length 45;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 8 CTCACGTTCCGACGACCACTATGCC 33
  ||||| ||||| ||||| |||||
Db 8 CTGCCGTCACGACGACCACTGTTGCC 33

RESULT 20
B2660777/c
LOCUS
DEFINITION B2660777 45 bp DNA linear GSS 31-JAN-2003
SALK 024235.56.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_024235.56.00.x, genomic
survey sequence.
ACCESSION B2660777
VERSION B2660777
KEYWORDS B2660777.1 GI:28173924
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 45)
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,
Gadrinab C., Jeske A., Karnes M., Kim C.J., Parker H., Prednis L.,

TITLE Shinn, P., Zimmerman, J. and Ecker, J.R.
JOURNAL A Sequence-Indexed Library of Insertion Mutations in the
COMMENT Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within 300 bases of the 5' end of
At3g51890.
Class: TDNA tagged.
Location/Qualifiers
1..45
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_024235.56.00.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 40.0%; Score 13.2; DB 8; Length 45;
Best Local Similarity 69.2%; Pred. No. 4.8e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 7 ACTCACGTTCCGACGACCACTATGG 32
  ||||| ||||| ||||| |||||
Db 44 ATTCTGCTGTTACGAAACCACTGTGG 19

RESULT 21
AUI02740/c
LOCUS
DEFINITION AUI02740 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC13229, mRNA sequence.
ACCESSION AUI02740
VERSION AUI02740.1 GI:13552261
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRC13229"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 4.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CTCACCGTTCCGACGACCACTATGCG 33
   ||| ||| ||| ||| ||| ||| |||
Db 33 CTCACGTTGAGGACCGCAGTAGGCG 8

RESULT 22
AUI05906
LOCUS          AUI05906          50 bp      mRNA      linear      EST 28-JAN-2004
DEFINITION    AUI05906 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
               HEF05852, mRNA sequence.
ACCESSION     AUI05906
VERSION       AUI05906.1 GI:13555427
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 50)
AUTHORS      Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Sese,J.,
               Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
               Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE        Diverse transcriptional initiation revealed by fine, large-scale
               mapping of mRNA start sites
JOURNAL       EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE       21270072
PUBMED        11375929
COMMENT       Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
               Email: yusuzuki@ims.u-tokyo.ac.jp
               Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
               Sugano,S. Construction and characterization of a full
               length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
               149-156 (1997).

FEATURES             source
   source
   1..50
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="HEP05852"
   /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match          40.0%; Score 13.2; DB 1; Length 50;
Best Local Similarity 69.2%; Pred. No. 4.9e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 8 CTCACCGTTCCGACGACCACTATGCG 33
   ||| ||| ||| ||| ||| ||| |||
Db 20 CTCATGTTCCGGGACACAGTAGGCG 45

RESULT 23
A2786726/c
LOCUS          A2786726          38 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION    2M0032H20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC2M0032H20 F, genomic survey sequence.
ACCESSION     A2786726
VERSION       A2786726.1 GI:12924776
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1..(bases 1 to 38)
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weisse,R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0032 row: H column: 20
               Seq primer: CGTTGTAAACGACGCGCCAGT
               Class: plasmid ends
               High quality sequence stop: 38.
               Location/Qualifiers
               1..38
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0032H20"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

ORIGIN
Query Match          39.4%; Score 13; DB 8; Length 38;
Best Local Similarity 76.2%; Pred. No. 5.8e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TGTACTCACCCTCCGCGAC 24
   ||| ||| ||| ||| ||| |||
Db 31 TGTCCACCGTACGACGTC 11

RESULT 24
A2786726/c
LOCUS          A2786726          42 bp      DNA      linear      GSS 01-APR-2004
DEFINITION    Arabidopsis thaliana T-DNA flanking sequence GK-135B08-012755,
               genomic survey sequence.
ACCESSION     A2786726
VERSION       A2786726.1 GI:21518160
KEYWORDS      GSS.
SOURCE        Arabidopsis thaliana (thale cress)
ORGANISM      Arabidopsis thaliana
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
               1..(bases 1 to 38)
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D.,Weisse,R.
               Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
               Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0032 row: H column: 20
               Seq primer: CGTTGTAAACGACGCGCCAGT
               Class: plasmid ends
               High quality sequence stop: 38.
               Location/Qualifiers
               1..38
               /organism="Mus musculus"
               /mol_type="genomic DNA"
               /strain="C57BL/6J"
               /db_xref="taxon:10090"
               /clone="UUGC2M0032H20"
               /sex="Male"
               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
               /clone_lib="Mouse 10kb plasmid UUGC1M library"
               /note="Vector: PWD42nv; Purified genomic DNA from M.
               musculus C57BL/6J (male) was obtained from the Jackson
               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptor DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptor mouse DNA was annealed to
               adaptor vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weissshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
MEDLINE
PUBMED
22755829
12874060

REFERENCE
AUTHORS
2
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weissshaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL
MEDLINE
PUBMED
23117147
14756321

REFERENCE
AUTHORS
3
Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weissshaar, B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
BioTechniques 35 (6), 1164-1168 (2003)

JOURNAL
PUBMED
14682050

REFERENCE
AUTHORS
4
Strizhov, N., Li, Y., Rosso, M.G. and Weissshaar, B.
Direct Submission
Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T209. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-135B08-012755"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA-derived sequences were removed."

ORIGIN
Query Match 39.4%; Score 13; DB 9; Length 42;
Best Local Similarity 65.5%; Pred. No. 5.9e+05;
Matches 19; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4 TGTACTCAGCGTTCGACACCATATGG 32
|||||
DB 12 TGGACTGGCCATGACGAGGAGACTATGG 40
|||||

RESULT 25
AG192231
AG192231
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-068K06.TJ, genomic survey sequence.
ACCESSION
AG192231
VERSION
AG192231.1 GI:45224407

KEYWORDS SOURCE ORGANISM

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE AUTHORS

1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of Library RP-43
Unpublished

TITLE JOURNAL AUTHORS

2 (bases 1 to 45)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission

TITLE JOURNAL

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.krribb.re.kr, URL: <http://phs-grc.krribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43. This BAC end was generated during the RAD process and may have higher chance of clone tracking errors.
PRIMERS

COMMENT

Sequencing: TJ
LIBRARY

FEATURES source

Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1..45
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-068K06.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN

Query Match 39.4%; Score 13; DB 9; Length 45;
Best Local Similarity 76.2%; Pred. No. 5.9e+05;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY DB

1 CGGTGTACTCAGCGTTCGCA 21
|||||
13 CGGTGTGTCTCCCTTCCCA 33
|||||

RESULT 26 AUI02583 LOCUS

DEFINITION
AUI02583 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HBWA420069, mRNA sequence.
AUI02583
AUI02583.1 GI:13552104

ACCESSION VERSION KEYWORDS

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS

1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

TITLE JOURNAL MEDLINE PUBMED

21270072
11375929
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.8%; Score 12.8; DB 8; Length 32;
Best Local Similarity 70.8%; Pred. No. 7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 8 CTCACCGTCCGCGACCACTATG 31
Db 4 CTCACGTATCCGCGTCCGCTATG 27

RESULT 29

LOCUS BI695278/c

DEFINITION 603345135F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5372912 5', mRNA sequence.

ACCESSION BI695278

VERSION BI695278.1 GI:15657907

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 36)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999).

Contact: Robert Strausberg, Ph.D.

Email: cgaps@remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11949 row: e column: 09

High quality sequence stop: 36.

Location/Qualifiers

FEATURES

source

1..36

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N-3"

/db_xref="taxon:10090"

/clone="IMAGE:5372912"

/tissue_type="tumor, biopsy sample"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_lib="NCI CGAP Mam2"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigator

providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match

Best Local Similarity 38.8%; Score 12.8; DB 4; Length 36;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY

1 CGGTGTACTCACCCTCCGACAC 24

Db

30 CGGGGACCCACCGCTCCGCGGAC 7

RESULT 30

LOCUS BX285871/c

DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-386C04-018253,

genomic survey sequence.

ACCESSION BX285871

VERSION BX285871.1 GI:28884867

KEYWORDS GSS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P., and Weissshaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for

the identification of T-DNA insertion mutants in Arabidopsis

thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

MEDLINE 22755829

PUBMED 12874060

REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

Weissshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for

flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

MEDLINE 23117147

PUBMED 14756321

REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and

Weissshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA

mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL 14682050

PUBMED 14682050

REFERENCE 4 (bases 1 to 46)

AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weissshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weissshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA.

It indicates an insertion close to or within gene At5g39070.

Details on the protocols used for generation of the sequence are

described in References 1-3. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project.

GABI-Kat is part of the German Plant Genomics program designated

'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers

1..46

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-386C04-018253"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecovPe="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pAC161 (GenBank accession number: AJ537514). The

lines contain one or more T-DNA insertions. The DNA

fragment(s) resulting from the PCR were directly sequenced

to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN


```

Query Match      38.8%; Score 12.8; DB 9; Length 46;
Best Local Similarity 62.5%; Pred. No. 7.2e+05;
Matches 20; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 GGTGTAACACCGTTCGACGACCACTATGGC 33
    ||||| ||||| ||||| ||||| |||||
Db 38 GCTATACCTAGCATTCACCAATCACTACAGTGGC 7

RESULT 31
LOCUS CR397300
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-417A05-026074,
genomic survey sequence.
ACCESSION CR397300
VERSION CR397300.1 GI:46938028
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weissshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Weissshaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
Weissshaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
MEDLINE 14682050
PUBMED
REFERENCE 4
AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weissshaar, B.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weissshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT It indicates an insertion close to or within gene At2g36200.
Details on the protocols used for generation of the sequence are
described in References 1-3. The sequences are generated at the MPI
for Plant Breeding Research in the context of the GABI-Kat project.
GABI-Kat is part of the German Plant Genomics program designated
'GABI'. Information on line availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
Location/Qualifiers
1..47
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PAC161 (GenBank accession number: AJ537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.

T-DNA derived sequences were removed."

ORIGIN
Query Match      38.8%; Score 12.8; DB 9; Length 47;
Best Local Similarity 87.5%; Pred. No. 7.2e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TGTACTCACCGTTCG 19
    ||||| ||||| ||||| |||||
Db 2 TGTACTCACCTTGGC 17

RESULT 32
LOCUS AU104159/c
DEFINITION AU104159 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00274, mRNA sequence.
ACCESSION AU104159
VERSION AU104159.1 GI:13553680
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PUBMED 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAT00274"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      38.8%; Score 12.8; DB 1; Length 50;
Best Local Similarity 70.8%; Pred. No. 7.3e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CGGTGTACTACCGTTCGACAGAC 24
    ||||| ||||| ||||| |||||
Db 24 CCGGGACGACGCTTCACAGAC 1

RESULT 33
LOCUS AU106328/c
DEFINITION AU106328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00983, mRNA sequence.
ACCESSION AU106328
VERSION AU106328.1 GI:13555849
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS (bases 1 to 50)

```


/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0023G09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 38.2%; Score 12.6; DB 8; Length 37;
Best Local Similarity 78.9%; Pred. No. 8.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GTACTCACCCTCCGACAG 23
|||||
Db 28 GTACTCACCCTATCCAGA 10
|||||

RESULT 36

BZ767361/c
LOCUS BZ767361 44 bp DNA linear GSS 13-MAR-2003
DEFINITION SALK_138740.35.70.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_138740.35.70.x, genomic survey sequence.

ACCESSION BZ767361
VERSION BZ767361.1 GI:28939914
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

AUTHORS

Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu

JOURNAL

COMMENT This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g00560.
Class: TDNA tagged.

Location/Qualifiers
1..44

FEATURES
source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"

ORIGIN

Query Match 38.2%; Score 12.6; DB 9; Length 46;
Best Local Similarity 66.7%; Pred. No. 8.8e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CGGTGTACTACCGTTCGACAGCAC 27
Db 30 CGTTTCATTCACTGCACCGCAGAGCGC 4
|||||

RESULT 38

/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_138740.35.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 38.2%; Score 12.6; DB 8; Length 44;
Best Local Similarity 78.9%; Pred. No. 8.8e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 15 TTCGCGACACCACTATGCG 33
|||||
Db 40 TTCGCGGCAACTATGCG 22
|||||

RESULT 37

TA82D010/c
LOCUS TA82D010 46 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 82d01, reverse sequence, genomic survey sequence.

ACCESSION AL459951
VERSION AL459951.1 GI:11860276
KEYWORDS GSS
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 46)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE

JOURNAL Direct Submission
COMMENT Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1..46
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="82d01"

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Best Local Similarity 66.7%; Pred. No. 8.8e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CGGTGTACTACCGTTCGACAGCAC 27
Db 30 CGTTTCATTCACTGCACCGCAGAGCGC 4
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R18118
LOCUS       R18118               49 bp    mRNA    linear    EST 14-APR-1995
DEFINITION  ve90c12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:125014 5' similar to SP:S02141 S02141 INTER-ALPHA-TRYPSIN
INHIIBITOR HEAVY CHAIN H3 - HUMAN ;, mRNA sequence.
R18118
ACCESSION  R18118.1 GI:771728
VERSION     R18118.1
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 49)
            Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
            Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
            Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
            Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
            Wilson, R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2101
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Insert Length: 2101 Std Error: 0.00
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            High quality sequence stop: 1.
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     source          Location/Qualifiers
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             /db_xref="GDB:477559"
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             /clone="IMAGE:125014"
             /sex="male"
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             /lab_host="PH10B (ampicillin resistant)"
             /clone_lib="Soares fetal liver spleen INFLS"
             /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
             with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
             1st strand cDNA was primed with a Pac I - oligo(dT) primer
             [5' AACTCGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'],
             double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Pac I and cloned into the Pac I
             and Eco RI sites of the modified p773 vector. Library
             went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match      38.2%; Score 12.6; DB 7; Length 49;
Best Local Similarity 66.7%; Pred. No. 8.9e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      6  TACTACCGTTCGGACACCTATGCG 32
        |||||
Db      21  TGCTACCGATGGCGACCCCACTGTGG 47

RESULT 39
AU102859
LOCUS       AU102859             50 bp    mRNA    linear    EST 28-JAN-2004
DEFINITION  Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
IMAGE:125014 5' similar to SP:S02141 S02141 INTER-ALPHA-TRYPSIN
INHIIBITOR HEAVY CHAIN H3 - HUMAN ;, mRNA sequence.
AU102859
ACCESSION  AU102859
VERSION     AU102859.1 GI:13552380
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 49)
            Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
            Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
            Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
            Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
            Wilson, R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Insert Size: 2101
            High quality sequence starts: 1 High quality sequence stops: 1
            Source: IMAGE Consortium, LLNL This clone is available royalty-free
            through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
            for further information. Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand
            Insert Length: 2101 Std Error: 0.00
            Seq primer: M13RP1
            High quality sequence stop: 1.
FEATURES             source
     source          Location/Qualifiers
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             /clone="IMAGE:125014"
             /sex="male"
             /dev_stage="20 week-post conception fetus"
             /lab_host="PH10B (ampicillin resistant)"
             /clone_lib="Soares fetal liver spleen INFLS"
             /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
             with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
             1st strand cDNA was primed with a Pac I - oligo(dT) primer
             [5' AACTCGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'],
             double-stranded cDNA was ligated to Eco RI adaptors
             (Pharmacia), digested with Pac I and cloned into the Pac I
             and Eco RI sites of the modified p773 vector. Library
             went through one round of normalization. Library
             constructed by Bento Soares and M.Fatima Bonaldo."
ORIGIN
Query Match      38.2%; Score 12.6; DB 7; Length 49;
Best Local Similarity 66.7%; Pred. No. 8.9e+05;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      6  TACTACCGTTCGGACACCTATGCG 32
        |||||
Db      21  TGCTACCGATGGCGACCCCACTGTGG 47

RESULT 39
AU102859
LOCUS       AU102859             50 bp    mRNA    linear    EST 28-JAN-2004
DEFINITION  Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
IMAGE:125014 5' similar to SP:S02141 S02141 INTER-ALPHA-TRYPSIN
INHIIBITOR HEAVY CHAIN H3 - HUMAN ;, mRNA sequence.
AU102859
ACCESSION  AU102859
VERSION     AU102859.1 GI:13552380
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 50)
            Hata, H., Ota, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K.,
            Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
            21270072
            PUBMED 11375929
            COMMENT Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
            Sugano, S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).
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     source          Location/Qualifiers
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             /clone="COL01421"
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Query Match      38.2%; Score 12.6; DB 1; Length 50;
Best Local Similarity 78.9%; Pred. No. 8.9e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  CGGTGTACTACCGTTCG 19
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Db      10  CGGTGCGCTCGCGGTTCTG 28

RESULT 40
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LOCUS       AZ482042             32 bp    DNA    linear    GSS 04-OCT-2000
DEFINITION  1M0306C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0306C20 R, genomic survey sequence.
AZ482042
ACCESSION  AZ482042
VERSION     AZ482042.1 GI:10643107
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 32)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0306 row: C column: 20
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends

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High quality sequence stop: 32.

FEATURES

source

Location/Qualifiers

1. .32

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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGC1M0306C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 37.6%; Score 12.4; DB 8; Length 32;
Best Local Similarity 92.9%; Pred. No. 1e+06;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CAGACCACTATGGC 33
Db 14 CAGACCACTATGGC 1

Search completed: November 23, 2004, 22:22:29
Job time : 1617.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 540.225 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631b-4
Perfect score: 30
Sequence: 1 tggactagctcttggtcatctcaccttct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1795872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_ats.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	100.0	30	6	AX802290 Sequence
2	19	63.3	31	6	BD181365 A method
3	19	63.3	31	6	AX147028 Sequence
4	19	63.3	31	6	AX523945 Sequence
5	19	63.3	31	6	AX524843 Sequence
6	19	63.3	33	6	I17523 Sequence 13
7	19	63.3	33	6	I28348 Sequence 1
8	17.6	58.7	48	6	AX777198 Sequence
9	16.4	54.7	46	6	AX379394 Sequence
10	16.2	54.0	39	6	AX804053 Sequence
11	15.8	52.7	26	6	AX800237 Sequence
12	15.6	52.0	49	9	U11510 Human RET p
13	15.2	50.7	22	6	AX420204 Sequence
14	15.2	50.7	22	6	AX528208 Sequence
15	15.2	50.7	22	6	AX528214 Sequence
16	15.2	50.7	22	6	AX554648 Sequence
17	15.2	50.7	24	6	AR230098 Sequence
18	15.2	50.7	24	6	AX022200 Sequence
19	15.2	50.7	24	6	AX030726 Sequence

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39	6	E14084	50.7	15.2	21	c
47	6	AR284878	50.7	15.2	22	c
31	6	AX249405	50.0	15	23	c
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30	6	CO801293	49.3	14.8	25	c
41	6	AX514149	49.3	14.8	26	c
41	6	AX520300	49.3	14.8	27	c
46	6	AR379395	49.3	14.8	28	c
46	6	AR379396	49.3	14.8	29	c
46	6	AR379397	49.3	14.8	30	c
47	6	AR290158	49.3	14.8	31	c
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36	6	AR303048	48.7	14.6	33	c
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42	6	AR443130	48.7	14.6	35	c
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34	6	CO817634	47.3	14.2	53	c
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39	6	AR151073	47.3	14.2	55	c
39	6	E15027	47.3	14.2	56	c
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39	6	BD014665	47.3	14.2	58	c
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42	6	AX612118	47.3	14.2	60	c
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45	6	AR401645	47.3	14.2	63	c
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48	6	AR008969	47.3	14.2	66	c
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28	6	AR090550	46.7	14	73	c
28	6	AR197585	46.7	14	74	c
28	6	AR259739	46.7	14	75	c
29	6	AX611610	46.7	14	76	c
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AR075804	Sequence
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AR197585	Sequence
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C75926	Homo sapien
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A19280	oligonucleo

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c 102	13.6	45.3	20	6	AX648136	AX648136 Sequence	c 175	13.2	44.0	50	6	CO008347	CO008347 Sequence
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c 107	13.6	45.3	24	6	AX445937	AX445937 Sequence	c 180	13	43.3	22	6	BD250601	BD250601 Identific
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c 109	13.6	45.3	26	6	AX703186	AX703186 Sequence	c 182	13	43.3	25	6	AX116600	AX116600 Sequence
c 110	13.6	45.3	28	6	AX183774	AX183774 Sequence	c 183	13	43.3	25	6	AX532893	AX532893 Sequence
c 111	13.6	45.3	29	6	AR014455	AR014455 Sequence	c 184	13	43.3	25	6	AX532894	AX532894 Sequence
c 112	13.6	45.3	29	6	AX922898	AX922898 Sequence	c 185	13	43.3	25	6	AX532895	AX532895 Sequence
c 113	13.6	45.3	31	6	AR195972	AR195972 Sequence	c 186	13	43.3	25	6	AX532896	AX532896 Sequence
c 114	13.6	45.3	35	6	A09922	A09922 Probe. 1/19	c 187	13	43.3	25	6	AX532897	AX532897 Sequence
c 115	13.4	44.7	17	6	AX500581	AX500581 Sequence	c 188	13	43.3	26	6	BD262546	BD262546 Informati
c 116	13.4	44.7	17	6	AX500582	AX500582 Sequence	c 189	13	43.3	26	6	AX037969	AX037969 Sequence
c 117	13.4	44.7	17	6	AX500583	AX500583 Sequence	c 190	13	43.3	27	6	AX473012	AX473012 Sequence
c 118	13.4	44.7	24	6	AX291457	AX291457 Sequence	c 191	13	43.3	27	6	BD003198	BD003198 HPPD Gene
c 119	13.4	44.7	25	6	AX502578	AX502578 Sequence	c 192	13	43.3	29	6	CO760897	CO760897 Sequence
c 120	13.4	44.7	25	6	AX502579	AX502579 Sequence	c 193	13	43.3	29	6	CO760898	CO760898 Sequence
c 121	13.4	44.7	25	6	AX502580	AX502580 Sequence	c 194	13	43.3	29	6	BD170744	BD170744 Human FG
c 122	13.4	44.7	25	6	AX502581	AX502581 Sequence	c 195	13	43.3	30	6	AR343503	AR343503 Sequence
c 123	13.4	44.7	25	6	AX502582	AX502582 Sequence	c 196	13	43.3	30	6	AR489851	AR489851 Sequence
c 124	13.4	44.7	25	6	AX502583	AX502583 Sequence	c 197	13	43.3	32	6	AR099893	AR099893 Sequence
c 125	13.4	44.7	25	6	AX502584	AX502584 Sequence	c 198	13	43.3	32	6	E10686	E10686 Primer. 9/1
c 126	13.4	44.7	25	6	AX502585	AX502585 Sequence	c 199	13	43.3	32	6	AR431427	AR431427 Sequence
c 127	13.4	44.7	25	6	AX502586	AX502586 Sequence	c 200	13	43.3	34	6	I12121	I12121 Sequence 26
c 128	13.4	44.7	25	6	AX502587	AX502587 Sequence	c 201	13	43.3	34	6	I41291	I41291 Sequence 26
c 129	13.4	44.7	25	6	AX502588	AX502588 Sequence	c 202	13	43.3	34	6	AX593266	AX593266 Sequence
c 130	13.4	44.7	28	6	A161780	A161780 Sequence	c 203	13	43.3	36	6	I36286	I36286 Sequence 16
c 131	13.4	44.7	29	6	AR00078	AR00078 mutagenic o	c 204	13	43.3	36	6	AX460070	AX460070 Sequence
c 132	13.4	44.7	31	6	AX249670	AX249670 Sequence	c 205	13	43.3	38	6	AX804041	AX804041 Sequence
c 133	13.4	44.7	32	6	AR204622	AR204622 Sequence	c 206	13	43.3	39	6	AR143459	AR143459 Sequence
c 134	13.4	44.7	36	6	AX207593	AX207593 Sequence	c 207	13	43.3	39	6	CO799136	CO799136 Sequence
c 135	13.4	44.7	41	6	AX515653	AX515653 Sequence	c 208	13	43.3	40	6	AX458423	AX458423 Sequence
c 136	13.4	44.7	41	6	AX518248	AX518248 Sequence	c 209	13	43.3	41	6	A74298	A74298 Sequence 10
c 137	13.4	44.7	42	6	I27648	I27648 Sequence 3	c 210	13	43.3	41	6	AR038839	AR038839 Sequence
c 138	13.4	44.7	42	6	AR379422	AR379422 Sequence	c 211	13	43.3	41	6	AX519835	AX519835 Sequence
c 139	13.4	44.7	45	6	AR321784	AR321784 Sequence	c 212	13	43.3	43	6	AX6382	AX6382 Sequence 30
c 140	13.4	44.7	47	6	AR289711	AR289711 Sequence	c 213	13	43.3	47	6	AR291253	AR291253 Sequence
c 141	13.4	44.7	49	6	BD247140	BD247140 Eukaryoti	c 214	13	43.3	48	3	MELRG5SB	M60442 Meloidogyne
c 142	13.2	44.0	21	6	BD088828	BD088828 A method	c 215	13	43.3	48	6	I33522	I33522 Sequence 1
c 143	13.2	44.0	21	6	BD089054	BD089054 A method	c 216	13	43.3	48	6	I33523	I33523 Sequence 2
c 144	13.2	44.0	21	12	AR068537	AR068537 Synthetic	c 217	13	43.3	48	6	I68897	I68897 Sequence 16
c 145	13.2	44.0	25	6	AX594722	AX594722 Sequence	c 218	13	43.3	48	6	I68901	I68901 Sequence 16
c 146	13.2	44.0	29	6	A73754	A73754 Sequence 3	c 219	13	43.3	48	6	AR205536	AR205536 Sequence
c 147	13.2	44.0	29	6	AR059886	AR059886 Sequence	c 220	13	43.3	48	6	AR253495	AR253495 Sequence
c 148	13.2	44.0	29	6	AX611170	AX611170 Sequence	c 221	13	43.3	48	6	AR253499	AR253499 Sequence
c 149	13.2	44.0	30	6	AR026347	AR026347 Sequence	c 222	13	43.3	48	6	AX076554	AX076554 Sequence
c 150	13.2	44.0	30	6	AR089150	AR089150 Sequence	c 223	13	43.3	48	6	AX426732	AX426732 Sequence
c 151	13.2	44.0	30	6	BD190689	BD190689 Productio	c 224	13	43.3	48	6	AX696548	AX696548 Sequence
c 152	13.2	44.0	30	6	BD271648	BD271648 Process f	c 225	13	43.3	48	6	AX696552	AX696552 Sequence
c 153	13.2	44.0	30	6	AR473504	AR473504 Sequence	c 226	13	43.3	48	6	BD130926	BD130926 Method of
c 154	13.2	44.0	30	6	AX611257	AX611257 Sequence	c 227	13	43.3	49	6	BD130927	BD130927 Method of
c 155	13.2	44.0	30	6	AX611260	AX611260 Sequence	c 228	13	43.3	50	6	AR032781	AR032781 Sequence
c 156	13.2	44.0	30	6	AX611261	AX611261 Sequence	c 229	13	43.3	50	6	I29521	I29521 Sequence 39
c 157	13.2	44.0	34	6	BD243124	BD243124 Hypersens	c 230	13	43.3	50	6	I91195	I91195 Sequence 39
c 158	13.2	44.0	34	6	E39868	E39868 Novel promo	c 231	13	43.3	50	6	AR209445	AR209445 Sequence
c 159	13.2	44.0	34	6	AR345085	AR345085 Sequence	c 232	13	43.3	50	6	AR282118	AR282118 Sequence
c 160	13.2	44.0	34	6	BD106646	BD106646 Hypersens	c 233	13	43.3	50	6	AR282119	AR282119 Sequence
c 161	13.2	44.0	35	3	DME544038	ARJ544038 Drosophil	c 234	13	43.3	50	6	AR282171	AR282171 Sequence
c 162	13.2	44.0	36	6	AR120415	AR120415 Sequence	c 235	13	43.3	50	6	AX427051	AX427051 Sequence
c 163	13.2	44.0	36	6	AR341106	AR341106 Sequence	c 236	12.8	42.7	17	6	AX266139	AX266139 Sequence
c 164	13.2	44.0	36	6	BD063424	BD063424 Streptoco	c 237	12.8	42.7	17	6	AX266140	AX266140 Sequence
c 165	13.2	44.0	42	6	A04432	A04432 Oligonucleo	c 238	12.8	42.7	18	6	AR294287	AR294287 Sequence

239	12.8	42.7	20	6	BD259929	BD59929 LIM miner	c 312	12.6	42.0	23	6	I23638	I23638 Sequence 60
240	12.8	42.7	20	6	AR227691	AR227691 Sequence	c 313	12.6	42.0	23	6	AR433502	AR433502 Sequence
241	12.8	42.7	20	6	AR282693	AR282693 Sequence	314	12.6	42.0	23	6	AR433503	AR433503 Sequence
242	12.8	42.7	20	6	AR369785	AR369785 Sequence	315	12.6	42.0	23	6	AR433504	AR433504 Sequence
243	12.8	42.7	20	6	AX101064	AX101064 Sequence	316	12.6	42.0	23	6	AR433505	AR433505 Sequence
244	12.8	42.7	20	6	AX600986	AX600986 Sequence	c 317	12.6	42.0	24	6	AX280512	AX280512 Sequence
245	12.8	42.7	20	6	BD073512	BD073512 Novel bon	c 318	12.6	42.0	25	6	CQ618736	CQ618736 Sequence
246	12.8	42.7	20	6	BD094869	BD094869 A method	c 319	12.6	42.0	25	6	CQ618737	CQ618737 Sequence
247	12.8	42.7	21	6	BD259938	BD259938 LIM miner	c 320	12.6	42.0	25	6	CQ618738	CQ618738 Sequence
248	12.8	42.7	21	6	AR227700	AR227700 Sequence	c 321	12.6	42.0	25	6	CQ618739	CQ618739 Sequence
249	12.8	42.7	21	6	AR282702	AR282702 Sequence	c 322	12.6	42.0	25	6	CQ618740	CQ618740 Sequence
250	12.8	42.7	21	6	AR298510	AR298510 Sequence	c 323	12.6	42.0	25	6	CQ618741	CQ618741 Sequence
251	12.8	42.7	21	6	AR369794	AR369794 Sequence	c 324	12.6	42.0	25	6	CQ618742	CQ618742 Sequence
252	12.8	42.7	21	6	BD073521	BD073521 Novel bon	325	12.6	42.0	25	6	CQ629414	CQ629414 Sequence
253	12.8	42.7	22	6	BD102271	BD102271 Method of	326	12.6	42.0	25	6	CQ629415	CQ629415 Sequence
254	12.8	42.7	24	6	BD259941	BD259941 LIM miner	327	12.6	42.0	25	6	CQ629416	CQ629416 Sequence
255	12.8	42.7	24	6	E50089	E50089 DNA encodin	328	12.6	42.0	25	6	CQ629417	CQ629417 Sequence
256	12.8	42.7	24	6	AR227703	AR227703 Sequence	329	12.6	42.0	25	6	CQ629418	CQ629418 Sequence
257	12.8	42.7	24	6	AR282705	AR282705 Sequence	330	12.6	42.0	25	6	CQ629419	CQ629419 Sequence
258	12.8	42.7	24	6	AR369797	AR369797 Sequence	331	12.6	42.0	25	6	CQ629420	CQ629420 Sequence
259	12.8	42.7	24	6	BD073524	BD073524 Novel bon	c 332	12.6	42.0	25	6	AR459799	AR459799 Sequence
260	12.8	42.7	25	6	AX534594	AX534594 Sequence	c 333	12.6	42.0	25	6	AR459800	AR459800 Sequence
261	12.8	42.7	25	6	AX534595	AX534595 Sequence	c 334	12.6	42.0	25	6	AR459801	AR459801 Sequence
262	12.8	42.7	26	6	AX921451	AX921451 Sequence	c 335	12.6	42.0	25	6	AR459802	AR459802 Sequence
263	12.8	42.7	27	6	AR040190	AR040190 Sequence	c 336	12.6	42.0	25	6	AR459803	AR459803 Sequence
264	12.8	42.7	27	6	AR184883	AR184883 Sequence	c 337	12.6	42.0	25	6	AR459804	AR459804 Sequence
265	12.8	42.7	27	6	AX702380	AX702380 Sequence	c 338	12.6	42.0	25	6	AR459805	AR459805 Sequence
266	12.8	42.7	29	6	BD174845	BD174845 Antibody-	339	12.6	42.0	25	6	AR470477	AR470477 Sequence
267	12.8	42.7	29	6	BD260456	BD260456 Secreted	340	12.6	42.0	25	6	AR470478	AR470478 Sequence
268	12.8	42.7	29	6	AX233420	AX233420 Sequence	341	12.6	42.0	25	6	AR470479	AR470479 Sequence
269	12.8	42.7	30	6	BD143278	BD143278 Oligonuc1	342	12.6	42.0	25	6	AR470480	AR470480 Sequence
270	12.8	42.7	30	6	AX248526	AX248526 Sequence	343	12.6	42.0	25	6	AR470481	AR470481 Sequence
271	12.8	42.7	31	6	I06237	I06237 Sequence 8	344	12.6	42.0	25	6	AR470482	AR470482 Sequence
272	12.8	42.7	34	6	I07307	I07307 Sequence 19	345	12.6	42.0	25	6	AR470483	AR470483 Sequence
273	12.8	42.7	34	6	BD013914	BD013914 Vermin da	c 346	12.6	42.0	25	6	AX609669	AX609669 Sequence
274	12.8	42.7	34	6	I05542	I05542 Sequence 8	c 347	12.6	42.0	26	6	AR349077	AR349077 Sequence
275	12.8	42.7	38	6	AR178217	AR178217 Sequence	c 348	12.6	42.0	26	6	AR349078	AR349078 Sequence
276	12.8	42.7	38	6	AR178716	AR178716 Sequence	349	12.6	42.0	26	6	AR349079	AR349079 Sequence
277	12.8	42.7	40	6	BD251230	BD251230 Oligonuc1	c 350	12.6	42.0	26	6	AR349080	AR349080 Sequence
278	12.8	42.7	40	6	AR205421	AR205421 Sequence	351	12.6	42.0	29	6	AR429703	AR429703 Sequence
279	12.8	42.7	40	6	AR220113	AR220113 Sequence	352	12.6	42.0	30	6	BD235556	BD235556 Methods a
280	12.8	42.7	40	6	AR221502	AR221502 Sequence	353	12.6	42.0	30	6	BD021856	BD021856 Method fo
281	12.8	42.7	40	6	AR254204	AR254204 Sequence	354	12.6	42.0	31	6	AX248913	AX248913 Sequence
282	12.8	42.7	40	6	AR282410	AR282410 Sequence	355	12.6	42.0	32	6	AX349884	AX349884 Sequence
283	12.8	42.7	40	6	AR368317	AR368317 Sequence	356	12.6	42.0	32	6	BD006910	BD006910 Inhibitio
284	12.8	42.7	41	6	AX515147	AX515147 Sequence	357	12.6	42.0	33	6	A45513	A45513 Sequence 42
285	12.8	42.7	41	6	AX515825	AX515825 Sequence	c 358	12.6	42.0	33	6	I08861	I08861 Sequence 1
286	12.8	42.7	41	6	AX517941	AX517941 Sequence	359	12.6	42.0	33	6	AR267694	AR267694 Sequence
287	12.8	42.7	41	6	AX521082	AX521082 Sequence	c 360	12.6	42.0	34	6	I06978	I06978 Sequence 2
288	12.8	42.7	41	6	A70338	A70338 Sequence 5	c 361	12.6	42.0	34	6	I07047	I07047 Sequence 2
289	12.8	42.7	43	6	AR117155	AR117155 Sequence	c 362	12.6	42.0	35	6	AX643576	AX643576 Sequence
290	12.8	42.7	43	6	CQ828067	CQ828067 Sequence	c 363	12.6	42.0	36	6	AX573339	AX573339 Sequence
291	12.8	42.7	43	6	CQ828097	CQ828097 Sequence	c 364	12.6	42.0	37	6	BD229946	BD229946 Novel DKR
292	12.8	42.7	43	6	AX404947	AX404947 Sequence	c 365	12.6	42.0	38	6	CQ784399	CQ784399 Sequence
293	12.8	42.7	43	6	AR284682	AR284682 Sequence	366	12.6	42.0	40	6	AX052779	AX052779 Sequence
294	12.8	42.7	47	6	AR289787	AR289787 Sequence	367	12.6	42.0	40	6	AX767221	AX767221 Sequence
295	12.8	42.7	47	6	AR290601	AR290601 Sequence	c 368	12.6	42.0	40	9	S08019	S08019 gamma delta
296	12.8	42.7	47	6	AR097534	AR097534 Sequence	c 369	12.6	42.0	41	6	AR020669	AR020669 Sequence
297	12.8	42.7	47	6	AX378326	AX378326 Sequence	c 370	12.6	42.0	41	6	AR121179	AR121179 Sequence
298	12.8	42.7	47	6	U65660	U65660 Mus muscul	c 371	12.6	42.0	41	6	AR160307	AR160307 Sequence
299	12.8	42.7	47	10	MMLOXL02	MMLOXL02	372	12.6	42.0	41	6	AX15367	AX15367 Sequence
300	12.8	42.7	50	6	CQ004805	CQ004805 Sequence	c 373	12.6	42.0	41	6	AX517862	AX517862 Sequence
301	12.8	42.7	50	6	AX538789	AX538789 Sequence	c 374	12.6	42.0	41	6	AX520898	AX520898 Sequence
302	12.6	42.0	20	6	BD221956	BD221956 Nucleic a	c 375	12.6	42.0	41	6	BD003594	BD003594 Methods a
303	12.6	42.0	20	6	I80914	I80914 Sequence 31	c 376	12.6	42.0	41	9	H5274594	H5274594 H sapiens j
304	12.6	42.0	20	6	AR211886	AR211886 Sequence	377	12.6	42.0	42	6	I32723	I32723 Sequence 50
305	12.6	42.0	20	6	AR230540	AR230540 Sequence	c 378	12.6	42.0	42	6	AX612115	AX612115 Sequence
306	12.6	42.0	20	6	AR310235	AR310235 Sequence	c 379	12.6	42.0	42	6	AX612117	AX612117 Sequence
307	12.6	42.0	20	6	AR350647	AR350647 Sequence	c 380	12.6	42.0	45	6	AX612113	AX612113 Sequence
308	12.6	42.0	20	6	AR494381	AR494381 Sequence	c 381	12.6	42.0	47	6	A40450	A40450 Sequence 77
309	12.6	42.0	23	6	I23635	I23635 Sequence 57	c 382	12.6	42.0	47	6	BD196577	BD196577 Prostatic
310	12.6	42.0	23	6	I23636	I23636 Sequence 58	c 383	12.6	42.0	47	6	BD196578	BD196578 Prostatic
311	12.6	42.0	23	6	I23637	I23637 Sequence 59	384	12.6	42.0	47	6	AR289463	AR289463 Sequence

385	12.6	42.0	47	6	AR289812	Sequence	458	12.4	41.3	41	6	AX519738	Sequence
386	12.6	42.0	47	6	AR291072	Sequence	459	12.4	41.3	41	6	AX521019	Sequence
387	12.6	42.0	47	6	AR292017	Sequence	460	12.4	41.3	42	6	A71375	Sequence 5
C 388	12.6	42.0	48	6	168898	Sequence 16	461	12.4	41.3	42	6	A78975	Sequence 5
C 389	12.6	42.0	48	6	168902	Sequence 17	462	12.4	41.3	42	6	BD003429	Sequence 5
C 390	12.6	42.0	48	6	AR253496	Sequence	463	12.4	41.3	42	6	BD003429	Sequence 5
C 391	12.6	42.0	48	6	AR253500	Sequence	464	12.4	41.3	46	6	AR392731	Sequence
C 392	12.6	42.0	48	6	AX696549	Sequence	C 464	12.4	41.3	47	6	BD221906	Nucleic a
C 393	12.6	42.0	48	6	AX696553	Sequence	C 465	12.4	41.3	47	6	AR211836	Sequence
C 394	12.6	42.0	49	6	CQ816324	Sequence	C 466	12.4	41.3	47	6	AR290041	Sequence
C 395	12.6	42.0	49	6	CQ818919	Sequence	C 467	12.4	41.3	47	6	AR290253	Sequence
396	12.6	42.0	50	6	AR112327	Sequence	C 468	12.4	41.3	47	6	AX194739	Sequence
397	12.6	42.0	50	6	CQ008492	Sequence	469	12.4	41.3	48	6	AX194739	Sequence 46
C 398	12.6	42.0	50	6	E33637	Sequence	470	12.4	41.3	48	10	PNU33863	Sequence
C 399	12.6	42.0	50	6	E33637	Detection o	471	12.4	41.3	48	10	S77042	T-cell rece
C 400	12.4	41.3	17	6	AX500580	Sequence	472	12.4	41.3	49	6	AX101291	Sequence
C 401	12.4	41.3	17	6	AX500584	Sequence	C 473	12.4	41.3	50	6	CQ816944	Sequence
402	12.4	41.3	20	6	AX732796	Sequence	C 474	12.4	41.3	50	6	AX068182	Sequence
403	12.4	41.3	20	6	BD28528	IL-17 hom	C 475	12.4	41.3	50	6	AX164945	Sequence
404	12.4	41.3	20	6	AR314211	Sequence	C 476	12.4	41.3	50	6	AX495663	Sequence
C 405	12.4	41.3	21	6	AR359753	Sequence	C 477	12.2	40.7	17	6	BD202860	Method an
C 406	12.4	41.3	21	6	AX095276	Sequence	C 478	12.2	40.7	17	6	BD241162	Methods a
C 407	12.4	41.3	22	6	AX095792	Sequence	C 479	12.2	40.7	17	6	CQ615807	Sequence
C 408	12.4	41.3	23	6	AX686739	Sequence	480	12.2	40.7	17	6	I37572	Sequence 58
C 409	12.4	41.3	23	6	BD266813	Methods f	481	12.2	40.7	17	6	I94422	Sequence 58
C 410	12.4	41.3	23	6	CQ753578	Sequence	C 482	12.2	40.7	17	6	AR456870	Sequence
C 411	12.4	41.3	23	6	E09974	Primer for	C 483	12.2	40.7	17	6	AR482663	Sequence
C 412	12.4	41.3	23	6	E09974	PCR primer	C 484	12.2	40.7	17	6	AX266135	Sequence
C 413	12.4	41.3	25	6	AR381729	Sequence	C 485	12.2	40.7	17	6	AX266136	Sequence
C 414	12.4	41.3	25	6	AX502577	Sequence	C 486	12.2	40.7	17	6	AX266143	Sequence
C 415	12.4	41.3	25	6	AX502589	Sequence	C 487	12.2	40.7	17	6	AX266144	Sequence
416	12.4	41.3	25	6	AX534592	Sequence	C 488	12.2	40.7	17	6	AX725150	Sequence
417	12.4	41.3	25	6	AX534593	Sequence	C 489	12.2	40.7	17	6	AX726799	Sequence
418	12.4	41.3	25	6	AX609787	Sequence	C 490	12.2	40.7	18	6	AR066856	Sequence
419	12.4	41.3	25	6	AX692209	Sequence	491	12.2	40.7	19	6	AX129585	Sequence
420	12.4	41.3	25	6	AX692210	Sequence	492	12.2	40.7	20	6	AR100060	Sequence
421	12.4	41.3	25	6	AX692211	Sequence	493	12.2	40.7	20	6	AR100061	Sequence
422	12.4	41.3	26	6	I12122	Sequence	494	12.2	40.7	20	6	AR136427	Sequence
423	12.4	41.3	26	6	I12122	Sequence 27	C 495	12.2	40.7	20	6	AR275085	Sequence
C 424	12.4	41.3	27	6	AR191412	Sequence	C 496	12.2	40.7	20	6	AR363587	Sequence
C 425	12.4	41.3	27	6	AR191412	Sequence	C 497	12.2	40.7	20	6	AR42097	Sequence
C 426	12.4	41.3	28	6	AR207923	Sequence	C 498	12.2	40.7	20	6	AR42097	Sequence
C 427	12.4	41.3	29	6	AR044258	Sequence	C 499	12.2	40.7	20	6	AX451710	Sequence
C 428	12.4	41.3	29	6	AR044258	Sequence	C 500	12.2	40.7	20	6	AX467189	Sequence
C 429	12.4	41.3	29	6	I18936	Sequence 8	C 501	12.2	40.7	20	6	BD168964	Drug resi
C 430	12.4	41.3	29	6	I24121	Sequence 8	C 502	12.2	40.7	21	6	I23544	Sequence 22
C 431	12.4	41.3	29	6	I35898	Sequence 13	C 503	12.2	40.7	21	6	I23549	Sequence 27
C 432	12.4	41.3	29	6	I36086	Sequence 40	C 504	12.2	40.7	21	6	AX154110	Sequence
C 433	12.4	41.3	29	6	I68869	Sequence 13	C 505	12.2	40.7	23	6	AR177338	Sequence
C 434	12.4	41.3	29	6	AR223530	Sequence	C 506	12.2	40.7	23	6	BD203807	5'EST and
C 435	12.4	41.3	29	6	AR223718	Sequence	C 507	12.2	40.7	23	6	BD247961	5' ESTs f
C 436	12.4	41.3	29	6	AR234845	Sequence	C 508	12.2	40.7	23	6	CQ771924	Sequence
C 437	12.4	41.3	29	6	AR234845	Sequence	C 509	12.2	40.7	23	6	AR306539	Sequence
C 438	12.4	41.3	29	6	AR235033	Sequence	C 510	12.2	40.7	23	6	AR340705	Sequence
C 439	12.4	41.3	29	6	AR253467	Sequence	C 511	12.2	40.7	23	6	AR412381	Sequence
C 440	12.4	41.3	29	6	AX611609	Sequence	C 512	12.2	40.7	23	6	AX061613	Sequence
C 441	12.4	41.3	29	6	AX696516	Sequence	C 513	12.2	40.7	23	6	AX884155	Sequence
C 442	12.4	41.3	29	6	AX935736	Sequence	C 514	12.2	40.7	23	6	AX939013	Sequence
443	12.4	41.3	30	6	AX146896	Sequence	C 515	12.2	40.7	23	6	AX968604	Sequence
444	12.4	41.3	30	6	AX146896	Sequence	C 516	12.2	40.7	23	6	AX969215	Sequence
C 445	12.4	41.3	31	6	AX105077	Sequence	C 517	12.2	40.7	23	6	BD023765	Sequence
C 446	12.4	41.3	31	6	AX248327	Sequence	C 518	12.2	40.7	23	6	BD073622	5'EST of
447	12.4	41.3	32	6	AX349880	Sequence	C 519	12.2	40.7	23	6	BD075900	5' EST of
448	12.4	41.3	33	6	BD237687	Therapeut	C 520	12.2	40.7	23	6	BD076078	5' EST of
449	12.4	41.3	33	6	AR473403	Sequence	C 521	12.2	40.7	23	6	BD076779	5' EST of
450	12.4	41.3	33	6	AX278205	Sequence	C 522	12.2	40.7	23	6	BD077440	5'EST of
451	12.4	41.3	33	6	BD138039	Expressio	C 523	12.2	40.7	23	6	BD077741	5'EST of
452	12.4	41.3	35	6	BD224795	Novel pla	C 524	12.2	40.7	23	6	BD085884	Elongatio
453	12.4	41.3	35	6	E10705	Primer. 9/1	C 525	12.2	40.7	23	6	BD107934	EST and e
C 454	12.4	41.3	41	6	AX513816	Sequence	C 526	12.2	40.7	23	6	BD131412	CDNA enco
455	12.4	41.3	41	6	AX515471	Sequence	C 527	12.2	40.7	23	6	BD139274	Extended
456	12.4	41.3	41	6	AX515544	Sequence	C 528	12.2	40.7	25	6	CQ618743	Sequence
C 457	12.4	41.3	41	6	AX517691	Sequence	C 529	12.2	40.7	25	6	CQ618744	Sequence
							C 530	12.2	40.7	25	6	CQ797993	Sequence

C 531	12.2	40.7	25	6	CQ797994	Sequence	604	12.2	40.7	41	6	AX514811	Sequence
C 532	12.2	40.7	25	6	AR459806	Sequence	605	12.2	40.7	41	6	AX517169	Sequence
C 533	12.2	40.7	25	6	AR459807	Sequence	606	12.2	40.7	41	6	AX519123	Sequence
C 534	12.2	40.7	25	6	AX566001	Sequence	607	12.2	40.7	46	6	AR148825	Sequence
C 535	12.2	40.7	25	6	AX566002	Sequence	608	12.2	40.7	46	10	MUSENV1	Mouse env m
C 536	12.2	40.7	25	6	AX766006	Sequence	609	12.2	40.7	47	6	E39260	Method for
C 537	12.2	40.7	25	6	AX766007	Sequence	610	12.2	40.7	47	6	E39260	Method for
C 538	12.2	40.7	26	6	AR026160	Sequence	611	12.2	40.7	47	6	AR288370	Sequence
C 539	12.2	40.7	26	6	AR026212	Sequence	612	12.2	40.7	47	6	AR289307	Sequence
C 540	12.2	40.7	26	6	AR026226	Sequence	613	12.2	40.7	47	6	AR289724	Sequence
C 541	12.2	40.7	26	6	AR026240	Sequence	614	12.2	40.7	48	6	A50035	Sequence 1
C 542	12.2	40.7	26	6	AR089196	Sequence	615	12.2	40.7	48	6	AR031654	Sequence
C 543	12.2	40.7	26	6	AR123651	Sequence	616	12.2	40.7	48	6	AR036479	Sequence
C 544	12.2	40.7	26	6	Q812851	Sequence	617	12.2	40.7	48	6	AR069438	Sequence
C 545	12.2	40.7	26	6	E61336	Probe for d	618	12.2	40.7	48	6	AR122695	Sequence
C 546	12.2	40.7	26	6	I82902	Sequence 4	619	12.2	40.7	48	6	AR122696	Sequence
C 547	12.2	40.7	26	6	I82954	Sequence 56	620	12.2	40.7	48	6	I73460	Sequence 12
C 548	12.2	40.7	26	6	I82968	Sequence 70	621	12.2	40.7	48	6	I90272	Sequence 13
C 549	12.2	40.7	26	6	I82982	Sequence 84	622	12.2	40.7	49	6	AR032506	Sequence
C 550	12.2	40.7	26	6	AR352022	Sequence	623	12.2	40.7	49	6	AR032506	Sequence
C 551	12.2	40.7	26	6	AR431088	Sequence	624	12.2	40.7	49	6	I29246	Sequence 11
C 552	12.2	40.7	26	6	AR431140	Sequence	625	12.2	40.7	49	6	I90920	Sequence 11
C 553	12.2	40.7	26	6	AR431154	Sequence	626	12.2	40.7	49	6	AR209170	Sequence
C 554	12.2	40.7	26	6	AR431168	Sequence	627	12.2	40.7	50	6	CO813874	Sequence
C 555	12.2	40.7	26	6	AR431168	Sequence	628	12.2	40.7	50	10	MMU41922	Sequence
C 556	12.2	40.7	26	6	AR828881	Sequence	629	12.2	40.7	50	10	MMU41988	Mus musculus
C 557	12.2	40.7	26	6	AR828933	Sequence	630	12.2	40.7	17	6	AX423530	Sequence
C 558	12.2	40.7	26	6	AX828947	Sequence	631	12.2	40.0	18	6	AR083094	Sequence
C 559	12.2	40.7	26	6	AX828961	Sequence	632	12.2	40.0	18	6	AR174871	Sequence
C 560	12.2	40.7	27	6	AR191128	Sequence	633	12.2	40.0	20	6	AR106431	Sequence
C 561	12.2	40.7	28	6	E30857	Process for	634	12.2	40.0	20	6	AR312440	Sequence
C 562	12.2	40.7	28	6	AR390869	Sequence	635	12.2	40.0	20	6	AX296090	Sequence
C 563	12.2	40.7	29	6	A56906	Sequence 2	636	12.2	40.0	20	6	AX683627	Sequence
C 564	12.2	40.7	29	6	AR139092	Sequence	637	12.2	40.0	21	11	DOG11A1A	Canis fam1
C 565	12.2	40.7	29	6	I64493	Sequence 7	638	12.2	40.0	22	6	AX241236	Sequence
C 566	12.2	40.7	30	6	BD271962	Cell surf	639	12.2	40.0	22	6	AX487704	Sequence
C 567	12.2	40.7	30	6	AR275195	Sequence	640	12.2	40.0	24	6	AR098104	Sequence
C 568	12.2	40.7	30	6	AR133703	Sequence	641	12.2	40.0	24	6	AR216929	Sequence
C 569	12.2	40.7	30	6	AX770023	Sequence	642	12.2	40.0	24	6	AX067818	Sequence
C 570	12.2	40.7	31	6	I12445	Sequence 15	643	12.2	40.0	24	6	AX283064	Sequence
C 571	12.2	40.7	31	6	I14507	Sequence 15	644	12.2	40.0	24	6	AX447390	Sequence
C 572	12.2	40.7	31	6	AX248925	Sequence	645	12.2	40.0	24	6	AX487514	Sequence
C 573	12.2	40.7	32	6	E10684	Primer. 9/1	646	12.2	40.0	24	6	AX487579	Sequence
C 574	12.2	40.7	32	6	AR014460	Sequence	647	12.2	40.0	24	6	BD084848	Modified
C 575	12.2	40.7	33	6	AR077823	Sequence	648	12.2	40.0	25	6	BD086399	KCNQ2 and
C 576	12.2	40.7	33	6	AR151063	Sequence	649	12.2	40.0	25	6	AR146789	Sequence
C 577	12.2	40.7	33	6	E15019	PCR primer	650	12.2	40.0	25	6	AX183844	Sequence
C 578	12.2	40.7	33	6	AR316462	Sequence	651	12.2	40.0	25	6	AX532892	Sequence
C 579	12.2	40.7	33	6	BD014655	Process f	652	12.2	40.0	25	6	AX532898	Sequence
C 580	12.2	40.7	34	6	BD188206	bHLH-PAS	653	12.2	40.0	27	6	AR167468	Sequence
C 581	12.2	40.7	34	6	BD225447	LYST prot	654	12.2	40.0	27	6	BD218432	SSX gene,
C 582	12.2	40.7	34	6	I02499	Sequence 3	655	12.2	40.0	27	6	AR189239	Sequence
C 583	12.2	40.7	34	6	AR362750	Sequence	656	12.2	40.0	27	6	AR305683	Sequence
C 584	12.2	40.7	34	6	AR373162	Sequence	657	12.2	40.0	27	6	AR402532	Sequence
C 585	12.2	40.7	35	6	BD169146	bHLH-PAS	658	12.2	40.0	27	6	AR402561	Sequence
C 586	12.2	40.7	35	6	BD272577	PRRSV vac	659	12.2	40.0	27	6	AR447192	Sequence
C 587	12.2	40.7	35	11	C75875	Homo sapien	660	12.2	40.0	27	6	AX107147	Sequence
C 588	12.2	40.7	36	6	AR146013	Sequence	661	12.2	40.0	27	6	AX118436	Sequence
C 589	12.2	40.7	36	6	E02844	DNA encodin	662	12.2	40.0	27	6	BD068032	Enzymatic
C 590	12.2	40.7	36	6	AR180904	Sequence	663	12.2	40.0	27	6	BD068061	Enzymatic
C 591	12.2	40.7	39	6	A67622	Sequence 42	664	12.2	40.0	28	6	AX234358	Sequence
C 592	12.2	40.7	39	6	AR089760	Sequence 46	665	12.2	40.0	28	6	AX597999	Sequence
C 593	12.2	40.7	39	6	AR089760	Sequence	666	12.2	40.0	30	6	A49578	Sequence 19
C 594	12.2	40.7	39	6	AR089764	Sequence	667	12.2	40.0	30	6	AR106272	Sequence
C 595	12.2	40.7	39	6	AR148717	Sequence	668	12.2	40.0	30	6	BD008840	Uses of a
C 596	12.2	40.7	39	6	AR151067	Sequence	669	12.2	40.0	30	6	BD097519	Methods f
C 597	12.2	40.7	39	6	E15023	PCR primer	670	12.2	40.0	31	6	BD002906	Gene comp
C 598	12.2	40.7	39	6	AR316466	Sequence	671	12.2	40.0	32	6	AX183759	Sequence
C 599	12.2	40.7	39	6	AX612039	Sequence	672	12.2	40.0	32	6	AX557074	Sequence
C 600	12.2	40.7	39	6	BD014659	Process f	673	12.2	40.0	33	6	AR038154	Sequence
C 601	12.2	40.7	40	6	E12972	Hybrid DNA/	674	12.2	40.0	33	6	AR094117	Sequence
C 602	12.2	40.7	40	6	AX802723	Sequence	675	12.2	40.0	33	6	AX184037	Sequence
C 603	12.2	40.7	40	6	AX803078	Sequence	676	12.2	40.0	33	6	AX589695	Sequence

677	12	40.0	33	6	BD106830	BD106830 Methods o	750	12	40.0	47	6	AX537339	AX537339 Sequence
678	12	40.0	34	6	AX283065	BD283065 Sequence	751	12	40.0	47	6	AX741679	AX741679 Sequence
679	12	40.0	35	6	BD190131	BD190131 Novel hum	752	12	40.0	47	6	AX776501	AX776501 Sequence
680	12	40.0	35	6	AX192030	AX192030 Sequence	753	12	40.0	47	6	BD063524	BD063524 Streptoco
681	12	40.0	37	6	AR193403	AR193403 Sequence	754	12	40.0	48	6	AX274412	AX274412 Sequence
682	12	40.0	37	6	AR491403	AR491403 Sequence	755	12	40.0	48	6	AX274568	AX274568 Sequence
683	12	40.0	37	6	AX234367	AX234367 Sequence	756	12	40.0	48	6	AX583479	AX583479 Sequence
684	12	40.0	38	6	CQ817646	CQ817646 Sequence	C 757	12	40.0	49	6	AX1174	AX1174 Sequence 8
685	12	40.0	38	6	CQ817647	CQ817647 Sequence	C 758	12	40.0	49	6	AR117404	AR117404 Sequence
686	12	40.0	39	6	AX34187	AX34187 Synthetic h	C 759	12	40.0	49	6	AR309043	AR309043 Sequence
687	12	40.0	39	6	AR128129	AR128129 Sequence	C 760	12	40.0	49	6	AX147410	AX147410 Sequence
688	12	40.0	39	6	BD265531	BD265531 Plastid t	761	12	40.0	49	6	AX662179	AX662179 Sequence
689	12	40.0	39	6	AR237493	AR237493 Sequence	762	12	40.0	50	6	AR444575	AR444575 Sequence
690	12	40.0	39	6	AX280672	AX280672 Sequence	763	12	40.0	50	6	AR444577	AR444577 Sequence
691	12	40.0	40	6	AR148734	AR148734 Sequence	C 764	12	40.0	50	6	AX160068	AX160068 Sequence
692	12	40.0	41	6	AX280671	AX280671 Sequence	765	12	40.0	50	6	AX694692	AX694692 Sequence
693	12	40.0	41	6	AX514233	AX514233 Sequence	766	12	40.0	50	9	HUMKREP8	L00204 Human K6b (
694	12	40.0	41	6	AX516287	AX516287 Sequence	C 767	11.8	39.3	17	6	AR072951	AR072951 Sequence
695	12	40.0	41	6	AX516352	AX516352 Sequence	768	11.8	39.3	17	6	BD202859	BD202859 Method an
696	12	40.0	41	6	AX516859	AX516859 Sequence	C 769	11.8	39.3	17	6	AR220084	AR220084 Sequence
697	12	40.0	41	6	AX519072	AX519072 Sequence	770	11.8	39.3	17	6	AX734694	AX734694 Sequence
698	12	40.0	41	6	AX519369	AX519369 Sequence	C 771	11.8	39.3	17	6	BD002277	BD002277 Cellulase
699	12	40.0	41	6	AX520386	AX520386 Sequence	C 772	11.8	39.3	17	6	BD010881	BD010881 Cellulase
700	12	40.0	41	6	AX520415	AX520415 Sequence	C 773	11.8	39.3	19	6	AR439937	AR439937 Sequence
701	12	40.0	42	6	A36516	A36516 Sequence 57	C 774	11.8	39.3	20	6	CQ819708	CQ819708 Sequence
702	12	40.0	42	6	AR080149	AR080149 Sequence	775	11.8	39.3	20	6	I71526	I71526 Sequence 67
703	12	40.0	42	6	BD266719	BD266719 Generatio	776	11.8	39.3	20	6	AR241092	AR241092 Sequence
704	12	40.0	42	6	E50930	E50930 DNA and uti	777	11.8	39.3	20	6	AX429373	AX429373 Sequence
705	12	40.0	42	6	AR238803	AR238803 Sequence	778	11.8	39.3	20	6	AX487019	AX487019 Sequence
706	12	40.0	42	6	AR363814	AR363814 Sequence	779	11.8	39.3	21	6	CQ815012	CQ815012 Sequence
707	12	40.0	42	6	AX079214	AX079214 Sequence	C 780	11.8	39.3	21	6	AX095302	AX095302 Sequence
708	12	40.0	42	6	AX080047	AX080047 Sequence	781	11.8	39.3	21	6	AX133261	AX133261 Sequence
709	12	40.0	42	6	AX080057	AX080057 Sequence	782	11.8	39.3	21	6	AX956310	AX956310 Sequence
710	12	40.0	42	6	AX338459	AX338459 Sequence	783	11.8	39.3	21	6	AX958200	AX958200 Sequence
711	12	40.0	43	6	BD1822384	BD1822384 An agent	784	11.8	39.3	21	6	BD091025	BD091025 ADAMTS po
712	12	40.0	43	6	E23312	E23312 Antibody ag	785	11.8	39.3	22	6	AR361979	AR361979 Sequence
713	12	40.0	43	6	E27081	E27081 Remedy for	C 786	11.8	39.3	22	6	AR361980	AR361980 Sequence
714	12	40.0	43	6	BD011912	BD011912 Ameliorat	787	11.8	39.3	22	6	AX192297	AX192297 Sequence
715	12	40.0	43	6	BD011968	BD011968 Therapeut	C 788	11.8	39.3	22	6	AX192298	AX192298 Sequence
716	12	40.0	43	6	BD012029	BD012029 Theraput	C 789	11.8	39.3	22	6	AX278540	AX278540 Sequence
717	12	40.0	43	6	BD012916	BD012916 Inhibitin	C 790	11.8	39.3	22	6	AX513097	AX513097 Sequence
718	12	40.0	43	6	BD095486	BD095486 Remedies	791	11.8	39.3	22	6	BD016730	BD016730 Promoter
719	12	40.0	43	6	BD095647	BD095647 Stable an	C 792	11.8	39.3	22	6	BD088534	BD088534 A method
720	12	40.0	43	6	BD140972	BD140972 An agent	C 793	11.8	39.3	22	6	BD171664	BD171664 Identific
721	12	40.0	44	6	AR058443	AR058443 Sequence 13	794	11.8	39.3	22	12	AB069511	AB069511 Synthetic
722	12	40.0	44	6	A95463	A95463 Sequence	795	11.8	39.3	23	6	BD230495	BD230495 Total gen
723	12	40.0	45	6	AR135328	AR135328 Sequence	796	11.8	39.3	23	6	CQ799765	CQ799765 Sequence
724	12	40.0	45	6	AR141103	AR141103 Sequence	C 797	11.8	39.3	23	6	AR267668	AR267668 Sequence
725	12	40.0	45	6	AR152395	AR152395 Sequence	798	11.8	39.3	23	6	AR345132	AR345132 Sequence
726	12	40.0	45	6	AR177526	AR177526 Sequence	C 799	11.8	39.3	23	6	AX428096	AX428096 Sequence
727	12	40.0	45	6	AR221749	AR221749 Sequence	C 800	11.8	39.3	23	6	AX709071	AX709071 Sequence
728	12	40.0	45	6	AR222529	AR222529 Sequence	C 801	11.8	39.3	23	6	BD103832	BD103832 A method
729	12	40.0	45	6	AR349242	AR349242 Sequence	C 802	11.8	39.3	24	6	BD230208	BD230208 Total gen
730	12	40.0	45	6	AX048221	AX048221 Sequence	C 803	11.8	39.3	24	6	BD230209	BD230209 Total gen
731	12	40.0	45	6	AX049382	AX049382 Sequence	C 804	11.8	39.3	24	6	E31368	E31368 Histidine k
732	12	40.0	45	6	AX052722	AX052722 Sequence	C 805	11.8	39.3	24	6	AR494807	AR494807 Sequence
733	12	40.0	45	6	AX053163	AX053163 Sequence	C 806	11.8	39.3	24	6	AX181781	AX181781 Sequence
734	12	40.0	45	6	AX268059	AX268059 Sequence	C 807	11.8	39.3	24	6	AX289759	AX289759 Sequence
735	12	40.0	46	6	BD237816	BD237816 Optical s	C 808	11.8	39.3	24	6	AX663757	AX663757 Sequence
736	12	40.0	46	6	AX026757	AX026757 Sequence	C 809	11.8	39.3	24	6	AX922586	AX922586 Sequence
737	12	40.0	47	6	AR032403	AR032403 Sequence	C 810	11.8	39.3	24	6	AX922588	AX922588 Sequence
738	12	40.0	47	6	AR120515	AR120515 Sequence	C 811	11.8	39.3	24	6	BD077184	BD077184 Method an
739	12	40.0	47	6	I29143	I29143 Sequence 15	C 812	11.8	39.3	25	6	AR150687	AR150687 Sequence
740	12	40.0	47	6	I90817	I90817 Sequence 15	C 813	11.8	39.3	25	6	BD183221	BD183221 A method
741	12	40.0	47	6	AR209067	AR209067 Sequence	C 814	11.8	39.3	25	6	CQ620230	CQ620230 Sequence
742	12	40.0	47	6	AR288840	AR288840 Sequence	C 815	11.8	39.3	25	6	CQ620231	CQ620231 Sequence
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744	12	40.0	47	6	AR290402	AR290402 Sequence	C 817	11.8	39.3	25	6	E16236	E16236 Primer 7/1
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1000 11.6 38.7 20 6 AX657567 Sequence

ALIGNMENTS

RESULT 1
AX802290
LOCUS AX802290 30 bp DNA linear PAT 24-NOV-2003
DEFINITION Sequence 2 from Patent WO03057910.
ACCESSION AX802290
VERSION AX802290.1 GI:38501181
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Pintel-Ober,J., Wenzig,P., Weindel,K., Bartl,K., Schoenbrunner,R.,
Malhotra,K., O'Donnell,P. and Kyger,E.
TITLE Use of silica material in an amplification reaction
JOURNAL Patent: WO 03057910-A 2 17-JUL-2003;
Roche Diagnostics GmbH (DE)
FEATURES
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/organism="synthetic construct"
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/note="Internal Control Specific Probes"

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Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30

RESULT 2
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LOCUS BD181365 31 bp DNA linear PAT 15-MAY-2003

DEFINITION A method for determination of a nucleic acid using a control.
ACCESSION BD181365
VERSION BD181365.1 GI:30792283
KEYWORDS JP 2002335981-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 31)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 4 26-NOV-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/4
PD 26-NOV-2002 JP 2002057515
PF 04-MAR-2001 EP 01105172.9
PR 02-MAR-2002 JP 2002057515
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
CC Description of Artificial Sequence: ST2535 probe sequence CC
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diol)
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FT Nregion (15).
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Query Match 63.3%; Score 19; DB 6; Length 31;
Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
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LOCUS AX147028 31 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 22 from Patent WO0137291.
ACCESSION AX147028
VERSION AX147028.1 GI:14346299
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Weindel,K., Riedling,M. and Geiger,A.
TITLE Magnetic glass particles, method for their preparation and uses
JOURNAL Patent: WO 0137291-A 22 25-MAY-2001;
Roche Diagnostics GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
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Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 4
LOCUS AX523945 31 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 4 from Patent EP1236804.
ACCESSION AX523945
VERSION AX523945.1 GI:25168876
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 4 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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Best Local Similarity 96.8%; Pred. No. 6.2e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 5
LOCUS AX524843 31 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 4 from Patent EP1236805.
ACCESSION AX524843
VERSION AX524843.1 GI:25169937
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 4 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 31
RESULT 6
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DEFINITION Sequence 13 from patent US 5491063.
ACCESSION I17523
VERSION I17523.1 GI:1597878
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Fisher,M.E. and Watson,R.M.
TITLE Methods for in-solution quenching of fluorescently labeled
oligonucleotide probes
JOURNAL Patent: US 5491063-A 13 13-FEB-1996;
FEATURES Location/Qualifiers
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Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1
RESULT 7
LOCUS I28348 33 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5571673.
ACCESSION I28348
VERSION I28348.1 GI:1819124
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Picone,T.K.H.
TITLE Methods for in-solution quenching of fluorescently labeled
oligonucleotide probes
JOURNAL Patent: US 5571673-A 1 05-NOV-1996;
FEATURES Location/Qualifiers
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Best Local Similarity 96.8%; Pred. No. 6.2e+02;
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Db 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1
RESULT 8
LOCUS AX777198 48 bp DNA linear PAT 14-JUL-2003
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Sequence 52 from Patent WO03040301.
DEFINITION
ACCESSION AX777198
VERSION AX777198.1 GI:32694346
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Deak,P., Frenz,L., Glover,D. and Midgley,C.
TITLE Cell cycle progression proteins
JOURNAL Patent: WO 03040301-A 52 15-MAY-2003;
Cyclacel Limited (GB)
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/notes="Primer"
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Best Local Similarity 83.3%; Pred.No. 2.9e+03;
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DB 41 GGCCTTGGTCCTTGGTCATCTCCC 18
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RESULT 9
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LOCUS AR379394 46 bp DNA linear PAT 18-DEC-2003
DEFINITION
Sequence 52 from patent US 6607878.
ACCESSION AR379394
VERSION AR379394.1 GI:40087028
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1
AUTHORS Unclassified.
TITLE (bases 1 to 46)
JOURNAL Sorge,J.A.
FEATURES
Collections of uniquely tagged molecules
Patent: US 6607878-A 52 19-AUG-2003;
Location/Qualifiers
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RESULT 10
AX804053/c
LOCUS AX804053 39 bp DNA linear PAT 25-NOV-2003
DEFINITION
Sequence 221 from Patent WO03060160.
ACCESSION AX804053
VERSION AX804053.1 GI:38521188
KEYWORDS
SOURCE
ORGANISM Oreochromis niloticus (Nile tilapia)
Oreochromis niloticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Perciformes;
Labroidae; Cichlidae; Oreochromis.
REFERENCE
1
AUTHORS Lie,Y., Slettan,A., Høevum,M. and Lingaas,P.

```

TITLE	Verification of food origin based on nucleic acid pattern									
JOURNAL	GenomAR ASA (NO)									
FEATURES	<p>source 1..39 Location/Qualifiers</p> <p>/organism="Oreochromis niloticus"</p> <p>/mol_type="unassigned DNA"</p> <p>/db_xref="taxon:8128"</p>									
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Query Match	54.0%;	Score 16.2;	DB 6;	Length 39;						
Best Local Similarity	72.4%;	Pred. No. 1.4e+04;								
Matches	21;	Conservative	0;	Mismatches	8;	Indels	0;	Gaps	0;	
Qy	1	TGGA	CTCAGTCCTTGGTCATCTCACCTTC	29						
Db	32	TGCAT	TCTGCTTGGTCATAGCTGTTTC	4						
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LOCUS	AX800237	Sequence 56 from Patent EP1327691.	26 bp	DNA	linear	PAT 13-OCT-2003				
DEFINITION										
ACCESSION	AX800237									
VERSION	AX800237.1	GI:37653480								
KEYWORDS	synthetic construct									
SOURCE	synthetic construct									
ORGANISM	artificial sequences.									
REFERENCE	1									
AUTHORS	Bai, Y. L. and Terng, H. J.									
TITLE	Detection of respiratory viruses									
JOURNAL	Patent: EP 1327691-A 56 16-JUL-2003;									
FEATURES	Dr. Chip Biotechnology Incorporation (TW)									
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Matches	17;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;	
Qy	2	GGACTCAGTCCTTGGTCATCT	22							
Db	22	GGAACCA	GTCCTTGGTCATGT	2						
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LOCUS	HSRETINT32	Human RET proto-oncogene, intron 16, 3' end.	49 bp	DNA	linear	PRI 01-APR-2002				
DEFINITION										
ACCESSION	U11510									
VERSION	U11510.1	GI:558792								
KEYWORDS	32 of 38									
SEGMENT	Homo sapiens (human)									
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
REFERENCE	1 (bases 1 to 49)									
AUTHORS	Ceccherini, I., Boccardi, R., Luo, Y., Pasini, B., Hofstra, R., Takahashi, M. and Romeo, G.									
TITLE	Exon structure and flanking intronic sequences of the human RET proto-oncogene									
JOURNAL	Biochem. Biophys. Res. Commun. 196 (3), 1288-1295 (1993)									
MEDLINE	94071887									
PUBMED	7902707									
REFERENCE	2 (bases 1 to 49)									

AUTHORS Ceccherini, I., Hofstra, R., Yin, L., Stulp, R., Barone, V., Stelwagen, T., Boccardi, R., Nijveen, H., Bolino, A., Seri, M., Ronchetto, P., Pasini, B., Bozzano, M., Buys, C. and Romeo, G.
TITLE DNA polymorphisms and conditions for SSCP analysis of the 20 exons of the ret proto-oncogene
JOURNAL Oncogene 9 (10), 3025-3029 (1994)
MEDLINE 94366753
PUBMED 8084609
REFERENCE 3 (bases 1 to 49)
AUTHORS Ceccherini, I.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-1994) Isabella Ceccherini, Laboratorio di Genetica Molecolare, Istituto Giannina Gaslini, Largo G. Gaslini, 5, Genova, 16148, Italy
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 Best Local Similarity 70.0%; Pred. No. 2.7e+04;
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 QY 1 TGGACTCAGTCTTGTCATCTCACCTTCT 30
 Db 16 TGGAGCCACTACTGGTCTTTCACTCTCT 45
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 AX420204/c
 LOCUS AX420204 22 bp DNA linear PAT 18-JUN-2002
 DEFINITION Sequence 93 from Patent WO0208289.
 ACCESSION AX420204
 VERSION AX420204.1 GI:21524455
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Padigar, M., Mezes, P., Mishra, V., Burgess, C., Casman, S. and Smithson, G.
 TITLE G-protein coupled receptors and nucleic acids encoding same
 JOURNAL Patent: WO 0208289-A 93 31-JAN-2002;
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 /db_xref="taxon:32630"
 /note="Ag1279/Ag2590 PCR Primer Sequence"
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 QY 10 TCCTTGGTCATCTCACCTTC 29
 Db 21 TCCTTTCATCTCTCTCTC 2
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 AX528208/c
 LOCUS AX528208 22 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 76 from Patent WO0226985.
 ACCESSION AX528208
 VERSION AX528208.1 GI:25172515

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Spytek, K.A., Casman, S., Padigar, M., Dickson, K., Vernet, C., Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., Edinger, S., Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M., Taylor, S., Gunther, E. and Tchernev, V.T.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226985-A 76 04-APR-2002;
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 QY 10 TCCTTGGTCATCTCACCTTC 29
 Db 21 TCCTTTCATCTCTCTCTC 2
 RESULT 15
 AX528214/c
 LOCUS AX528214 22 bp DNA linear PAT 21-NOV-2002
 DEFINITION Sequence 82 from Patent WO0226985.
 ACCESSION AX528214
 VERSION AX528214.1 GI:25172521
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1
 AUTHORS Spytek, K.A., Casman, S., Padigar, M., Dickson, K., Vernet, C., Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., Edinger, S., Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M., Taylor, S., Gunther, E. and Tchernev, V.T.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226985-A 82 04-APR-2002;
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 /db_xref="taxon:32630"
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 Db 21 TCCTTTCATCTCTCTCTC 2
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 AX554648/c
 LOCUS AX554648 22 bp DNA linear PAT 27-NOV-2002
 DEFINITION Sequence 202 from Patent WO0246229.
 ACCESSION AX554648
 VERSION AX554648.1 GI:25898315
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

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artificial sequences.
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REFERENCE
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
          Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
          Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 202 13-JUN-2002;
          Curagen Corporation (US)
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Db 21 TCCTTTCATCTCTCCTTC 2
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AR230098/c
LOCUS AR230098 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6451557.
ACCESSION AR230098
VERSION AR230098.1 GI:27270082
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Method for producing, in yeast, a hydroxylated triple helical
protein, and yeast host cells useful in said method
JOURNAL Patent: US 6451557-A 7 17-SEP-2002;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTGACCTCCCTTC 1
RESULT 18
AX022200/c
LOCUS AX022200 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from Patent EP0950098.
ACCESSION AX022200
VERSION AX022200.1 GI:10045866
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: EP 0950098-A 7 20-OCT-1999;
          COMMW SCIENT IND RES ORG (AU)
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artificial sequences.
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REFERENCE
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
          Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
          Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 202 13-JUN-2002;
          Curagen Corporation (US)
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KEYWORDS
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ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Method for producing, in yeast, a hydroxylated triple helical
protein, and yeast host cells useful in said method
JOURNAL Patent: US 6451557-A 7 17-SEP-2002;
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QY 10 TCCTTGGTCATCTCACCTTC 29
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LOCUS AX022200 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from Patent EP0950098.
ACCESSION AX022200
VERSION AX022200.1 GI:10045866
KEYWORDS
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ORGANISM unidentified
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AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: EP 0950098-A 7 20-OCT-1999;
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AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
          Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
          Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 202 13-JUN-2002;
          Curagen Corporation (US)
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ACCESSION AR230098
VERSION AR230098.1 GI:27270082
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ORGANISM Unknown.
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1 (bases 1 to 24)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Method for producing, in yeast, a hydroxylated triple helical
protein, and yeast host cells useful in said method
JOURNAL Patent: US 6451557-A 7 17-SEP-2002;
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QY 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTGACCTCCCTTC 1
RESULT 18
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LOCUS AX022200 24 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 7 from Patent EP0950098.
ACCESSION AX022200
VERSION AX022200.1 GI:10045866
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
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AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: EP 0950098-A 7 20-OCT-1999;
          COMMW SCIENT IND RES ORG (AU)
FEATURES
source Location/Qualifiers
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REFERENCE
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
          Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
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TITLE Novel proteins and nucleic acids encoding same
JOURNAL Patent: WO 0246229-A 202 13-JUN-2002;
          Curagen Corporation (US)
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QY 10 TCCTTGGTCATCTCACCTTC 29
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RESULT 17
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LOCUS AR230098 24 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent WO9818918.
ACCESSION AX030726
VERSION AX030726.1 GI:10278240
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: WO 9818918-A 7 07-MAY-1998;
          RAMSHAW JOHN ALAN MAURICE (AU) ; GALANIS MARIA (AU) ; COMMW SCIENT
          IND RES ORG (AU) ; VAUGHAN PAUL RICHARD (AU) ; WERKMEISTER JEROME
          ANTHONY (AU)
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Best Local Similarity 85.0%; Pred. No. 4.2e+04;
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QY 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTGACCTCCCTTC 1
RESULT 20
BD008647/c
LOCUS BD008647 24 bp DNA linear PAT 31-JAN-2002
DEFINITION Stable expression of the triple helical protein.
ACCESSION BD008647
VERSION BD008647.1 GI:18637020
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 24)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Stable expression of the triple helical protein
JOURNAL Patent: JP 2001502548-A 7 27-FEB-2001;
          COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
          OS
COMMENT OS Unidentified
          PN JP 2001502548-A/7
          PD 27-FEB-2001
          PF 29-OCT-1997 JP 1998519817
          PR
          PI PAUL RICHARD VAUGHAN, MARIA GALANIS, JOHN ALAN MAURICE RAMSHAW,
          PI JEROME ANTHONY WERKMEISTER
          PC C12N15/12,C12N15/81,C12N15/53,C07K14/78,A61K38/39 CC
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  Best Local Similarity 85.0%; Pred. No. 4.2e+04;
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Qy 10 TCCTTGGTCATCTCACCTTC 29
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RESULT 21
LOCUS E14084 39 bp DNA linear PAT 28-JUL-1999
DEFINITION Primer.
ACCESSION E14084
VERSION E14084.1 GI:5708767
KEYWORDS JP 1997268200-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 39)
AUTHORS Muramatsu, S. and Zushi, M.
TITLE RAT THROMBOMODULIN
JOURNAL Patent: JP 1997268200-A 13 14-OCT-1997;
        ASAHII CHEM IND CO LTD
COMMENT OS None
        OC Artificial sequences.
        PN JP 1997268200-A/13
        PD 14-OCT-1997
        PF 01-APR-1996 JP 1996078494
        PI MURAMATSU SHUJI, ZUSHI MICHITAKA
        PC
C07K14/745,A01K67/027,C07H21/04,C12N15/09,C12P21/02//A61K38/00, PC
(C12P21/02,
PC C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key
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FT /organism='Artificial sequences'.
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  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 7 CAGTCCTTGGTCATCTCACC 26
Db 14 CAGTCCTTGGCTAATCTGACC 33

RESULT 22
LOCUS AR284878 47 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 930 from patent US 6528260.
ACCESSION AR284878
VERSION AR284878.1 GI:29721782
KEYWORDS
SOURCE Unknown.

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Qy 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTGACCTCCCTTC 1

RESULT 23
LOCUS AX249405/c 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1484 from Patent WO0166800.
ACCESSION AX249405
VERSION AX249405.1 GI:15864028
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cargill, M., Ireland, J. S. and Lander, E. S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1484 13-SEP-2001;
        WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
FEATURES
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  Best Local Similarity 72.0%; Pred. No. 5.2e+04;
  Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TGGACTCAGTCCTTGGTCATCTCAC 25
Db 31 TGGACTAAGCCTTTGKCCATCGCCC 7

RESULT 24
LOCUS AX800208 20 bp DNA linear PAT 13-OCT-2003
DEFINITION Sequence 27 from Patent EP1327691.
ACCESSION AX800208
VERSION AX800208.1 GI:37653451
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bai, Y. L. and Terng, H. J.
TITLE Detection of respiratory viruses
JOURNAL Patent: EP 1327691-A 27 16-JUL-2003;
        Dr. Chip Biotechnology Incorporation (TW)
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Query Match	49.3%; Score 14.8; DB 6; Length 20;									
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Matches	16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;									
QY	3	GACTCAGTCCTTGTCATCT 22								
Db	1	GAACCACTCTTGTCATCT 20								
RESULT 25										
LOCUS	CQ801293 30 bp DNA linear PAT 05-MAY-2004									
DEFINITION	Sequence 154 from Patent WO2004033689.									
ACCESSION	CQ801293									
VERSION	CQ801293.1 GI:47058049									
KEYWORDS	synthetic construct									
SOURCE	synthetic construct									
ORGANISM	artificial sequences.									
REFERENCE	1									
AUTHORS	Blondelet-Rouault,M.H., Dominguez,H., Darbon-Rongere,E., Gerbaud,C., Gondran,A., Karray,F., Lacroix,P., Oestreicher-mermet-Bouvier,N., Pernodet,J.L. and Tuphile K.									
TITLE	Polypeptides involved in spiramycin biosynthesis, nucleotide sequences encoding said polypeptides and uses thereof									
JOURNAL	Patent: WO 2004033689-A 154 22-APR-2004; Aventis Pharma S.A. (FR); CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)									
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RESULT 26										
LOCUS	AX514149 41 bp DNA linear PAT 05-OCT-2002									
DEFINITION	Sequence 347 from Patent WO02052044.									
ACCESSION	AX514149									
VERSION	AX514149.1 GI:23560508									
KEYWORDS	Homo sapiens (human)									
SOURCE	Homo sapiens									
ORGANISM	Homo sapiens									
REFERENCE	1									
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
TITLE	Nakamura,Y., Sekine,A., Iida,A. and Saito,S.									
JOURNAL	Detection of genetic polymorphisms									
	Patent: WO 02052044-A 347 04-JUL-2002;									
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QY	5	CTCAGTCCTTGTCATCTCA 24								
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LOCUS	AX520300 41 bp DNA linear PAT 05-OCT-2002									
DEFINITION	Sequence 6498 from Patent WO02052044.									
ACCESSION	AX520300									
VERSION	AX520300.1 GI:23570842									
KEYWORDS	Homo sapiens (human)									
SOURCE	Homo sapiens									
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REFERENCE	1									
AUTHORS	Nakamura,Y., Sekine,A., Iida,A. and Saito,S.									
TITLE	Detection of genetic polymorphisms									
JOURNAL	Patent: WO 02052044-A 6498 04-JUL-2002;									
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LOCUS	AR379395 46 bp DNA linear PAT 18-DEC-2003									
DEFINITION	Sequence 53 from patent US 6607878.									
ACCESSION	AR379395									
VERSION	AR379395.1 GI:40087029									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 46)									
AUTHORS	Sorge,J.A.									
TITLE	Collections of uniquely tagged molecules									
JOURNAL	Patent: US 6607878-A 53 19-AUG-2003;									
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LOCUS	AR379396 46 bp DNA linear PAT 18-DEC-2003									
DEFINITION	Sequence 54 from patent US 6607878.									
ACCESSION	AR379396									

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VERSION AR379396.1 GI:40087030
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Sorge,J.A.
TITLE Collections of uniquely tagged molecules
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Db 41 GACTCAGACCTTGTGCACTGACGTT 16
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LOCUS AR379397/c 46 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6607878.
ACCESSION AR379397
VERSION AR379397.1 GI:40087031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 46)
AUTHORS Sorge,J.A.
TITLE Collections of uniquely tagged molecules
JOURNAL Patent: US 6607878-A 55 19-AUG-2003;
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Db 41 GACTCAGACCTTGTGCACTGACGTT 16
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RESULT 31
LOCUS AR290158 47 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1893 from patent US 6537751.
ACCESSION AR290158
VERSION AR290158.1 GI:31677442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 47)
AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE Biallelic markers for use in constructing a high density
    disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 1893 25-MAR-2003;
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RESULT 32
LOCUS BD262074 36 bp DNA linear PAT 17-JUL-2003
DEFINITION Antineoplastic viral agent containing toxin gene under regulation
    by oncotyete-inducible transcriptional factor.
ACCESSION BD262074
VERSION BD262074.1 GI:33071842
KEYWORDS JP 2002539796-A/17.
SOURCE synthetic construct
    artificial sequences.
    1 (bases 1 to 36)
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.
TITLE Antineoplastic viral agent containing toxin gene under regulation
    by oncotyete-inducible transcriptional factor
JOURNAL Patent: JP 2002539796-A 17 26-NOV-2002;
COMMENT BTG INTERNATIONAL LTD
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    PN JP 2002539796-A/17
    PD 26-NOV-2002
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    PR 24-MAR-1999 GB 9906815.7
    PI RICHARD IGGO,MICHELE BRUNORI
    PC C12N15/09,A61K35/76,A61K48/00,A61P35/04,C12N7/00,C12N15/00 CC
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DEFINITION Sequence 20 from patent US 6544507.
ACCESSION AR303048
VERSION AR303048.1 GI:31691672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.A.
TITLE Anti-neoplastic viral agents
    Patent: US 6544507-A 20 08-APR-2003;
JOURNAL Location/Qualifiers
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ACCESSION AR303048
VERSION AR303048.1 GI:31691672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Iggo,R. and Brunori,M.A.
TITLE Anti-neoplastic viral agents
    Patent: US 6544507-A 20 08-APR-2003;
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 DEFINITION Sequence 20 from Patent WO0056909.
 ACCESSION AX036808
 VERSION AX036808.1 GI:11226287
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Brunori, M. and Iigo, R.
 TITLE Anti-neoplastic viral agents comprising toxin gene under control of
 tumour cell-derived transcription factors
 JOURNAL Patent: WO 0056909-A 20 28-SEP-2000;
 BRUNORI MICHELE (CH); IGO RICHARD (CH); BTG INT LTD (GB)
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 ACCESSION AR443130
 VERSION AR443130.1 GI:42670876
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 42)
 AUTHORS Frenken, L.G., Howell, S., Ledebor, A.M. and van der Logt, C.P.
 TITLE Multivalent antigen-binding proteins
 JOURNAL Patent: US 6670453-A 28 30-DEC-2003;
 FEATURES Location/Qualifiers
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 ACCESSION AR207700
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 49)
 AUTHORS Weidenhammer, E.M., Wang, L., Xu, X., Heller, M.J. and Kahl, B.F.
 TITLE Methods for gene expression monitoring on electronic microarrays
 JOURNAL Patent: US 6379897-A 40 30-APR-2002;
 FEATURES Location/Qualifiers
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 ACCESSION AR265026
 VERSION AR265026.1 GI:29693413
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 49)
 AUTHORS Weidenhammer, E.M., Wang, L., Xu, X., Heller, M.J. and Kahl, B.F.
 TITLE Quantitative analysis methods on active electronic microarrays
 JOURNAL Patent: US 6492122-A 40 10-DEC-2002;
 FEATURES Location/Qualifiers
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 ACCESSION CQ008348
 VERSION CQ008348.1 GI:41015046
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Shimkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 methods of use thereof
 JOURNAL Patent: WO 0147944-A 6988 05-JUL-2001;

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  JP 1997056380-A/17.
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  REFERENCE
  1 (bases 1 to 24)
    Tanida,E., Oue,C., Yagi,S., Hasegawa,A., Kiyozawa,K. and Yano,A.
    ASIALOGLYCOPROTEIN RECEPTOR DERIVATIVE AND ITS USE
    Patent: JP 1997056380-A 17 04-MAR-1997;
    TONEN CORP, INTERNATL REAGENTS CORP, KIZOZAWA KENDOU
  COMMENT
  OS None
  OC Artificial sequences.
  PN JP 1997056380-A/17
  PD 04-MAR-1997
  PF 21-AUG-1995 JP 1995212118
  PI TANIDA EMIKO, OUE CHIHARU, YAGI SHINTARO, HASEGAWA AKIRA, PI
  KIZOZAWA KENDOU,
  YANO AKIHIKO
  PC C12N15/09,C07H21/04,C07K14/705,C12N1/21,C12N5/10,C12P21/02, PC
  G01N33/53
  PC G01N33/566,G01N33/576,(C12N1/21,C12R1:19),(C12N5/10,C12R1:91),
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SUMMARIES

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5	19	63.3	33	2	AAT32453 Probe, SK
6	17.6	58.7	48	10	ADK11540 RNai prim
7	16.8	56.0	38	10	ADG78921 Schizophr
8	16.6	55.3	25	9	ACI99856 Human mic
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10	16.4	54.7	46	2	AAV55829 PCR mutag
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12	16.2	54.0	39	10	ADD19586 Oreochrom
13	16	53.3	25	9	ACK01932 Human mic
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16	15.6	52.0	50	6	ABZ04927 Human leu
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18	15.4	51.3	25	9	ACK12515 Human mic
19	15.4	51.3	31	4	AAI30996 Human sin
20	15.2	50.7	22	6	AAD29041 Human G-p
21	15.2	50.7	22	6	AAD29038 Human G-p

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C 96	14	46.7	23	10	ADP88702	Adf88702 Reverse p	169	13.6	45.3	39	3	AA33303	Low adeno
C 97	14	46.7	24	2	AAV04689	Aav04689 Connexin	170	13.6	45.3	39	3	AA33303	Human ade
C 98	14	46.7	24	12	ADJ14729	Adj14729 Debrisoqu	171	13.6	45.3	39	3	AA19425	Human ade
C 99	14	46.7	24	12	ADJ14498	Adj14498 Debrisoqu	172	13.6	45.3	39	10	AB295119	Human ade
100	14	46.7	24	12	ADJ060832	Adj060832 Human deb	173	13.6	45.3	39	11	ABD18990	Human ade
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103	14	46.7	25	9	ACK27601	Ack27601 Human mic	176	13.6	45.3	41	6	ABO84170	Human sul
C 104	14	46.7	25	9	ACK180489	Ack180489 Human mic	177	13.6	45.3	41	6	ABO84170	Huntingto
C 105	14	46.7	25	9	ACK113245	Ack113245 Human mic	178	13.6	45.3	43	12	ADJ45023	Plant cdn
C 106	14	46.7	28	6	ABK66582	Abk66582 Human gen	179	13.6	45.3	47	3	AA268174	Human map
C 107	14	46.7	24	6	AA334581	Aa334581 Forward p	180	13.6	45.3	47	3	AA267268	Human map
C 108	14	46.7	44	3	AAZ01299	Aaz01299 PCR prime	181	13.4	44.7	17	6	ABV80643	Human HTP
C 109	14	46.7	47	3	AAZ68639	Aaz68639 Human map	182	13.4	44.7	17	6	ABV80642	Human HTP
C 110	14	46.7	50	6	ABZ00894	Abz00894 Human leu	183	13.4	44.7	17	6	ABV80644	Human HTP
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C 112	13.8	46.0	23	12	ADP72582	Adp72582 Human APM	185	13.4	44.7	23	10	ADB61411	Human HDA
C 113	13.8	46.0	23	12	ADG14741	Adg14741 OBG3 3'UT	186	13.4	44.7	24	6	ABI88834	Human HDA
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C 115	13.8	46.0	25	9	ACK196204	Ack196204 Human mic	188	13.4	44.7	25	6	ABV82648	Human HTP
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C 118	13.8	46.0	28	3	AAA97799	Aaa97799 T. haloph	191	13.4	44.7	25	6	ABV82645	Human HTP
C 119	13.8	46.0	28	3	AAA97800	Aaa97800 T. haloph	192	13.4	44.7	25	6	ABV82645	Human HTP
C 120	13.8	46.0	29	12	ADI28588	Adi28588 Interleuk	193	13.4	44.7	25	6	ABV82639	Human HTP
C 121	13.8	46.0	36	2	AAQ11736	Aaq11736 Sequence	194	13.4	44.7	25	6	ABV82642	Human HTP
C 122	13.8	46.0	36	5	AA081911	Aa081911 S. cerevi	195	13.4	44.7	25	6	ABV82644	Human HTP
C 123	13.8	46.0	37	12	ADJ67929	Adj67929 A. aeolic	196	13.4	44.7	25	6	ABV82649	Human HTP
C 124	13.8	46.0	37	12	ADJ68141	Adj68141 A. aeolic	197	13.4	44.7	25	6	ABV82643	Human HTP
C 125	13.8	46.0	37	12	ADK01219	Adk01219 DNA polym	198	13.4	44.7	25	6	ABV82643	Human HTP
C 126	13.8	46.0	37	12	ADJ79438	Adj79438 A. aeolic	199	13.4	44.7	25	9	ACI94384	Human HTP
C 127	13.8	46.0	37	12	ADJ84878	Adj84878 Bacterial	200	13.4	44.7	25	9	ACH54631	Human mic
C 128	13.8	46.0	37	12	ADM77566	Adm77566 DNA polym	201	13.4	44.7	25	9	ACH55566	DNA targe
C 129	13.8	46.0	37	12	ADM66333	Adm66333 A. aeolic	202	13.4	44.7	27	10	ADD01570	DNA targe
C 130	13.8	46.0	37	12	ADP04386	Adp04386 A. aeolic	203	13.4	44.7	28	2	AAV57967	Human mve
C 131	13.8	46.0	37	12	ADP82463	Adp82463 Aquifex a	204	13.4	44.7	30	2	AAV57967	Human mve
C 132	13.8	46.0	41	6	ABZ47662	Abz47662 Human ATP	205	13.4	44.7	30	12	AD012455	Single mu
C 133	13.8	46.0	41	6	ABZ45067	Abz45067 Human ATP	206	13.4	44.7	30	12	AD012500	Single mu
C 134	13.8	46.0	47	3	AAH88371	Aah88371 CNS disor	207	13.4	44.7	30	12	AD079909	CENPC1 PC
C 135	13.8	46.0	47	3	AAH88371	Aah88371 CNS disor	208	13.4	44.7	31	4	AAI131261	Human sin
C 136	13.8	46.0	50	5	ABU00122	Abu00122 Human sil	209	13.4	44.7	32	6	ABL53952	Leukaemia
C 137	13.8	46.0	50	6	ABZ04509	Abz04509 Human leu	210	13.4	44.7	32	10	ADD73391	Human MLL
C 138	13.6	45.3	20	8	ABZ58618	Abz58618 Cytochrom	211	13.4	44.7	32	10	ADD01586	Human Fc
C 139	13.6	45.3	20	8	ACC43102	Acc43102 OProbe us	212	13.4	44.7	33	10	AD01586	Human Fc
C 140	13.6	45.3	20	10	ADH94016	Adh94016 Human glu	213	13.4	44.7	36	4	ADJ12894	Rhesus ro
C 141	13.6	45.3	20	12	ADH67343	Adh67343 Human glu	214	13.4	44.7	36	4	ADJ12894	Bcl-2-IGH
C 142	13.6	45.3	20	12	ADJ24395	Adj24395 Human end	215	13.4	44.7	36	4	ADJ12893	Anti-sens
C 143	13.6	45.3	22	5	AAH27178	Aah27178 PCR prime	216	13.4	44.7	37	3	AA006622	5' PCR pr
C 144	13.6	45.3	22	6	AAZ36078	Aaz36078 Human cML	217	13.4	44.7	39	2	AAV10819	Human MSH
C 145	13.6	45.3	23	6	ABK65145	Abk65145 PCR prime	218	13.4	44.7	39	12	ADL64388	Human sin
C 146	13.6	45.3	24	6	ABQ08721	Abq08721 Oligonuc	219	13.4	44.7	40	2	AA770652	Fibrin cl
C 147	13.6	45.3	24	6	ABQ08721	Abq08721 Oligonuc	220	13.4	44.7	40	12	ADI28600	Woodchuck
C 148	13.6	45.3	24	6	ABQ08680	Abq08680 Oligonuc	221	13.4	44.7	41	6	ABZ49250	Human aid
C 149	13.6	45.3	25	9	ACI13008	Act13008 Human mic	222	13.4	44.7	42	2	AA739249	PCR suppr
C 150	13.6	45.3	25	9	ACI93221	Act93221 Human mic	223	13.4	44.7	42	2	AAV26802	PCR suppr
C 151	13.6	45.3	25	9	ACI73514	Act73514 Human mic	224	13.4	44.7	44	5	AAAF16775	EPSPS com
C 152	13.6	45.3	25	9	ACT142197	Act142197 Human mic	225	13.4	44.7	44	5	AAAF16763	S. typhimu
C 153	13.6	45.3	25	9	ACT00251	Act00251 Human mic	226	13.4	44.7	45	3	AAZ95271	Linker fo
C 154	13.6	45.3	26	6	ABSS9067	Abss9067 Human G-p	227	13.4	44.7	50	2	AAAT23193	Human gen
C 155	13.6	45.3	26	12	ADG47269	Adg47269 LTR U5 se	228	13.4	44.7	50	6	ABZ00529	Human leu
C 156	13.6	45.3	28	4	AAH91201	Aah91201 Human inf	229	13.2	44.0	19	10	ADF75536	Sense siN
C 157	13.6	45.3	28	10	ADJ33233	Adj33233 Probe rT1	230	13.2	44.0	19	10	ADF75536	Antisense
C 158	13.6	45.3	29	2	AAQ67090	Aaq67090 Human TNF	231	13.2	44.0	20	8	ACC46996	Human pho
C 159	13.6	45.3	29	2	AAQ67211	Aaq67211 Mutant TN	232	13.2	44.0	20	10	ABZ98527	Human ICA
C 160	13.6	45.3	29	6	ABV99429	Abv99429 Human NOV	233	13.2	44.0	20	11	ABD31558	Human ICA
C 161	13.6	45.3	29	6	ADJ17702	Adj17702 Labelled	234	13.2	44.0	20	12	ADJ60377	Oligonuc1
C 162	13.6	45.3	29	12	ADN42790	Adn42790 Human NOV	235	13.2	44.0	20	12	ADJ54516	Human B7-
C 163	13.6	45.3	30	2	AAQ38558	Aaq38558 T cell re	236	13.2	44.0	20	12	ADJ23933	Human end
C 164	13.6	45.3	30	2	AAQ02263	Aaq02263 T cell re	237	13.2	44.0	20	12	ADJ23933	Human end
C 165	13.6	45.3	31	2	AAQ62562	Aaq62562 Granule b	238	13.2	44.0	20	12	ADO45866	Human Oli
C 166	13.6	45.3	31	3	AAZ96707	Aaz96707 T cell an	239	13.2	44.0	21	6	ABL44254	Human chr
C 167	13.6	45.3	35	1	AAAN94233	Aaan94233 Sequence	240	13.2	44.0	21	6	ABL44254	Human chr

C 241	13.2	44.0	22	4	AA514515	Aa514515 Human GST	314	13	43.3	29	12	AD128586	Adi28586 Interleuk
C 242	13.2	44.0	22	6	ABA00040	AbA00040 TREN-1 se	315	13	43.3	30	2	AAV19100	Aav19100 Bacillus
C 243	13.2	44.0	23	6	ABS78800	ABs78800 Human NOV	C 316-	13	43.3	30	2	AAV54150	Aav54150 Primer fo
C 244	13.2	44.0	25	9	ACI29158	ACi29158 Human mic	317	13	43.3	30	2	AAV18004	Aav18004 Primer us
C 245	13.2	44.0	25	9	ACI00355	ACi00355 Human mic	C 318	13	43.3	30	12	ADO56313	Ado56313 Human cyc
C 246	13.2	44.0	25	9	ACK10841	ACk10841 Human mic	319	13	43.3	31	8	ACD43835	ACd43835 Human gen
C 247	13.2	44.0	25	9	ACI29159	ACi29159 Human mic	320	13	43.3	32	2	AAI18048	Aai18048 Sense pri
C 248	13.2	44.0	25	9	ADA01830	ADa01830 Mouse car	321	13	43.3	32	3	AAA51225	Aaa51225 3' primer
C 249	13.2	44.0	25	10	ADP171569	ADp171569 Mouse car	C 322	13	43.3	32	6	ABK11956	ABk11956 E. coli v
C 250	13.2	44.0	25	12	ADP14216	ADp14216 Renal cel	C 323	13	43.3	32	10	ADF68136	Adf68136 Stabilise
C 251	13.2	44.0	26	2	AAV36894	AAv36894 Nucleotid	324	13	43.3	33	12	ADN97476	Adn97476 Artificia
C 252	13.2	44.0	26	4	AAI66798	AAi66798 Barley HV	325	13	43.3	34	10	ABZ58800	Abz58800 Cinnamyci
C 253	13.2	44.0	27	3	AA887770	AAa88770 Respirato	326	13	43.3	35	2	AAQ87358	Aaq87358 Human fam
C 254	13.2	44.0	29	2	AA556371	AAv556371 Streptoco	327	13	43.3	35	2	AAQ92510	Aaq92510 Human imm
C 255	13.2	44.0	30	2	AAV55607	AAv55607 Primer fo	328	13	43.3	35	2	AAV37304	AAv37304 PCR prime
C 256	13.2	44.0	30	3	AA88769	AAa88769 Respirato	329	13	43.3	35	3	AAAL3316	Aaal3316 PCR prime
C 257	13.2	44.0	30	12	ADO79574	Ado79574 KIAA0783	330	13	43.3	35	6	ABA94788	ABa94788 HCV-AB 68
C 258	13.2	44.0	31	4	AAI30117	AAi30117 Human ein	331	13	43.3	36	6	ABK12310	ABk12310 Marinococ
C 259	13.2	44.0	34	2	AAV83986	AAv83986 PCR prime	C 332	13	43.3	36	8	ABSS58071	ABs58071 Rhodobact
C 260	13.2	44.0	34	3	AAAI4935	AAa14935 PCR prime	333	13	43.3	36	8	ABSS58072	ABs58072 Pea rbcS-
C 261	13.2	44.0	34	5	AAF85602	AAf85602 Acremoniu	C 334	13	43.3	37	2	AAV99401	AAv99401 Oligonuc1
C 262	13.2	44.0	36	2	AAV27501	AAv27501 Streptoco	C 335	13	43.3	38	10	ADD19574	Adi19574 Oreochrom
C 263	13.2	44.0	36	6	ABQ84969	ABq84969 Streptoco	C 336	13	43.3	38	12	ADO26066	Ado26066 Arabidrops
C 264	13.2	44.0	36	10	ADC45372	Adc45372 S. pneumo	C 337	13	43.3	39	12	ADN12341	Adn12341 hagt clon
C 265	13.2	44.0	37	12	ADI38942	Adi38942 Phosphorr	338	13	43.3	40	6	AAH48523	Aah48523 Nucleic a
C 266	13.2	44.0	41	6	ABZ45239	ABz45239 Human car	C 339	13	43.3	41	2	AAQ56317	Aaq56317 Probe for
C 267	13.2	44.0	41	6	ABZ47355	ABz47355 Human ATP	340	13	43.3	41	4	AAH74191	Aah74191 s1 RNA bi
C 268	13.2	44.0	41	6	ABZ44561	ABz44561 Human ATP	341	13	43.3	41	4	AAH74190	Aah74190 s1 RNA bi
C 269	13.2	44.0	41	6	ABZ50498	ABz50498 Human car	C 342	13	43.3	41	6	ABSS60060	ABs60060 Human DNA
C 270	13.2	44.0	42	3	AAAI2095	AAa12095 Human ICA	C 343	13	43.3	41	6	ABZ50314	ABz50314 Human cyt
C 271	13.2	44.0	44	10	ADF72048	Adf72048 Human ABC	344	13	43.3	42	2	AAV09726	AAv09726 Adenoviru
C 272	13.2	44.0	46	2	AA55828	AAx55828 PCR mutag	C 345	13	43.3	43	4	ACC57826	Acc57826 Primer B-
C 273	13.2	44.0	46	2	AA55834	AAx55834 PCR mutag	346	13	43.3	46	3	AAA75226	Aaa75226 Nucleotid
C 274	13.2	44.0	46	2	AA55833	AAx55833 PCR mutag	C 347	13	43.3	46	12	ADJ14733	Adj14733 Debrisoqu
C 275	13.2	44.0	46	2	AA55826	AAx55826 PCR mutag	C 348	13	43.3	46	12	ADJ14502	Adj14502 Debrisoqu
C 276	13.2	44.0	46	2	AA55827	AAx55827 PCR mutag	C 349	13	43.3	46	12	ADO60836	Ado60836 Human deb
C 277	13.2	44.0	47	2	AA552574	AAx552574 Human gen	C 350	13	43.3	46	12	ADO60991	Ado60991 Human deb
C 278	13.2	44.0	47	3	AAZ67989	AAz67989 Human map	C 351	13	43.3	47	3	AAZ67200	AAz67200 Human map
C 279	13.2	44.0	47	3	AAZ67175	AAz67175 Human map	352	13	43.3	47	3	AAZ67200	AAz67200 Human map
C 280	13.2	44.0	48	2	AAV13614	AAv13614 Hepatitis	353	13	43.3	47	3	AAZ68460	AAz68460 Human map
C 281	13.2	44.0	50	4	AAI33779	AAi33779 Human SNP	C 354	13	43.3	47	12	ADJ14732	Adj14732 Debrisoqu
C 282	13.2	44.0	50	6	ABK01525	ABz01525 Human leu	C 355	13	43.3	47	12	ADJ14501	Adj14501 Debrisoqu
C 283	13	43.3	50	6	ABK18566	ABk18566 Human ERG	C 356	13	43.3	47	12	ADO60835	Ado60835 Human deb
C 284	13	43.3	20	2	AAQ76305	AAq76305 Neomycin-	C 357	13	43.3	47	12	ADO60603	Ado60603 Human deb
C 285	13	43.3	20	2	AAV67146	AAv67146 PCR prime	C 358	13	43.3	47	12	ADO60990	Ado60990 Human deb
C 286	13	43.3	20	8	ABS58165	ABs58165 Streptomy	359	13	43.3	48	2	AAZ159754	AAz159754 Target tr
C 287	13	43.3	22	2	AZ41006	Aaz41006 Human cel	C 360	13	43.3	48	2	AAZ10912	AAz10912 Probe #4
C 288	13	43.3	22	2	AZ22097	Aaz22097 Human cel	C 361	13	43.3	48	5	AAZ10912	AAz10912 Probe #4
C 289	13	43.3	22	8	ABV75134	ABv75134 Human CII	362	13	43.3	48	6	ABK22421	ABk22421 Human ERG
C 290	13	43.3	22	10	AA60473	AA60473 Human c-I	C 363	13	43.3	48	10	ADC02709	Adc02709 Ex vivo s
C 291	13	43.3	22	10	ADH76940	ADh76940 Neo F PCR	C 364	13	43.3	48	10	ADC02705	Adc02705 Ex vivo s
C 292	13	43.3	22	10	ADH76944	ADh76944 Neo F PCR	C 365	13	43.3	48	12	ADIS8384	Adi58384 Human int
C 293	13	43.3	22	10	ABV75297	ABv75297 Nucleotid	C 366	13	43.3	48	12	ADIS8380	Adi58380 Human int
C 294	13	43.3	25	3	AZ58162	Aaz58162 Neomycin	C 367	13	43.3	48	12	ADM28758	Adm28758 Mouse OPG
C 295	13	43.3	25	4	AAH38927	AAh38927 SNP speci	368	13	43.3	49	2	AAZ10913	AAz10913 Probe #5
C 296	13	43.3	25	6	ABV91693	ABv91693 Human POS	C 369	13	43.3	50	2	AAQ69643	Aaq69643 Human pre
C 297	13	43.3	25	6	ABV91692	ABv91692 Human POS	C 370	13	43.3	50	2	AAAT64105	Aat64105 Human pre
C 298	13	43.3	25	6	ABV91689	ABv91689 Human POS	C 371	13	43.3	50	2	AAAT64105	Aat64105 Human pre
C 299	13	43.3	25	6	ABV91691	ABv91691 Human POS	C 372	13	43.3	50	2	AAAT64105	Aat64105 Human pre
C 300	13	43.3	25	6	ABV91690	ABv91690 Human POS	C 373	13	43.3	50	2	AAAT64105	Aat64105 Human pre
C 301	13	43.3	25	9	ACI93081	ACi93081 Human mic	C 374	13	43.3	50	6	ABK82884	ABk82884 DNA bindi
C 302	13	43.3	25	9	ACK17019	ACk17019 Human mic	C 375	13	43.3	50	6	ABK30176	ABk30176 CYP2D6 ge
C 303	13	43.3	25	9	ACI81535	ACi81535 Human mic	376	13	43.3	50	6	ABZ04284	ABz04284 Human leu
C 304	13	43.3	25	9	ACI41824	ACi41824 Human mic	C 377	13	43.3	50	12	ADB80423	Adb80423 Duplex ol
C 305	13	43.3	25	9	ACK02539	ACk02539 Human mic	378	12.8	42.7	17	4	ABA80685	ABa80685 LDLR muta
C 306	13	43.3	25	9	ACI42863	ACi42863 Human mic	C 379	12.8	42.7	17	4	ABA80684	ABa80684 LDLR muta
C 307	13	43.3	25	12	ADJ93541	Adj93541 Mouse Mel	380	12.8	42.7	18	3	AAZ71666	Aaz71666 Human bla
C 308	13	43.3	26	5	AAF17192	AAf17192 Informati	381	12.8	42.7	19	11	ADO15037	Ado15037 Human PDG
C 309	13	43.3	27	2	AAV15726	AAv15726 Primer AT	C 382	12.8	42.7	19	11	ADO14726	Ado14726 Human PDG
C 310	13	43.3	27	6	ABK81875	ABk81875 Lung spec	383	12.8	42.7	19	12	ADQ61553	Adq61553 Anti-ORC1
C 311	13	43.3	29	3	AAK93141	AAk93141 29-mer ol	384	12.8	42.7	20	2	AAAX24316	Aax24316 Rat bone
C 312	13	43.3	29	6	ABN81594	ABn81594 Human FGF	385	12.8	42.7	20	3	AAc87720	Aac87720 Rat LIM m
C 313	13	43.3	29	12	ADI28587	Adi28587 Interleuk	C 386	12.8	42.7	20	4	AAf62435	Aaf62435 A thalian

314	13	43.3	29	12	AD128586	Adi28586 Interleu
315	13	43.3	30	2	AAV19100	Aav19100 Bacillus
C 316-	13	43.3	30	2	AAV54150	Aav54150 Primer fo
317	13	43.3	30	2	AAV18004	Aav18004 Primer us
C 318	13	43.3	30	12	ADO56313	Ado56313 Human cyc
319	13	43.3	31	8	ACD43835	ACd43835 Human gen
320	13	43.3	32	2	AAI18048	Aai18048 Sense pri
321	13	43.3	32	3	AAA51225	Aaa51225 3' primer
C 322	13	43.3	32	6	ABK11956	ABk11956 E. coli v
C 323	13	43.3	32	10	ADF68136	Adf68136 Stabilise
324	13	43.3	33	12	ADN97476	Adn97476 Artificia
325	13	43.3	34	10	ABZ58800	Abz58800 Cinnamyci
326	13	43.3	35	2	AAQ87358	Aaq87358 Human lam
327	13	43.3	35	2	AAQ92510	Aaq92510 Human imm
328	13	43.3	35	2	AAV37304	AAv37304 PCR prime
329	13	43.3	35	3	AAAL3316	Aaal3316 PCR prime
330	13	43.3	35	6	ABA94788	ABa94788 HCV-AB 68
331	13	43.3	36	6	ABK12310	ABk12310 Marinococ
C 332	13	43.3	36	8	ABSS58071	ABs58071 Rhodobact
333	13	43.3	36	8	ABSS58072	ABs58072 Pea rbcS-
C 334	13	43.3	37	2	AAV99401	AAv99401 Oligonuc1
C 335	13	43.3	38	10	ADD19574	Adi19574 Oreochrom
C 336	13	43.3	38	12	ADO26066	Ado26066 Arabidops
C 337	13	43.3	39	12	ADN12341	Adn12341 hAGT clon
338	13	43.3	40	6	AAH48523	Aah48523 Nucleic a
C 339	13	43.3	41	2	AAQ56317	Aaq56317 Probe for
340	13	43.3	41	4	AAH74191	Aah74191 s1 RNA bi
341	13	43.3	41	4	AAH74190	Aah74190 s1 RNA bi
C 342	13	43.3	41	6	ABSS60060	ABs60060 Human DNA
C 343	13	43.3	41	6	ABZ50314	ABz50314 Human cyt
344	13	43.3	42	2	AAV09726	AAv09726 Adenoviru
C 345	13	43.3	44	8	ACC57826	Acc57826 Primer B-
346	13	43.3	46	3	AAA75226	Aaa75226 Nucleotid
C 347	13	43.3	46	12	ADJ14733	Adj14733 Debrisoqu
C 348	13	43.3	46	12	ADJ14502	Adj14502 Debrisoqu
C 349	13	43.3	46	12	ADO60836	Ado60836 Human deb
C 350	13	43.3	46	12	ADO60991	Ado60991 Human deb
C 351	13	43.3	46	12	ADO60604	Ado60604 Human deb
352	13	43.3	47	3	AAZ67200	Aaz67200 Human map
353	13	43.3	47	3	AAZ68460	Aaz68460 Human map
C 354	13	43.3	47	12	ADJ14732	Adj14732 Debrisoqu
C 355	13	43.3	47	12	ADJ14501	Adj14501 Debrisoqu
C 356	13	43.3	47	12	ADO60835	Ado60835 Human deb
C 357	13	43.3	47	12	ADO60603	Ado60603 Human deb
C 358	13	43.3	47	12	ADO60990	Ado60990 Human deb
359	13	43.3	48	2	AAT59754	Aat59754 Target tr
C 360	13	43.3	48	2	AAZ10912	Aaz10912 Probe #4
C 361	13	43.3	48	5	AAZ57787	AAz57787 Oligonucl
362	13	43.3	48	6	ABK22421	ABk22421 Human ERG
C 363	13	43.3	48	10	ADC02709	Adc02709 Ex vivo s
C 364	13	43.3	48	10	ADC02705	Adc02705 Ex vivo s
C 365	13	43.3	48	12	ADI58384	Adi58384 Human int
C 366	13	43.3	48	12	ADI58380	Adi58380 Human int
C 367	13	43.3	48	12	ADM28758	Adm28758 Mouse OPG
368	13	43.3	49	2	AAZ10913	Aaz10913 Probe #5
C 369	13	43.3	50	2	AAQ69643	Aaq69643 Human pre
C 370	13	43.3	50	2	AAI16105	Aai16105 Human pre
C 371	13	43.3	50	2	AAZ17393	Aaz17393 Test sequ
C 372	13	43.3	50	2	AAZ52142	Aaz52142 Synthetic
373	13	43.3	50	2	AAZ52090	Aaz52090 Synthetic
C 374	13	43.3	50	6	ABK82884	ABk82884 DNA bindi
C 375	13	43.3	50	6	ABK30176	ABk30176 CYP2D6 ge
376	13	43.3	50	6	ABZ04284	ABz04284 Human leu
C 377	13	43.3	50	12	AD80423	ADe80423 Duplex ol
378	12.8	42.7	17	4	ABA80685	ABa80685 LDLR muta
C 379	12.8	42.7	17	4	ABA80684	ABa80684 LDLR muta
380	12.8	42.7	18	3	AAZ71666	Aaz71666 Human bia
381	12.8	42.7	19	11	AD015037	ADo15037 Human PDG
C 382	12.8	42.7	19	11	AD014726	ADo14726 Human PDG
383	12.8	42.7	19	12	ADG61553	ADg61553 Anti-ORC1
384	12.8	42.7	20	2	AAZ24316	Aaz24316 Rat bone
C 385	12.8	42.7	20	3	AAZ87720	Aac87720 Rat LIM m
C 386	12.8	42.7	20	4	AAF62245	AAf62245 A thalian

387	12.8	42.7	20	4	AAH45766	Aah45766 Human E2F	460	12.8	42.7	41	6	ABZ50435	Human cyt
388	12.8	42.7	20	8	ABT21294	Abt21294 Multiplex	C 461	12.8	42.7	41	6	ABZ43230	Human ATP
389	12.8	42.7	20	8	ABT43285	Abt43285 Neuroblas	462	12.8	42.7	41	8	ACC42873	Zinc fing
390	12.8	42.7	20	8	ABT32434	Abt32434 Neuroblas	463	12.8	42.7	41	8	ACC42874	Zinc fing
391	12.8	42.7	20	10	ADD68974	Add68974 Human B-c	C 464	12.8	42.7	41	10	AAI56520	Probe 2 r
392	12.8	42.7	20	10	ACC58348	Acc58348 Rat LIM m	465	12.8	42.7	43	2	AAV11896	L. lactis
393	12.8	42.7	21	2	AAX26585	Aax26585 Human pol	466	12.8	42.7	43	12	ADP67587	Gene aada
394	12.8	42.7	21	2	AAX24326	Aax24326 Human bon	C 467	12.8	42.7	45	2	AAT61001	L-galacto
395	12.8	42.7	21	3	AAZ75889	Aaz75889 Human bia	C 468	12.8	42.7	47	2	AAQ14691	Sclavo pe
396	12.8	42.7	21	3	AAZ75889	Aaz75889 Human bia	C 469	12.8	42.7	47	2	AAQ14691	Sclavo pe
397	12.8	42.7	21	4	AAZ75889	Aaz75889 Human LIM	C 470	12.8	42.7	47	3	AAZ67429	Human map
398	12.8	42.7	21	4	AAZ75889	Aaz75889 Human gen	C 471	12.8	42.7	47	3	AAZ67429	Human map
399	12.8	42.7	22	4	AAI66687	Aai66687 Human LIM	472	12.8	42.7	47	5	AAAF80124	Primer us
400	12.8	42.7	22	4	AAI66687	Aai66687 Human CBT	C 473	12.8	42.7	47	5	AAAF80124	Primer us
401	12.8	42.7	23	6	ABA90543	Ab90543 Lactococc	C 474	12.8	42.7	50	4	AAI30237	Human SNP
402	12.8	42.7	24	3	AAZ75889	Aaz75889 Human LIM	C 475	12.8	42.7	50	6	ABA00181	Primer SN
403	12.8	42.7	24	5	AAH21789	Aah21789 Mouse GAS	476	12.8	42.7	50	6	ABZ06619	Human leu
404	12.8	42.7	24	10	ACC58354	Acc58354 Human LIM	C 476	12.8	42.7	50	6	ABZ07009	Human leu
405	12.8	42.7	25	6	ABV93390	Abv93390 Human POS	477	12.6	42.0	19	8	ACA96045	Flavonoid
406	12.8	42.7	25	6	ABV93391	Abv93391 Human POS	478	12.6	42.0	20	2	AAT76856	Primer fo
407	12.8	42.7	25	9	ACK13150	Ack13150 Human mic	479	12.6	42.0	20	3	AAZ87094	PCR prime
408	12.8	42.7	25	9	ACK193419	Ack193419 Human mic	480	12.6	42.0	20	3	AAZ87094	PCR prime
409	12.8	42.7	25	9	ACK25817	Ack25817 Human mic	481	12.6	42.0	20	10	ABZ97933	Hepatitis
410	12.8	42.7	25	9	ACK27434	Ack27434 Human mic	482	12.6	42.0	20	10	ABZ97933	Hepatitis
411	12.8	42.7	25	9	ACK22696	Ack22696 Human mic	C 483	12.6	42.0	20	11	ABD30964	Human RAN
412	12.8	42.7	25	9	ACK22697	Ack22697 Human mic	C 484	12.6	42.0	20	12	ADH67609	Human glu
413	12.8	42.7	25	9	ACK183762	Ack183762 Human mic	485	12.6	42.0	20	12	ADH67404	Human glu
414	12.8	42.7	25	9	ACK183762	Ack183762 Human mic	486	12.6	42.0	20	12	ADJ59798	Oligonuc
415	12.8	42.7	25	9	ACK194909	Ack194909 Human mic	487	12.6	42.0	20	12	ADJ59798	Oligonuc
416	12.8	42.7	25	9	ACK06380	Ack06380 Human mic	C 488	12.6	42.0	20	12	ADJ24370	Human end
417	12.8	42.7	25	9	ACK196843	Ack196843 Human mic	C 489	12.6	42.0	20	12	ADO45288	Human oli
418	12.8	42.7	25	9	ACK25816	Ack25816 Human mic	C 490	12.6	42.0	21	2	AAV51534	PCR prime
419	12.8	42.7	25	9	ACK124444	Ack124444 Human mic	C 491	12.6	42.0	21	4	AAH62307	Human bia
420	12.8	42.7	25	9	ACK108338	Ack108338 Human mic	C 492	12.6	42.0	21	9	AAH62307	Cytokine
421	12.8	42.7	25	9	ACK184257	Ack184257 Human mic	C 493	12.6	42.0	21	12	ADO42740	Human NOV
422	12.8	42.7	25	9	ACK174163	Ack174163 Human mic	C 494	12.6	42.0	22	2	AAV51534	Ze mays
423	12.8	42.7	25	9	ACK154881	Ack154881 Human mic	C 495	12.6	42.0	22	2	AAV79997	Primer us
424	12.8	42.7	25	9	ACK13151	Ack13151 Human mic	496	12.6	42.0	24	5	ABJ197683	Endogenou
425	12.8	42.7	25	9	ACK13151	Ack13151 Human mic	C 497	12.6	42.0	24	5	ABJ197683	Pregnancy
426	12.8	42.7	25	9	ACK63453	Ack63453 DNA targe	C 498	12.6	42.0	24	8	ABX89541	Synthetic
427	12.8	42.7	26	6	ADH49160	Adh49160 NOV64 pro	C 499	12.6	42.0	24	8	ABX12339	Fluoresce
428	12.8	42.7	27	2	AAV67621	Aav67621 Human fit	500	12.6	42.0	25	6	ABN14163	Human GDM
429	12.8	42.7	27	2	AAV94404	Aav94404 Canine IL	C 501	12.6	42.0	25	6	ABN14167	Human GDM
430	12.8	42.7	27	6	ABJ60796	Abj60796 GPCR rea	C 502	12.6	42.0	25	6	ABN03487	Human GDM
431	12.8	42.7	28	8	AAI60796	Aai60796 Human CVS	503	12.6	42.0	25	6	ABN03488	Human GDM
432	12.8	42.7	28	10	ADC36293	Adc36293 Weed cont	504	12.6	42.0	25	6	ABN14162	Human GDM
433	12.8	42.7	29	4	AAZ10820	Aaz10820 Probe for	505	12.6	42.0	25	6	ABN14166	Human GDM
434	12.8	42.7	29	4	AAZ10820	Aaz10820 Probe for	506	12.6	42.0	25	6	ABN14165	Human GDM
435	12.8	42.7	29	5	AAZ10820	Aaz10820 Probe for	C 507	12.6	42.0	25	6	ABN03484	Human GDM
436	12.8	42.7	29	6	ABA91024	Ab91024 Biotinyla	C 508	12.6	42.0	25	6	ABN03489	Human GDM
437	12.8	42.7	29	10	ABT15869	Abt15869 Anti-huma	C 509	12.6	42.0	25	6	ABN03485	Human GDM
438	12.8	42.7	29	12	ADO56421	Ado56421 Human cyc	C 510	12.6	42.0	25	6	ABN03486	Human GDM
439	12.8	42.7	30	6	ABK91859	Abk91859 Mouse mag	C 511	12.6	42.0	25	6	ABN03490	Human GDM
440	12.8	42.7	30	12	ADP08456	Adp08456 PCR prime	512	12.6	42.0	25	6	ABN14164	Human GDM
441	12.8	42.7	31	4	AAI29918	Aai29918 Human sin	C 513	12.6	42.0	25	6	AD45008	Peammomys
442	12.8	42.7	33	4	AAH49655	Aah49655 Protein k	C 514	12.6	42.0	25	9	ACK30579	Human mic
443	12.8	42.7	33	4	AAH49655	Aah49655 Protein k	515	12.6	42.0	25	9	ACK30579	Human mic
444	12.8	42.7	33	8	ACC42802	Acc42802 Ribosome	C 516	12.6	42.0	25	9	ACK30578	Human mic
445	12.8	42.7	33	8	ABX12797	Abx12797 PCR prime	517	12.6	42.0	25	9	ACK30578	Human mic
446	12.8	42.7	33	10	ADP76129	Adp76129 Mutagenic	C 518	12.6	42.0	25	9	ACK30578	Human mic
447	12.8	42.7	33	10	ADP76128	Adp76128 Mutagenic	519	12.6	42.0	25	9	ACK30578	Human mic
448	12.8	42.7	38	6	ABZ52901	Abz52901 PCR prime	520	12.6	42.0	25	9	ACK30578	Human mic
449	12.8	42.7	38	6	ABZ52901	Abz52901 PCR prime	C 521	12.6	42.0	25	9	ACK30578	Human mic
450	12.8	42.7	40	3	ABA97725	Ab97725 Therman t	522	12.6	42.0	25	9	ACK30578	Human mic
451	12.8	42.7	40	3	ABA97725	Ab97725 Therman t	523	12.6	42.0	25	9	ACK30578	Human mic
452	12.8	42.7	40	10	AAA62656	Aaa62656 Beta-lact	C 524	12.6	42.0	25	9	ACK30578	Human mic
453	12.8	42.7	41	4	AAH74191	Aah74191 sl RNA bi	525	12.6	42.0	25	12	ADP75841	PCR prime
454	12.8	42.7	41	4	AAH74191	Aah74191 sl RNA bi	C 526	12.6	42.0	26	2	AAT72340	Human Pap
455	12.8	42.7	41	6	ABA01655	Ab01655 Human reg	C 527	12.6	42.0	26	2	AAT72341	Human Pap
456	12.8	42.7	41	6	ABZ55302	Abz55302 Human reg	C 528	12.6	42.0	26	2	AAT72342	Human Pap
457	12.8	42.7	41	6	ABZ49153	Abz49153 Human ald	529	12.6	42.0	26	2	AAT72343	Human Pap
458	12.8	42.7	41	6	ABZ44958	Abz44958 Human ald	530	12.6	42.0	28	6	ABK98985	Feline PC
459	12.8	42.7	41	6	ABZ47105	Abz47105 Human ATP	531	12.6	42.0	29	8	ABZ68983	PCR prime
	12.8	42.7	41	6	ABZ44885	Abz44885 Human cyt	532	12.6	42.0	30	2	AAV18700	Homo sapi

533	12.6	42.0	30	3	AAZ50179	Aaz50179 PCR prime	606	12.4	41.3	20	2	AAQ31848	Aeq31848 Primer GG
534	12.6	42.0	30	3	AAZ46111	Aaa46111 Human G p	c 607	12.4	41.3	20	2	AAQ31840	Aeq31840 Primer bi
c 535	12.6	42.0	30	3	AAA46112	Aaa46112 Human G p	c 608	12.4	41.3	20	2	AAAX95422	Aax95422 PCR prime
c 536	12.6	42.0	30	12	ADG86485	Adg86485 Human hCH	c 609	12.4	41.3	20	12	ADH72827	Ach72827 Hypoxia r
537	12.6	42.0	30	12	ADG86484	Adg86484 Human hCH	c 610	12.4	41.3	21	10	ADC26353	Adc26353 NOV prote
538	12.6	42.0	30	12	ADP20277	Adp20277 G protein	c 611	12.4	41.3	22	6	AAAL49024	Aal49024 Murine PA
c 539	12.6	42.0	30	12	ADP20278	Adp20278 G protein	c 612	12.4	41.3	22	6	ABX97351	Abx97351 Human NOV
c 540	12.6	42.0	31	2	ATAT38854	Atat38854 Primer fo	c 613	12.4	41.3	22	8	ABX72401	Abx72401 Human NOV
c 541	12.6	42.0	31	4	AAI30504	Aai30504 Human sin	c 614	12.4	41.3	22	12	ADNG2254	Adng2254 Human NOV
c 542	12.6	42.0	31	8	ACC44511	Acc44511 HIV fragm	c 615	12.4	41.3	23	2	AAAT01534	Aat01534 Human her
543	12.6	42.0	32	2	AAV18399	Aav18399 Synthetic	c 616	12.4	41.3	23	2	AAAT03719	Aat03719 Human her
c 544	12.6	42.0	32	2	AAAX59033	Aax59033 Human tra	c 617	12.4	41.3	23	3	AAA47528	Aaa47528 Primer fo
545	12.6	42.0	32	6	ABL91400	Abi91400 Chlamydia	c 618	12.4	41.3	23	12	ADHI0689	Adhi0689 Human CX3
c 546	12.6	42.0	32	10	ADK71640	Adk71640 Drug-tole	c 619	12.4	41.3	23	12	ADI44500	Adi44500 P. praten
547	12.6	42.0	33	2	AAQ69213	Aaq69213 Recombina	c 620	12.4	41.3	24	2	AAV11542	Aav11542 Recombina
548	12.6	42.0	33	2	AAAT58965	Aat58965 Primer OT	c 621	12.4	41.3	24	12	ADL70387	Adl70387 Target se
549	12.6	42.0	33	3	AAA49409	Aaa49409 Primer us	c 622	12.4	41.3	24	12	ADLO1711	Adol1711 Single mu
c 550	12.6	42.0	34	2	AAQ29333	Aaq29333 Retinoic	c 623	12.4	41.3	25	3	AAZ37265	Aaz37265 PCR prime
551	12.6	42.0	35	1	AAAG0581	Aan60581 Sequence	c 624	12.4	41.3	25	6	ABV82638	Abv82638 Human HTP
552	12.6	42.0	35	2	AAAT08566	Atat08566 Human CSF	c 625	12.4	41.3	25	6	ABV82650	Abv82650 Human HTP
553	12.6	42.0	35	2	AAV66887	Aav66887 Human imm	c 626	12.4	41.3	25	6	ABV93389	Abv93389 Human POS
554	12.6	42.0	35	4	AAAD10997	Aad10997 Forward p	c 627	12.4	41.3	25	6	ABV93388	Abv93388 Human POS
555	12.6	42.0	35	8	ABZ24417	Abz24417 Primer RP	c 628	12.4	41.3	25	8	ADB03956	Adb03956 Human MDZ
556	12.6	42.0	35	8	ABV76084	Abv76084 Primer RP	c 629	12.4	41.3	25	8	ADB03955	Adb03955 Human MDZ
557	12.6	42.0	35	10	ADD06167	Add06167 Rhabdovir	c 630	12.4	41.3	25	8	ADB03957	Adb03957 Human MDZ
c 558	12.6	42.0	36	6	AAAL49318	Aal49318 Rat Glut1	c 631	12.4	41.3	25	8	ADB03958	Adb03958 Human MDZ
559	12.6	42.0	37	3	AAAO8890	Aaa08890 PCR prime	c 632	12.4	41.3	25	9	ACI49090	Ac149090 Human mlc
560	12.6	42.0	37	6	ABK98987	Abk98987 Feline PC	c 633	12.4	41.3	25	9	ACK03973	Ack03973 Human mlc
c 561	12.6	42.0	37	12	ADJ92414	Adj92414 Human Cys	c 634	12.4	41.3	25	9	ACI86824	Ac186824 Human mlc
c 562	12.6	42.0	37	12	ADJ92410	Adj92410 Human Cys	c 635	12.4	41.3	25	9	ACK24895	Ack24895 Human mlc
c 563	12.6	42.0	38	12	ADM36296	Adm36296 Modified	c 636	12.4	41.3	25	9	ACI36583	Ac136583 Human mlc
564	12.6	42.0	40	2	AAT70799	Aat70799 Stenotic	c 637	12.4	41.3	25	9	ACI06410	Ac106410 Human mlc
565	12.6	42.0	40	2	AAT71195	Aat71195 HPV type	c 638	12.4	41.3	25	9	ACI58763	Ac158763 Human mlc
c 566	12.6	42.0	40	4	AAAC91703	Aac91703 Mouse fat	c 639	12.4	41.3	25	9	ACI88219	Ac188219 Human mlc
c 567	12.6	42.0	40	8	ACA61849	Acc61849 Human C5a	c 640	12.4	41.3	25	9	ACI13244	Ac113244 Human mlc
568	12.6	42.0	40	10	ADI57945	Adi57945 Monoclonia	c 641	12.4	41.3	25	9	ACI164681	Ac1164681 Human mlc
c 569	12.6	42.0	40	12	ADF90241	Adf90241 Human HMG	c 642	12.4	41.3	25	9	ACI99858	Ac199858 Human mlc
c 570	12.6	42.0	41	2	AAV26914	Aav26914 Human C5a	c 643	12.4	41.3	25	9	ACI07783	Ac107783 Human mlc
c 571	12.6	42.0	41	2	AAV50020	Aav50020 PCR prime	c 644	12.4	41.3	25	9	ACI99859	Ac199859 Human mlc
c 572	12.6	42.0	41	2	AAAX18236	Aax18236 Primer #2	c 645	12.4	41.3	25	9	ACI97509	Ac197509 Human mlc
c 573	12.6	42.0	41	3	AAAB88387	Aab88387 Human C5a	c 646	12.4	41.3	25	9	ACK28622	Ack28622 Human mlc
c 574	12.6	42.0	41	4	AAAF27382	Aaf27382 Human C5a	c 647	12.4	41.3	25	9	ACK27600	Ack27600 Human mlc
c 575	12.6	42.0	41	4	AAI65753	Aai65753 PCR prime	c 648	12.4	41.3	25	9	ACI11747	Ac111747 Human mlc
c 576	12.6	42.0	41	12	ADI37091	Adi37091 Yeast cel	c 649	12.4	41.3	25	9	ACI88218	Ac188218 Human mlc
577	12.6	42.0	42	2	AAQ54958	Aaq54958 cyd-lacZ	c 650	12.4	41.3	25	9	ACI64680	Ac164680 Human mlc
c 578	12.6	42.0	42	8	ABT34125	Abt34125 Human pig	c 651	12.4	41.3	25	9	ACI46710	Ac146710 Human mlc
c 579	12.6	42.0	42	8	AAZ01036	Aaz01036 Probe for	c 652	12.4	41.3	25	9	ACI00776	Ac100776 Human mlc
c 580	12.6	42.0	42	8	AAZ01035	Aaz01035 Probe for	c 653	12.4	41.3	25	9	ACK11683	Ack11683 Human mlc
c 581	12.6	42.0	42	8	AAZ66851	Aaz66851 Human map	c 654	12.4	41.3	25	9	ACI86335	Ac186335 Human mlc
c 582	12.6	42.0	42	10	ADF34426	Adf34426 Murine 5'	c 655	12.4	41.3	25	9	ACI80498	Ac180498 Human mlc
c 583	12.6	42.0	42	12	ADM90556	Adm90556 Mouse 5'	c 656	12.4	41.3	25	10	ADC61196	Adc61196 Full-leng
c 584	12.6	42.0	42	12	AAV15688	Aav15688 PCR prime	c 657	12.4	41.3	25	12	ADPI5002	Adpi5002 Renal cel
585	12.6	42.0	48	3	AAAC58561	Aac58561 Human DNA	c 658	12.4	41.3	25	12	ADPI5005	Adpi5005 Renal cel
c 586	12.6	42.0	48	10	ADC02710	Adc02710 Ex vivo s	c 659	12.4	41.3	25	12	ADPI5004	Adpi5004 Renal cel
c 587	12.6	42.0	48	10	ADC02706	Adc02706 Ex vivo s	c 660	12.4	41.3	27	2	AAAX74150	Aax74150 Mouse fit
c 588	12.6	42.0	48	12	ADI58385	Adi58385 Human int	c 661	12.4	41.3	27	2	AAV94070	Aav94070 Human IL-
c 589	12.6	42.0	48	12	ADI58381	Adi58381 Human int	c 662	12.4	41.3	27	12	ADMA1126	Adm41126 GeneRacer
c 590	12.6	42.0	49	10	ADFI6998	Adfi6998 Human alb	c 663	12.4	41.3	28	4	AAAD13133	Aad13133 Human mem
c 591	12.6	42.0	49	12	ADO38208	Ado38208 HIV envel	c 664	12.4	41.3	28	4	AAQ83999	Aaq83999 pMON5853
c 592	12.6	42.0	49	12	ADO38097	Ado38097 HIV envel	c 665	12.4	41.3	29	3	AAA04598	Aaa04598 Polymorph
593	12.6	42.0	50	2	AAAX30010	Aax30010 Detector	c 666	12.4	41.3	29	3	AAA04598	Aaa04598 Polymorph
594	12.6	42.0	50	3	AAK99538	Aak99538 50-mer ol	c 667	12.4	41.3	29	6	ABSV74250	Absv74250 Interleuk
595	12.6	42.0	50	4	AAAL33924	Aal33924 Human SNP	c 668	12.4	41.3	29	6	ABSV74062	Absv74062 Interleuk
c 596	12.6	42.0	50	6	ABZ03457	Abz03457 Human leu	c 669	12.4	41.3	29	10	ADC02673	Adc02673 Ex vivo s
c 597	12.6	42.0	50	6	ABZ08145	Abz08145 Human leu	c 670	12.4	41.3	29	10	ADC02107	Adc02107 Ex vivo s
c 598	12.6	42.0	50	6	ABV80641	Abv80641 Human HTP	c 671	12.4	41.3	29	10	ADC02374	Adc02374 Ex vivo s
c 599	12.6	42.0	50	6	ABV80645	Abv80645 Human HTP	c 672	12.4	41.3	29	12	ADI58348	Adi58348 Human int
c 600	12.4	41.3	17	6	ABV80645	Abv80645 Human HTP	c 673	12.4	41.3	30	2	AAV21494	Aav21494 Plaemid p
601	12.4	41.3	17	8	ABT38793	Abt38793 Tumour su	c 674	12.4	41.3	30	4	AAAF84418	Aaf84418 Human WAV
602	12.4	41.3	17	10	ADE25272	Adc25272 Plant gro	c 675	12.4	41.3	30	4	AAAF84418	Aaf84418 Human WAV
603	12.4	41.3	17	10	ADF49915	Adf49915 Human BCL	c 676	12.4	41.3	30	10	ABZ23494	Abz23494 PCR prime
c 604	12.4	41.3	19	10	ADF49501	Adf49501 Human BCL	c 677	12.4	41.3	30	12	ADI37222	Adi37222 Mouse PN-
c 605	12.4	41.3	19	10	ADP47193	Adp47193 Mouse alp	c 678	12.4	41.3	30	12	ADP08793	Adp08793 PCR prime

C 679	12.4	41.3	30	12	ADP08806	Adp08806 PCR prime	752	12.2	40.7	19	10	ADG36508	ADG36508 HIV siNA
C 680	12.4	41.3	31	4	AAD03503	Aad03503 Dog p-gly	C 753	12.2	40.7	19	10	ADG35458	ADG35458 HIV siNA
C 681	12.4	41.3	31	10	ADE15940	Adel15940 Silkworm	C 754	12.2	40.7	20	3	AAA12081	Aaa12081 Human ICA
C 682	12.4	41.3	32	6	ABL91396	Ab191396 Chlamydia	C 755	12.2	40.7	20	3	AAA61966	Aaa61966 Human MEK
C 683	12.4	41.3	32	2	ABA19836	Aba19836 Bacteriop	C 756	12.2	40.7	20	3	AAA61965	Aaa61965 Human MEK
C 684	12.4	41.3	33	3	AAA29784	Aaa29784 Bacteriop	C 757	12.2	40.7	20	4	AAC67702	Aac67702 Oligonucle
C 685	12.4	41.3	33	5	AAD21590	Aad21590 Bacteriop	C 758	12.2	40.7	20	4	AAD41824	Aad41824 Target su
C 686	12.4	41.3	33	8	ABZ70725	Abz70725 Human Bol	C 759	12.2	40.7	20	6	AAD41825	Aad41825 Target su
C 687	12.4	41.3	33	10	ACF57878	Acf57878 Human SCN	C 760	12.2	40.7	20	6	AA141039	Aa141039 3'F1TC la
C 688	12.4	41.3	33	12	ADL72630	Adl72630 Foldback	C 761	12.2	40.7	20	6	AA141039	Aa141039 3'F1TC la
C 689	12.4	41.3	35	3	AAA37474	Aaa37474 Arabidops	C 762	12.2	40.7	20	6	AA141039	Aa141039 3'F1TC la
C 690	12.4	41.3	38	12	ADK67669	Adk67669 T7 promot	C 763	12.2	40.7	20	6	AA141039	Aa141039 3'F1TC la
C 691	12.4	41.3	39	9	ADA15916	Ada15916 Primer fo	C 764	12.2	40.7	20	6	AA141039	Aa141039 3'F1TC la
C 692	12.4	41.3	39	11	ABD18991	Abd18991 Human ade	C 765	12.2	40.7	20	6	ABV72771	Abv72771 Digoxigen
C 693	12.4	41.3	41	6	ABA97154	Aba97154 Human pro	C 766	12.2	40.7	20	6	ABK90665	Abk90665 FITC labe
C 694	12.4	41.3	41	6	ABA97155	Aba97155 Human pro	C 767	12.2	40.7	20	6	ABK90666	Abk90666 FITC labe
C 695	12.4	41.3	41	6	ABA00595	Abaa00595 LIM homol	C 768	12.2	40.7	20	6	ACC44142	Acc44142 HIV integ
C 696	12.4	41.3	41	6	ABA00596	Abaa00596 LIM homol	C 769	12.2	40.7	20	6	ACC44141	Acc44141 HIV integ
C 697	12.4	41.3	41	6	ABZ49831	Abz49831 Human car	C 770	12.2	40.7	20	8	ACC00274	Acc00274 Target pl
C 698	12.4	41.3	41	6	ABZ43647	Abz43647 Human car	C 771	12.2	40.7	20	8	ACC00273	Acc00273 Target pl
C 699	12.4	41.3	41	6	ABL55242	Ab155242 Myelin P0	C 772	12.2	40.7	20	8	ABS56185	Abs56185 PCR prime
C 700	12.4	41.3	41	6	ABL48376	Ab148376 Cytohesin	C 773	12.2	40.7	20	8	ABS56185	Abs56185 PCR prime
C 701	12.4	41.3	41	8	ABZ70727	Abz70727 Human Bol	C 774	12.2	40.7	20	10	ADG43931	Adg43931 Human DYR
C 702	12.4	41.3	41	12	ADL70390	Adl70390 Target se	C 775	12.2	40.7	20	10	ADG43931	Adg43931 Human DYR
C 703	12.4	41.3	42	2	AAV35222	Aav35222 E. coli G	C 776	12.2	40.7	20	10	ABZ88622	Abz88622 Human OLI
C 704	12.4	41.3	42	2	AAV28133	Aav28133 GroEL api	C 777	12.2	40.7	20	11	ABD24852	Abd24852 AI095492-
C 705	12.4	41.3	42	10	ADG44249	Adg44249 Anti-path	C 778	12.2	40.7	20	11	ABD24852	Abd24852 AI095492-
C 706	12.4	41.3	42	10	ADG44235	Adg44235 Anti-path	C 779	12.2	40.7	20	12	ADJ29661	Adj29661 AAG26698-
C 707	12.4	41.3	42	10	ADG44238	Adg44238 Anti-path	C 780	12.2	40.7	20	12	ADJ29661	Adj29661 AAG26698-
C 708	12.4	41.3	42	10	ADG44236	Adg44236 Anti-path	C 781	12.2	40.7	20	12	ADJ23427	Adj23427 Human end
C 709	12.4	41.3	43	2	AAV19604	Aav19604 Human int	C 782	12.2	40.7	20	12	ADO47435	Ado47435 Anti-HIV
C 710	12.4	41.3	43	2	AAV19573	Aav19573 Human int	C 783	12.2	40.7	21	2	AAQ85724	Aaq85724 Anti-HIV
C 711	12.4	41.3	43	2	AAV15393	Aav15393 Interfero	C 784	12.2	40.7	21	2	AAQ85724	Aaq85724 Anti-HIV
C 712	12.4	41.3	43	2	AAV15367	Aav15367 Interfero	C 785	12.2	40.7	21	3	AAQ85724	Aaq85724 Anti-HIV
C 713	12.4	41.3	46	2	AAV06352	Aav06352 Phosphati	C 786	12.2	40.7	21	6	ABK12106	Abk12106 HIV Gag P
C 714	12.4	41.3	47	3	AAZ87009	Aaz87009 RBP-7 bia	C 787	12.2	40.7	21	11	ADL08483	Adl08483 Human can
C 715	12.4	41.3	47	3	AAZ66228	Aaz66228 Human map	C 788	12.2	40.7	21	11	ADL08483	Adl08483 Human can
C 716	12.4	41.3	47	3	AAZ67790	Aaz67790 Human map	C 789	12.2	40.7	21	12	ADJ60119	Adj60119 Oligonucle
C 717	12.4	41.3	47	4	AAH88369	Aah88369 CNS disor	C 790	12.2	40.7	21	12	ADJ60119	Adj60119 Oligonucle
C 718	12.4	41.3	47	4	AAI66149	Aai66149 Hepatitis	C 791	12.2	40.7	21	12	ADO45608	Ado45608 Human oli
C 719	12.4	41.3	48	2	AAI04995	Aai04995 Bacteriop	C 792	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 720	12.4	41.3	48	8	ACA09597	Aca09597 Necrosis	C 793	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 721	12.4	41.3	49	4	AAE81330	Aae81330 Human cac	C 794	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 722	12.4	41.3	50	4	AAE67710	Aae67710 HSI fragm	C 795	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 723	12.4	41.3	50	5	ABL00149	Ab100149 Human sil	C 796	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 724	12.4	41.3	50	6	ABQ95778	Abq95778 Tumour su	C 797	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 725	12.4	41.3	50	6	ABZ03330	Abz03330 Human leu	C 798	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 726	12.4	41.3	50	6	ABZ02112	Abz02112 Human leu	C 799	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 727	12.4	41.3	50	6	ABZ04715	Abz04715 Human leu	C 800	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 728	12.4	41.3	50	6	ABZ04942	Abz04942 Human leu	C 801	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 729	12.4	41.3	50	6	ABZ00546	Abz00546 Human leu	C 802	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 730	12.4	41.3	50	6	ABZ05064	Abz05064 Human leu	C 803	12.2	40.7	23	2	AAQ62402	Aaq62402 Vector pv
C 731	12.4	41.3	50	6	ABZ04065	Abz04065 Human leu	C 804	12.2	40.7	23	3	AAQ62402	Aaq62402 Vector pv
C 732	12.4	41.3	50	12	ADO28825	Ado28825 Fibrillar	C 805	12.2	40.7	23	3	AAQ62402	Aaq62402 Vector pv
C 733	12.2	40.7	17	2	AAK63953	Aak63953 Rabbit st	C 806	12.2	40.7	23	5	AAQ62402	Aaq62402 Vector pv
C 734	12.2	40.7	17	2	AAK22660	Aak22660 Integrin	C 807	12.2	40.7	23	5	AAQ62402	Aaq62402 Vector pv
C 735	12.2	40.7	17	3	AAA36052	Aaa36052 Human gen	C 808	12.2	40.7	23	8	AAQ62402	Aaq62402 Vector pv
C 736	12.2	40.7	17	4	ABA80688	Aba80688 LDLR muta	C 809	12.2	40.7	23	10	AAQ62402	Aaq62402 Vector pv
C 737	12.2	40.7	17	4	ABA80689	Aba80689 LDLR muta	C 810	12.2	40.7	23	11	AAQ62402	Aaq62402 Vector pv
C 738	12.2	40.7	17	4	ABA80680	Aba80680 LDLR muta	C 811	12.2	40.7	24	1	AAQ62402	Aaq62402 Vector pv
C 739	12.2	40.7	17	4	ABA80681	Aba80681 LDLR muta	C 812	12.2	40.7	25	6	AAQ62402	Aaq62402 Vector pv
C 740	12.2	40.7	17	6	ABN00555	Abn00555 Human GDM	C 813	12.2	40.7	25	6	AAQ62402	Aaq62402 Vector pv
C 741	12.2	40.7	17	8	ACC65590	Acc65590 Murine ol	C 814	12.2	40.7	25	6	AAQ62402	Aaq62402 Vector pv
C 742	12.2	40.7	18	8	ACC67239	Acc67239 Murine ol	C 815	12.2	40.7	25	6	AAQ62402	Aaq62402 Vector pv
C 743	12.2	40.7	18	2	AAQ82204	Aaq82204 Chromosom	C 816	12.2	40.7	25	6	AAQ62402	Aaq62402 Vector pv
C 744	12.2	40.7	19	3	AAH83217	Aah83217 cdk7 ribo	C 817	12.2	40.7	25	8	AAQ62402	Aaq62402 Vector pv
C 745	12.2	40.7	19	5	AAH58379	Aah58379 Cell-cycl	C 818	12.2	40.7	25	8	AAQ62402	Aaq62402 Vector pv
C 746	12.2	40.7	19	10	ADE27263	Adel27263 Stearoyl-	C 819	12.2	40.7	25	8	AAQ62402	Aaq62402 Vector pv
C 747	12.2	40.7	19	10	ADE27553	Adel27553 Stearoyl-	C 820	12.2	40.7	25	8	AAQ62402	Aaq62402 Vector pv
C 748	12.2	40.7	19	10	ADG36192	Adg36192 HIV siNA	C 821	12.2	40.7	25	9	AAQ62402	Aaq62402 Vector pv
C 749	12.2	40.7	19	10	ADG35454	Adg35454 HIV siNA	C 822	12.2	40.7	25	9	AAQ62402	Aaq62402 Vector pv
C 750	12.2	40.7	19	10	ADG36196	Adg36196 HIV siNA	C 823	12.2	40.7	25	9	AAQ62402	Aaq62402 Vector pv
C 751	12.2	40.7	19	10	ADG35770	Adg35770 HIV siNA	C 824	12.2	40.7	25	9	AAQ62402	Aaq62402 Vector pv

C 825	12.2	40.7	25	9	ACK14105	ACK14105 Human mic	898	12.2	40.7	31	8	ACD43689	ACD43689 Human gen
C 826	12.2	40.7	25	9	ACK15027	ACK15027 Human mic	899	12.2	40.7	32	2	AAT18046	AAT18046 Sense pri
C 827	12.2	40.7	25	9	ACK5065	ACK5065 Human mic	900	12.2	40.7	33	2	AAQ67095	AAQ67095 Human TNF
C 828	12.2	40.7	25	9	ACK196205	ACK196205 Human mic	901	12.2	40.7	33	2	AAQ67215	AAQ67215 Mutant TN
C 829	12.2	40.7	25	9	ACK196205	ACK196205 Human mic	902	12.2	40.7	33	2	AAQ67215	AAQ67215 Sense pri
C 830	12.2	40.7	25	9	ACK162221	ACK162221 Human mic	903	12.2	40.7	33	2	AAV13820	AAV13820 Sense pri
C 831	12.2	40.7	25	9	ACK192666	ACK192666 Human mic	904	12.2	40.7	33	2	AAV13820	AAV13820 Primer fo
C 832	12.2	40.7	25	9	ACK152734	ACK152734 Human mic	905	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 833	12.2	40.7	25	9	ACK165931	ACK165931 Human mic	906	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 834	12.2	40.7	25	9	ACK165931	ACK165931 Human mic	907	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 835	12.2	40.7	25	9	ACK187713	ACK187713 Human mic	908	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 836	12.2	40.7	25	9	ACK187713	ACK187713 Human mic	909	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 837	12.2	40.7	25	9	ACK06806	ACK06806 Human mic	910	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 838	12.2	40.7	25	9	ACK175396	ACK175396 Human mic	911	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 839	12.2	40.7	25	9	ACK175397	ACK175397 Human mic	912	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 840	12.2	40.7	25	9	ACK139293	ACK139293 Human mic	913	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 841	12.2	40.7	25	9	ACK112545	ACK112545 Human mic	914	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 842	12.2	40.7	25	9	ACK165537	ACK165537 Human mic	915	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 843	12.2	40.7	25	9	ACK07270	ACK07270 Human mic	916	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 844	12.2	40.7	25	9	ACK141126	ACK141126 Human mic	917	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 845	12.2	40.7	25	9	ACK15818	ACK15818 Human mic	918	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 846	12.2	40.7	25	9	ACK144058	ACK144058 Human mic	919	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 847	12.2	40.7	25	9	ACK148041	ACK148041 Human mic	920	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 848	12.2	40.7	25	9	ACK148577	ACK148577 Human mic	921	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 849	12.2	40.7	25	9	ACK54893	ACK54893 DNA target	922	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 850	12.2	40.7	25	12	ADM66525	ADM66525 Human coa	923	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 851	12.2	40.7	25	12	ADM66524	ADM66524 Human coa	924	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 852	12.2	40.7	25	12	ADP18080	ADP18080 Renal cel	925	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 853	12.2	40.7	25	12	ADP18079	ADP18079 Renal cel	926	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 854	12.2	40.7	26	2	AAQ32845	AAQ32845 "Drop-in/	927	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 855	12.2	40.7	26	2	AAQ30090	AAQ30090 Sequence	928	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 856	12.2	40.7	26	2	AAQ74489	AAQ74489 Probe for	929	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 857	12.2	40.7	26	2	AAQ74564	AAQ74564 Probe for	930	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 858	12.2	40.7	26	2	AAQ74536	AAQ74536 Probe for	931	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 859	12.2	40.7	26	2	AAQ74550	AAQ74550 Probe for	932	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 860	12.2	40.7	26	2	AAQ86618	AAQ86618 Human imm	933	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 861	12.2	40.7	26	2	AAQ15563	AAQ15563 Human imm	934	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 862	12.2	40.7	26	2	AAQ40188	AAQ40188 HIV target	935	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 863	12.2	40.7	26	2	AAV55993	AAV55993 Human cel	936	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 864	12.2	40.7	26	2	AAV66341	AAV66341 Human imm	937	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 865	12.2	40.7	26	2	AAV23183	AAV23183 HIV regio	938	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 866	12.2	40.7	26	10	AAQ25655	AAQ25655 Human imm	939	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 867	12.2	40.7	26	10	ADF43588	ADF43588 HIV detec	940	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 868	12.2	40.7	26	10	ADF75976	ADF75976 Complement	941	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 869	12.2	40.7	26	10	ADF75924	ADF75924 DNA hybri	942	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 870	12.2	40.7	26	10	ADF75990	ADF75990 RNA Hybri	943	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 871	12.2	40.7	26	10	ADF76004	ADF76004 Complement	944	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 872	12.2	40.7	26	10	ABV74096	ABV74096 HIV PCR p	945	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 873	12.2	40.7	26	12	ADO47270	ADO47270 LTR U5 se	946	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 874	12.2	40.7	27	2	AAQ27975	AAQ27975 Primer E.	947	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 875	12.2	40.7	27	2	AAQ73866	AAQ73866 Mouse flt	948	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 876	12.2	40.7	27	2	AAV13611	AAV13611 Hepatitis	949	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 877	12.2	40.7	27	6	ABS63389	ABS63389 Human Fv	950	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 878	12.2	40.7	27	6	ABS67771	ABS67771 Antibody	951	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 879	12.2	40.7	27	12	ADF91540	ADF91540 Human TNF	952	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 880	12.2	40.7	28	2	AAV17941	AAV17941 Simian er	953	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 881	12.2	40.7	28	3	AZ49126	AZ49126 PCR prime	954	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 882	12.2	40.7	28	10	ADG37163	ADG37163 RbA rela	955	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 883	12.2	40.7	29	2	AAQ94527	AAQ94527 Human/mur	956	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 884	12.2	40.7	29	2	AAQ94516	AAQ94516 Human/mur	957	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 885	12.2	40.7	29	2	AAQ34756	AAQ34756 Probe for	958	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 886	12.2	40.7	29	2	AAQ38630	AAQ38630 Chimaeric	959	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 887	12.2	40.7	29	2	AAQ38641	AAQ38641 Chimaeric	960	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 888	12.2	40.7	29	2	AAQ42075	AAQ42075 Human bet	961	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 889	12.2	40.7	30	3	AAQ53134	AAQ53134 Chimeric	962	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 890	12.2	40.7	30	4	AAQ88177	AAQ88177 Murine CS	963	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 891	12.2	40.7	30	12	ADQ12252	ADQ12252 Single re	964	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 892	12.2	40.7	30	12	ADQ12298	ADQ12298 Single mu	965	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 893	12.2	40.7	30	12	ADQ48556	ADQ48556 Human neu	966	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 894	12.2	40.7	31	2	AAQ46948	AAQ46948 Chronic m	967	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 895	12.2	40.7	31	2	AAV67716	AAV67716 Nucleotid	968	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 896	12.2	40.7	31	2	AAV67535	AAV67535 Nucleotid	969	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime
C 897	12.2	40.7	31	2	AAV67535	AAV67535 Nucleotid	970	12.2	40.7	33	2	AAV13820	AAV13820 PCR prime

c 971 12 40.0 20 2 AAT17566
 c 972 12 40.0 20 2 AAT17564
 c 973 12 40.0 20 2 AAX93651
 c 974 12 40.0 20 3 AAG63906
 c 975 12 40.0 20 4 AAD20444
 c 976 12 40.0 20 5 AAF69688
 c 977 12 40.0 20 5 ABA82295
 c 978 12 40.0 20 6 ABK23092
 c 979 12 40.0 20 6 ABI96132
 c 980 12 40.0 20 8 ACC45875
 c 981 12 40.0 20 10 ADB98373
 c 982 12 40.0 20 10 ABZ5978
 c 983 12 40.0 20 12 ADG98202
 c 984 12 40.0 20 12 ADI66976
 c 985 12 40.0 20 12 ADI66915
 c 986 12 40.0 20 12 ADK96478
 c 987 12 40.0 20 12 ADK96675
 c 988 12 40.0 21 2 AAV01121
 c 989 12 40.0 21 2 AAV67401
 c 990 12 40.0 21 3 AAA95916
 c 991 12 40.0 21 4 AAF96817
 c 992 12 40.0 21 4 AAH62122
 c 993 12 40.0 22 4 AAS23793
 c 994 12 40.0 22 6 ABZ30785
 c 995 12 40.0 22 10 ADF87878
 c 996 12 40.0 23 6 AAL46190
 c 997 12 40.0 23 9 ADA25523
 c 998 12 40.0 23 10 ADG29581
 c 999 12 40.0 24 2 AAV68426
 1000 12 40.0 24 2 AAX57133

ALIGNMENTS

RESULT 1
 ACF35783
 ID ACF35783 standard; DNA; 30 BP.
 XX
 AC ACF35783;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Internal control (IC)-specific probe ST2535Cy5F15.
 KW Nucleic acid purification; nucleic acid amplification; cancer;
 KW sickle cell anemia; blood screening; probe; ss.

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /tag= a
 FT /note= "Cys fluorophore attached to 5' terminus"
 FT modified_base 13..14 /tag= b
 FT /note= "HEX label incorporated between these nucleotides"
 FT
 PN WO2003057910-A2.

XX
 PD 17-JUL-2003.
 XX
 PF 04-JAN-2003; 2003WO-EP000039.
 XX
 PR 08-JAN-2002; 2002US-0347327P.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Pintel-Ober J, Wenzig P, Weindel K, Schoenbrunner R;
 PI Mallotra K, O'donnell P, Kyger E;
 XX
 DR WPI; 2003-587135/55.

XX
 PT Purification and amplification of target nucleic acid from biological
 PT sample used in diagnosis of cancer or in screening blood, involves
 PT binding target nucleic acid with unmodified silica surface, followed by
 PT amplification.
 XX
 PS Example 1; Page 23; 33pp; English.
 XX
 CC The invention relates to purification and amplification of target nucleic
 CC acid from biological sample. The method involves and binding target
 CC nucleic acid (TNA) in the sample with a material comprising an unmodified
 CC silica surface, separating the material from the sample and amplifying
 CC TNA in the presence of the material. The method is useful in diagnosis of
 CC certain diseases such as inherited diseases like sickle cell anemia and
 CC certain types of cancer or in screening blood for presence of target
 CC nucleic acid from virus. The method improves reaction efficiency and
 CC detection sensitivity of target nucleic acids. The present sequence
 CC represents an internal control (IC)-specific probe used in the method of
 CC the invention
 XX
 SQ Sequence 30 BP; 4 A; 10 C; 5 G; 11 T; 0 U; 0 Other;

Query Match 100.0%; Score 30; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.0017;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 30
 |||||
 Db 1 TGGACTCAGTCTTGGTCATCTCACCTTCT 30

RESULT 2
 AAD43286
 ID AAD43286 standard; DNA; 31 BP.
 XX
 AC AAD43286;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE ST2535 probe used to illustrate the methods of the invention.
 KW Amplification; target nucleic acid; probe; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1 /tag= a
 FT /note= "Linked to Cy5 where Cy5 is Oligonucleotid-
 FT derivatisation with pentamethin-di-indocarbocyanin using
 FT alkylphosphatidyl-linker"
 FT stem_loop 2..12 /tag= b
 FT misc_binding 2..15 /tag= c
 FT /bound_moiety= "Nucleotides 12-9"
 FT misc_binding 9..12 /tag= d
 FT /bound_moiety= "Nucleotides 5-2"
 FT misc_feature 13..14 /tag= e
 FT /note= "Linked via HEXs where HEXs is Oligonucleotid-
 FT derivatisation with hexachloro-6-carboxy-fluorescein
 FT using 2-(Amino-cyclohexyl)propan-1,3-diol-linker"
 FT stem_loop 15..26 /tag= f
 FT misc_binding 15..17 /tag= g
 FT /bound_moiety= "Nucleotides 26-24"
 FT misc_binding 24..26 /tag= h
 FT /bound_moiety= "Nucleotides 17-15"
 FT modified_base 31


```

FT FT /*tag= i
FT FT /mod_base= OTHER
FT FT /note= "phosphorylated"
PN PN EP1236805-A1.
XX XX
PD PD 04-SEP-2002.
XX XX
XX XX 27-FEB-2002; 2002EP-00004483.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX XX
XX XX Jaeger S;
XX XX
XX XX WPI; 2002-610695/66.
XX XX
XX XX Amplification of a target nucleic acid region using a specific control
XX XX sequence.
XX XX
XX XX Example 1; Fig 3; 28pp; English.
XX XX
XX XX The invention relates to a method for amplification of a target nucleic
XX XX acid region in a sample using a specific control sequence. The invention
XX XX is also directed to a method of determination of a target nucleic acid
XX XX using a special control nucleic acid. Nucleic acids of the invention are
XX XX used as a control in a reaction for amplifying target nucleic acids and
XX XX as a control in a hybridisation reaction for determination of target
XX XX nucleic acids. The present sequence is a probe used to illustrate the
XX XX methods of the invention. Note: This sequence is stated to be same as
XX XX that shown as SEQ ID NO:4 in sequence listing. However this sequence has
XX XX additional T at its 3' end
XX XX
XX XX Sequence 31 BP; 4 A; 10 C; 5 G; 12 T; 0 U; 0 Other;
XX XX
XX XX Query Match 100.0%; Score 30; DB 6; Length 31;
XX XX Best Local Similarity 100.0%; Pred. NO. 0.0017;
XX XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
XX XX
RESULT 3
RAD43738
ID AAD43738 standard; DNA; 31 BP.
XX XX
XX XX AAD43738;
XX XX
XX XX 14-NOV-2002 (first entry)
XX XX
XX XX ST535 probe to illustrate the method of the invention.
DE ST535 target nucleic acid; control nucleic acid; probe; ss.
XX XX
XX XX Amplification; target nucleic acid; control nucleic acid; probe; ss.
XX XX
XX XX Unidentified.
XX XX
XX XX Key Location/Qualifiers
XX XX misc_feature 1
XX XX /*tag= a
XX XX /note= "Linked to Cy5 where Cy5 is Oligonucleotid-
XX XX derivatisation with pentamethin-di-indocarbocyanin using
XX XX alkylphosphatidyl-linker"
XX XX 2..12
XX XX /*tag= b
XX XX 2..5
XX XX /*tag= c
XX XX /bound_moiety= "Nucleotides 12-9"
XX XX 9..12
XX XX /*tag= d
XX XX

```

```

FT FT misc_feature /bound_moiety= "Nucleotides 5-2"
FT FT 13..14
FT FT /*tag= e
FT FT /note= "Linked via HEXs where HEXs is Oligonucleotid-
FT FT derivatisation with hexachloro-6-carboxy-fluorescein
FT FT using 2-(Amino-cyclohexyl)propan-1,3-diol-linker"
FT FT 15..26
FT FT /*tag= f
FT FT 15..17
FT FT /*tag= g
FT FT /bound_moiety= "Nucleotides 26-24"
FT FT 24..26
FT FT /*tag= h
FT FT /bound_moiety= "Nucleotides 17-15"
FT FT 31
FT FT /*tag= i
FT FT /mod_base= OTHER
FT FT /note= "Phosphorylated"
XX XX
XX XX EP1236804-A1.
XX XX
XX XX 04-SEP-2002.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX
XX XX 02-MAR-2001; 2001EP-00105172.
XX XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX XX
XX XX Jaeger S;
XX XX
XX XX WPI; 2002-610694/66.
XX XX
XX XX Amplification of a target nucleic acid region using control sequences.
XX XX
XX XX Example 1; Fig 2; 29pp; English.
XX XX
XX XX The invention relates to a method for amplification of a target nucleic
XX XX acid region. The method is useful for amplification of a nucleic acid
XX XX molecule using control nucleic acid sequences. The control nucleic acid
XX XX sequences are at least in part parallel-complementary to the sequence of
XX XX the target nucleic acid. The present sequence is ST2535 probe used to the
XX XX method of the invention. Note: This sequence is stated to be same as that
XX XX shown as SEQ ID NO:4 in sequence listing. However this sequence has
XX XX additional T at its 3' end
XX XX
XX XX Sequence 31 BP; 4 A; 10 C; 5 G; 12 T; 0 U; 0 Other;
XX XX
XX XX Query Match 100.0%; Score 30; DB 6; Length 31;
XX XX Best Local Similarity 100.0%; Pred. NO. 0.0017;
XX XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
XX XX
RESULT 4
AAH25420
ID AAH25420 standard; DNA; 31 BP.
XX XX
XX XX AAH25420;
XX XX
XX XX 22-AUG-2001 (first entry)
XX XX
XX XX Nucleotide sequence of a detection probe.
XX XX
XX XX Magnetic glass particle; nucleic acid purification; probe; ss.
XX XX
XX XX Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX XX

```

```
FT modified_base 1 /*tag= a
FT /*note= "derivatisation with a pentamethine-di-
FT indocarbocyanine via an alkylphosphatidyl linker"
FT misc_feature 14 /*tag= b
FT /*note= "2-(amino-cyclohexyl)-propane-1,3-diol-linker
FT modified_base 30 /*tag= c
FT /*note= "derivatised with a 3'-terminal phosphate group"
FT
FT WO200137291-A1.
XX
XX 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-EP011459.
XX
XX 17-NOV-1999; 99EP-00122853.
XX 12-MAY-2000; 2000EP-00110165.
XX
XX (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
XX Weindel K, Riedling M, Geiger A;
XX WPI; 2001-381247/40.
XX
XX Novel composition of magnetic glass particles for purification of DNA or
XX RNA in automated processes.
XX
XX Example 7; Page 101; 105pp; English.
XX
XX The specification describes a composition of magnetic glass particles,
XX which contain at least one magnetic object with a mean diameter between 5
XX -500 nm. The composition is useful for the purification of nucleic acids.
XX The composition can be used to process large quantities of nucleic acid
XX samples, because it does not involve the particles being centrifuged or
XX the fluids being drawn through glass fiber filters. The present sequence
XX represents a probe which is used in the course of the invention
XX
XX Sequence 31 BP; 4 A; 10 C; 5 G; 11 T; 0 U; 1 Other;
XX
XX Query Match 63.3%; Score 19; DB 4; Length 31;
XX Best Local Similarity 96.8%; Pred. No. 1.2e+02;
XX Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
XX 1 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 31
XX
XX RESULT 5
XX AAT32453/c
XX ID AAT32453 standard; DNA; 33 BP.
XX
XX AC AAT32453;
XX
XX 17-JAN-1997 (first entry)
XX
XX Probe, SK535, for detection of internal quantification standard.
XX
XX Probe; internal quantification standard; amplification; detection; ss.
XX
XX Synthetic.
XX
XX EP713921-A2.
XX
XX 29-MAY-1996.
XX
XX 15-NOV-1995; 95EP-00117981.
XX
XX 23-NOV-1994; 94US-00347657.
XX
```

```
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Picone TK;
XX
XX WPI; 1996-261341/27.
XX
XX Detecting a change in length of an oligonucleotide with a light-emitting
XX label - by measuring light emission in the presence of a DNA binding cpd.
XX
XX Example 1; Page 11; 16pp; English.
XX
XX The present sequence is the oligonucleotide probe SK535, which is
XX hexachlorofluorescein labelled, and used for the detection of an internal
XX quantification standard (IQS). The amplification of the IQS is used to
XX prep. a standard curve, to which the amplification of an unknown sample,
XX which is detected using a fluorescein labelled probe, is compared
XX
XX Sequence 33 BP; 12 A; 5 C; 11 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 63.3%; Score 19; DB 2; Length 33;
XX Best Local Similarity 96.8%; Pred. No. 1.2e+02;
XX Matches 30; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 TGGACTCAGTCCT-TGGTCATCTCACCTTCT 30
XX 31 TGGACTCAGTCCTCTGGTCATCTCACCTTCT 1
XX
XX RESULT 6
XX ADK11540/c
XX ID ADK11540 standard; DNA; 48 BP.
XX
XX AC ADK11540;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX RNAi primer 53 for isolating Drosophila genes.
XX
XX ss; cytosolic; cardiovascular; immunosuppressive; nephrotropic;
XX antirheumatic; antiarthritic; dermatological; antipsoriatic;
XX antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis;
XX cardiovascular disorder; autoimmune disease; glomerulonephritis;
XX rheumatoid arthritis; dermatological disorder; psoriasis;
XX inflammatory disorder; malaria; emphysema; alopecia; primer.
XX
XX Drosophila melanogaster.
XX
XX WO20003040301-A2.
XX
XX 15-MAY-2003.
XX
XX 23-OCT-2002; 2002WO-GB004780.
XX
XX 05-NOV-2001; 2001GB-00026506.
XX 27-NOV-2001; 2001GB-00028384.
XX 11-FEB-2002; 2002GB-00003185.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Deak P, Frenz L, Glover D, Midgley C;
XX
XX WPI; 2003-441540/41.
XX
XX New Drosophila polypeptides and polynucleotides, useful for diagnosing,
XX preventing and/or treating disorders, such as cancer, glomerulonephritis,
XX rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
XX
XX Disclosure; Page 79; 265pp; English.
XX
XX The invention relates to novel Drosophila species DNA sequences and their
XX encoded proteins with their corresponding human homologues. The proteins
XX or their encoding polynucleotides are useful in a method of prevention,
XX treatment or diagnosis of a disease in an individual, and used to
```

CC identify a substance capable of binding to the polypeptide or modulating
 CC the function of the polypeptide comprising incubating the polypeptide
 CC with a candidate substance and determining whether the substance binds to
 CC the polypeptide. The compositions are administered to an individual in
 CC need of such treatment. The method of diagnosis, in which the presence or
 CC absence of a polynucleotide is detected in a biological sample, comprises
 CC brining the biological sample containing the nucleic acid such as DNA or
 CC RNA into contact with a probe comprising a fragment of at least 15
 CC nucleotides of the polynucleotide, and detecting any duplex formed
 CC between the probe and nucleic acid in the sample. The method also
 CC comprises providing an antibody capable of binding to the polypeptide,
 CC incubating a biological sample with the antibody to allow the formation
 CC of an antibody-antigen complex, and determining whether antibody-antigen
 CC complex comprising the antibody is formed. The disease comprises a
 CC proliferative disease such as cancer. The antibody or identified
 CC substance is also useful in inhibiting the function of a polypeptide
 CC and/or regulating a cell division cycle function. The diseases also
 CC include cardiovascular disorders, autoimmune diseases such as
 CC glomerulonephritis and rheumatoid arthritis, and dermatological disorders
 CC such as psoriasis, inflammatory, fungal, and parasitic disorders such as
 CC malaria, emphysema and alopecia. The Drosophila sequences were isolated
 CC by a knockout mutation method using a P element and short interfering RNA
 CC (siRNA). Identification and isolation of the genes was done using RNAi
 CC primer targeted to the siRNA sequences. This sequence corresponds to
 CC primer used to amplify the Drosophila genes.

XX SQ Sequence 48 BP; 17 A; 11 C; 11 G; 9 T; 0 U; 0 Other;
 Query Match 58.7%; Score 17.6; DB 10; Length 48;
 Best Local Similarity 83.3%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 4;

Oy 2 GGACTCAGTCTTGTCATCTCAC 25
 |||||
 Db 41 GGCCTTGCTCTGGTCATCTCCC 18

RESULT 7
 ADG78921/c
 ID ADG78921 standard; DNA; 38 BP.
 AC ADG78921;
 XX
 DT 11-MAR-2004 (first entry)
 DE Schizophrenia diagnosis method-related PCR-sequencing primer #8.
 KW schizophrenia; polymorphism detection; calcineurin; CN;
 KW CN-interacting molecule; PCR; primer; ss; sequencing.
 OS Unidentified.

XX WO2003082210-A2.
 XX 09-OCT-2003.
 XX 26-MAR-2003; 2003WO-US009578.
 XX 26-MAR-2002; 2002US-0367944P.
 FR 07-MAR-2003; 2003US-0452813P.
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA (UYRU) UNIV ROCKEFELLER.

XX Gerber DJ, Karaviorgou M, Miyakawa T, Toneygawa S;
 XX WPI; 2003-803944/75.
 XX Diagnosing schizophrenia or susceptibility to schizophrenia comprises
 PT detecting a polymorphic variant of a polymorphism in a coding or non-
 PT coding portion of a gene encoding a calcineurin (CN) subunit or a CN
 PT interacting molecule.

PS Disclosure; Page 162; 177pp; English.
 CC The invention comprises a method of diagnosing schizophrenia or a
 CC susceptibility to schizophrenia. The method involves detecting a
 CC polymorphism in a gene encoding a calcineurin (CN) subunit or CN-
 CC interacting molecule. The method of the invention is useful for the
 CC diagnosis of schizophrenia or a susceptibility to schizophrenia. The
 CC present DNA sequence represents a PCR-sequencing primer that was used in
 CC the exemplification of the invention.

XX SQ Sequence 38 BP; 12 A; 13 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 56.0%; Score 16.8; DB 10; Length 38;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 2 GGACTCAGTCTTGTCATCTCACCTTC 29
 |||||
 Db 31 GGACTCAGTATTGGTCATAGCTGTTTC 4

RESULT 8
 ACI99856
 ID ACI99856 standard; DNA; 25 BP.
 XX ACI99856;
 XX 14-OCT-2003 (first entry)
 DE Human microarray DNA oligonucleotide SEQ ID NO 99847.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (APFY-) APFYMATRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 99847; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 3 A; 8 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 55.3%; Score 16.6; DB 9; Length 25;
 Best Local Similarity 82.6%; Pred. No. 1.3e+03;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GACTCAGTCTCTGGTGCATCTCAC 25
 |||||
 DB 3 GACTCAGTCTCTGGTGCATCTCAC 25

RESULT 9
 AAQ35233/c

ID AAQ35233 standard; DNA; 24 BP.

XX

AC AAQ35233;

XX

DT 25-MAR-2003 (revised)

DT 25-MAR-1993 (first entry)

XX

DE ANF detection primer 167-191.

XX

KW Primer; atrial natriuretic factor; ANF; recombination; hormone; atrial;
 KW cardiomyocytes; arterial pressure; cardiac output; vascular resistance;
 KW intravascular volume; FOI; hypotension; familial orthostatic intolerance;
 KW dizziness; mitral valve prolapse; clearance receptor; PCRFPLP;
 KW linkage relationship; ss.

OS Synthetic.

PN WO9300445-A1.

XX

PD 07-JAN-1993.

XX

PF 04-JUN-1992; 92WO-US004764.

XX

PR 20-JUN-1991; 91US-00718006.

XX

PA (UYVA-) UNIV VANDERBILT.

XX

PI Phillips JA, Vnencak-Jones CL;

XX

DR WPI; 1993-036390/04.

XX

PT Detecting gene deletions e.g. growth hormone deficiency - comprises PCR

PT amplification of fusion fragment and enzyme digestion.

XX

PS Disclosure; Page 30; 46pp; English.

XX The sequences given in AAQ35233-34 are primers which were used to amplify
 CC the atrial natriuretic factor (ANF) gene and to detect possible
 CC recombination events. ANF is a small peptide hormone synthesised by
 CC atrial cardiomyocytes. Infusion of ANF in man causes decreased arterial
 CC pressure due to decreased cardiac output and vascular resistance and
 CC decreased intravascular volume. Individuals with familial orthostatic
 CC intolerance (FOI) develop hypotension and dizziness on standing and may
 CC have mitral valve prolapse. Individuals in certain FOI kindreds have
 CC paradoxical increases in ANF levels on standing suggesting possible
 CC abnormalities in ANF or its clearance receptors. An intragenic ANF PCRFPLP
 CC was identified to map ANF and its linkage relationship to FOI was
 CC studied. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 24 BP; 8 A; 6 C; 8 G; 2 T; 0 U; 0 Other;

Query Match

54.7%; Score 16.4; DB 2; Length 24;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 GTCCTTGGTCACTCTCACC 26
 |||||
 DB 24 GTCCTTGGTCACTCTCACC 7

RESULT 10

AAK55829/c

ID AAK55829 standard; DNA; 46 BP.

XX

AC AAK55829;

XX

DT 09-JUL-1999 (first entry)

XX

DE PCR mutagenesis primer #912 from WO9918240 Example 6.

XX

KW Labelling; tag; molecular species; identification; property;
 KW characteristic; hybridisation; amplification; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO9918240-A2.

XX

PD 15-APR-1999.

XX

PF 05-OCT-1998; 98WO-US020874.

XX

PR 06-OCT-1997; 97US-00944410.

XX

PA (STRA-) STRATAGENE.

XX

PI Sorge JA;

XX

DR WPI; 1999-264040/22.

XX

PT Uniquely tagged molecules identifiable by a unique property or

PT characteristic.

XX

PS Example 6; Page 94; 138pp; English.

XX

CC The present invention describes a composition comprising a mixture of
 CC different species of molecules where each species is linked to a tag that
 CC is unique to that species and that encodes at least two variable
 CC positions on that species, where the tags can be identified without the
 CC need for first isolating each of the tags prior to identification. Liquid
 CC phase hybridisation system may be used for simultaneous identification of
 CC a large subset of targets out of a very large collection of similar of
 CC dissimilar molecular species. It may also be used to create tagged
 CC molecules that identify any collection of molecular species, e.g.
 CC peptides, antibodies, nucleic acids. Method bar codes collections or
 CC probes or analytes for use in a liquid phase hybridisation method. Tagged
 CC probes able to detect small changes or mutations in the target specimen.
 CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
 CC the concentration of the probe would not be limited by the solid support,
 CC both the target nucleic acids and the probes can diffuse toward each
 CC other, and signal amplification through cycling reactions could occur.
 CC Sequencing DNA with tags in combination with DNA amplification techniques
 CC means that there is no need for traditional sequencing methods or
 CC attaching to a solid phase, either the materials to be analysed or the
 CC tags. The present sequence represents a PCR primer which is used in an
 CC example from the present invention

SQ Sequence 46 BP; 11 A; 13 C; 12 G; 10 T; 0 U; 0 Other;

Query Match

54.7%; Score 16.4; DB 2; Length 46;

Best Local Similarity 76.9%; Pred. No. 1.8e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GACTCAGTCTCTGGTGCATCTCACCTT 28

|||||

DB 41 GACTCAGACCTTGTGATCTGACCTT 16

RESULT 11
ACK23341
ID ACK23341 standard; DNA; 25 BP.
XX
AC ACK23341;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 123322.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; diallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
FN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
WPI; 2003-567953/53.
XX
New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
XX
Claim 1; SEQ ID NO 123322; 9pp; English.
XX
The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.
XX
Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying allelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html
XX
Sequence 25 BP; 5 A; 8 C; 6 G; 6 T; 0 U; 0 Other;
Query Match 54.0%; Score 16.2; DB 9; Length 25;
Best Local Similarity 85.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 CAGTCTTGTCATCTCACT 27
DB 5 CAGTCCGTGTCATCACTT 25

RESULT 12
ADD19586/c
ID ADD19586 standard; DNA; 39 BP.
XX
AC ADD19586;
XX
DT 15-JAN-2004 (first entry)
XX
DE Oreochromis niloticus SNP OLA primer SEQ ID NO:221.
XX
KW single nucleotide polymorphism; SNP; fish; Salmo salar;
KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
KW detection; primer; ss.
XX
OS Synthetic.
OS Oreochromis niloticus.
XX
FN WO2003060160-A2.
XX
PD 24-JUL-2003.
XX
PF 17-JAN-2003; 2003WO-IB000112.
XX
PR 18-JAN-2002; 2002US-0349950P.
PR 16-AUG-2002; 2002US-0404200P.
XX
PA (GENO-) GENOMAR ASA.
XX
PI Lie O, Slettan A, Hoyum M, Lingaas F;
XX
WPI; 2003-627388/59.
XX
Novel isolated nucleic acid molecule comprising single nucleotide polymorphism associated with fish, useful for forming PCR primers which are used for detecting single nucleotide polymorphisms in fish nucleic acids.
XX
Claim 6; SEQ ID NO 221; 233pp; English.
XX
The present invention describes an isolated nucleic acid (I) comprising a single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs; and (ii) a nucleic acid having nucleotide sequence that hybridises to (i), or its complement under highly stringent hybridisation conditions. Also described: (1) an isolated oligonucleotide (II) comprising at least 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites, or their complement; (2) a primer pair (III) suitable for use in PCR, comprising two (II) capable of amplifying a nucleotide sequence chosen from S. salar SNPs and O. niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod polymorphic sites and seabass polymorphic sites; and determining (M1) the origin of fish sample comprising providing a parent genotype database comprising a collection of candidate parent genotypes, where each of the candidate parent genotype represents a distinct origin, and comparing a sample genotype to the parent genotype database, where a match between the sample genotype and one of the candidate parent genotype identifies to the origin of the sample. (M1) is useful for determining the origin of a fish sample such as family salmonidae, S. salar, Tilapia, O. niloticus, rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for detecting nucleic acid molecule comprising SNP in a sample, which involves contacting the sample containing nucleic acids with one or more (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus SNPs, and identifying nucleic acid that hybridises to (II). (II) is useful for detecting nucleic acid molecule comprising a polymorphic sequence in a sample, comprising contacting the sample containing nucleic acids with one or more (II) which is derived from O. niloticus microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic sites or seabass polymorphic sites, and identifying a nucleic acid that hybridises to (II). (III) is useful for detecting nucleic acid molecule comprising a microsatellite sequence in sample. The present sequence is used in the exemplification of the present invention.


```
XX 09-JAN-2003 (first entry)
XX Human leukocyte gene expression profiling probe SEQ ID NO 405.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX Homo sapiens.
XX WO2000257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 338; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 8 A; 14 C; 10 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 52.0%; Score 15.6; DB 6; Length 50;
XX Best Local Similarity 70.0%; Pred. No. 4.2e+03;
XX Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
XX ||||| ||| ||| ||||| |||
XX Db 13 TGCACCCAGTTCCTCTTATCTCAACTTAT 42
XX
XX RESULT 16
XX ABZ04927
XX ID ABZ04927 standard; DNA; 50 BP.
XX
XX AC ABZ04927;
XX
XX DT 09-JAN-2003 (first entry)
XX
XX DE Human leukocyte gene expression profiling probe SEQ ID NO 4918.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
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```
OS Homo sapiens.
XX WO2000257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quertermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1; Page 486; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
XX Sequence 50 BP; 8 A; 14 C; 11 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 52.0%; Score 15.6; DB 6; Length 50;
XX Best Local Similarity 70.0%; Pred. No. 4.2e+03;
XX Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
XX ||||| ||| ||| ||||| |||
XX Db 13 TGCACCCAGTTCCTCTTATCTCAACTTAT 42
XX
XX RESULT 17
XX ADP12630
XX ID ADP12630 standard; DNA; 50 BP.
XX
XX AC ADP12630;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE 50-mer oligonucleotide array probe #13.
XX
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; probe; ss.
XX
XX OS Homo sapiens.
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
XX
XX 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
```

XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX WPI; 2004-400724/37.
 XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 2; SEQ ID NO 2639; 1762pp; English.
 XX
 CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents an
 CC array probe to identify mRNA genes of the invention.
 XX
 SQ Sequence 50 BP; 8 A; 14 C; 10 G; 18 T; 0 U; 0 Other;
 Query Match 52.0%; Score 15.6; DB 12; Length 50;
 Best Local Similarity 70.0%; Pred. NO. 4.2e+03;
 Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
 |||||
 Db 13 TGCACCCAGTCTCCTTTATCTCACTTAT 42
 |||||
 RESULT 18
 ACK12515
 ID ACK12515 standard; DNA; 25 BP.
 XX
 AC ACK12515;
 XX
 DT 14-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 112496.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 PA (AFFY-) AFFYMETRIX INC.
 XX
 PI Mittmann MP;
 XX
 DR WPI; 2003-567953/53.
 XX
 XX New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX
 PS Claim 1; SEQ ID NO 112496; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 8 C; 5 G; 6 T; 0 U; 0 Other;
 Query Match 51.3%; Score 15.4; DB 9; Length 25;
 Best Local Similarity 76.0%; Pred. NO. 4.5e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GGACTCAGTCCTTGGTCATCTCACCC 26
 |||||
 Db 1 GGACTTCGACATGTGTAATCCACC 25
 |||||
 RESULT 19
 AA130996/c
 ID AA130996 standard; DNA; 31 BP.
 XX
 AC AA130996;
 XX
 DT 18-OCT-2001 (first entry)
 XX
 DE Human single nucleotide polymorphism (SNP) MHC2TA 5.
 XX
 KW Human; resequence; genotype; disease; forensic; paternity testing;
 KW single nucleotide polymorphism; SNP; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(16,A)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200166800-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-US007268.
 XX
 PR 07-MAR-2000; 2000US-0187510P.
 PR 22-MAY-2000; 2000US-0206129P.
 XX
 PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Cargill M, Ireland JS, Lander ES;
 XX
 DR WPI; 2001-522952/57.
 XX
 PT Nucleic acid molecules from the human genome which include polymorphic
 PT sites, useful in methods for predicting the presence, absence or severity

PT of a particular phenotype or disorder (e.g. diabetes) associated with a
 XX particular genotype.

PS Claim 1; Page 121; 145pp; English.

XX The invention relates to the identification of nucleic acid molecules
 CC (AA129513-AA13134) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing

XX SQ Sequence 31 BP; 7 A; 8 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 51.3%; Score 15.4; DB 4; Length 31;
 Best Local Similarity 76.0%; Pred. No. 4.7e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCAC 25
 ||||| || ||||| ||||| |||||
 Db 31 TGGACTAAGCCTTGGCCATGCC 7

RESULT 20

AAAD29041/c
 ID AAD29041 standard; DNA; 22 BP.

XX AC AAD29041;

XX DT 07-MAY-2002 (first entry)

XX DE Human G-protein coupled-receptor 7 gene expressing reverse PCR primer #1.

XX KW G-protein coupled-receptor; GPCR; therapy; diabetes; obesity; anorexia;
 KW cancer; neurodegenerative disorders; Alzheimer's; Parkinson's; dementia;
 KW haematopoietic disorder; immune disorder; cardiac disorder; haemostatic;
 KW Crohn's disease; angina pectoris; schizophrenia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; hypotension; hypertension; neuroleptic;
 KW human immuno deficiency virus; HIV; neuroprotective; immunomodulatory;
 KW asthma; immunogen; vaccine; nontropic; anorectic; anabolic; cytostatic;
 KW depression; ulcer; cardiant; hypotensive; hypertensive; osteoporosis;
 KW anticonvulsant; antiinflammatory; gastrointestinal; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200208289-A2.

XX PD 31-JAN-2002.

XX PF 26-JUL-2001; 2001WO-US023576.

XX PR 26-JUL-2000; 2000US-0221336P.

XX PR 05-OCT-2000; 2000US-0238333P.

XX PR 10-JAN-2001; 2001US-0260675P.

XX PR 22-FEB-2001; 2001US-0271025P.

XX PR 23-MAR-2001; 2001US-0278164P.

XX PR 02-APR-2001; 2001US-0280876P.

XX PA (CURA-) CURAGEN CORP.

XX PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Smithson G;

XX DR WPI; 2002-148464/19.

XX XX New G-protein coupled-receptor polypeptides and nucleic acids encoding
 XX PT them are useful in therapeutics e.g. cancer.

XX PS Example 1; Page 149; 168pp; English.

XX The present invention relates to an isolated G-protein coupled-receptor

CC (GPCRX) polypeptide and its nucleic acid. GPCR is useful in treating or
 CC preventing a GPCR-associated disorder and the predisposition to a
 CC disease associated with altered expression levels of this polypeptide.
 CC GPCR is useful for treating or preventing disorders such as; diabetes,
 CC obesity, anorexia, cancer, neurodegenerative disorders, Alzheimer's,
 CC Parkinson's, haematopoietic disorders, immune disorders, asthma, cardiac
 CC disorders, Crohn's disease, angina pectoris, ulcer, schizophrenia,
 CC depression, dementia, Huntington's disease, Gilles de la Tourette's
 CC syndrome, human immuno deficiency virus (HIV), hypotension, hypertension
 CC and osteoporosis. GPCR can be used as an immunogen to produce antibodies
 CC specific for the invention, as vaccines and in screening for potential
 CC agonistic and antagonistic compounds. The present sequence is human GPCR
 CC gene expressing PCR primer

XX SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 5.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTC 29
 ||||| ||||| ||||| |||||
 Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 21

AAAD29038/c

ID AAD29038 standard; DNA; 22 BP.

XX AC AAD29038;

XX DT 07-MAY-2002 (first entry)

XX DE Human G-protein coupled-receptor 6a gene expressing reverse PCR primer.

XX KW G-protein coupled-receptor; GPCR; therapy; diabetes; obesity; anorexia;
 KW cancer; neurodegenerative disorders; Alzheimer's; Parkinson's; dementia;
 KW haematopoietic disorder; immune disorder; cardiac disorder; haemostatic;
 KW Crohn's disease; angina pectoris; schizophrenia; Huntington's disease;
 KW Gilles de la Tourette's syndrome; hypotension; hypertension; neuroleptic;
 KW human immuno deficiency virus; HIV; neuroprotective; immunomodulatory;
 KW asthma; immunogen; vaccine; nontropic; anorectic; anabolic; cytostatic;
 KW depression; ulcer; cardiant; hypotensive; hypertensive; osteoporosis;
 KW anticonvulsant; antiinflammatory; gastrointestinal; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200208289-A2.

XX PD 31-JAN-2002.

XX PF 26-JUL-2001; 2001WO-US023576.

XX PR 26-JUL-2000; 2000US-0221336P.

XX PR 05-OCT-2000; 2000US-0238333P.

XX PR 10-JAN-2001; 2001US-0260675P.

XX PR 22-FEB-2001; 2001US-0271025P.

XX PR 23-MAR-2001; 2001US-0278164P.

XX PR 02-APR-2001; 2001US-0280876P.

XX PA (CURA-) CURAGEN CORP.

XX PI Padigar M, Mezes P, Mishra V, Burgess C, Casman S, Smithson G;

XX DR WPI; 2002-148464/19.

XX XX New G-protein coupled-receptor polypeptides and nucleic acids encoding
 XX PT them are useful in therapeutics e.g. cancer.

XX PS Example 1; Page 146; 168pp; English.

XX The present invention relates to an isolated G-protein coupled-receptor

CC (GPCRX) polypeptide and its nucleic acid. GPCR is useful in treating or

CC preventing a GPCR-associated disorder and the predisposition to a
 CC disease associated with altered expression levels of this polypeptide.
 CC GPCR is useful for treating or preventing disorders such as; diabetes,
 CC obesity, anorexia, cancer, neurodegenerative disorders, Alzheimer's,
 CC Parkinson's, haematopoietic disorders, immune disorders, asthma, cardiac
 CC disorders, Croun's disease, angina pectoris, ulcer, schizophrenia,
 CC depression, dementia, Huntington's disease, Gilles de la Tourette's
 CC syndrome, human immuno deficiency virus (HIV), hypotension, hypertension
 CC and osteoporosis. GPCR can be used as an immunogen to produce antibodies
 CC specific for the invention, as vaccines and in screening for potential
 CC agonistic and antagonistic compounds. The present sequence is human GPCR
 CC gene expressing PCR primer
 XX

SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 5.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
 ||||| ||||| ||||| |||||
 Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 22
 ID ABN89142/c
 XX ABN89142 standard; DNA; 22 BP.
 AC ABN89142;
 XX
 XX
 DT 28-AUG-2002 (first entry)
 DE Human GPCR2 reverse PCR primer SEQ ID NO:82.

XX Human; GPCR; GPCR; G protein-coupled receptor; antiatherosclerotic;
 KW anorectic; antibacterial; fungicide; protozoacide; virucide; analgesic;
 KW cytotatic; immunomodulator; metabolic; antiasthmatic; antiparkinsonian;
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
 KW antinfertility; neuroprotective; antianigmal; cardiant; antiulcer;
 KW antiallergic; nootropic; tranquiliser; neuroleptic; antidepressant;
 KW antimanic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;
 KW autoimmune disorder; infectious disease; PCR primer; ss.

OS Homo sapiens.
 OS Synthetic.

XX WO200226985-A2.

PN 04-APR-2002.

PD 28-SEP-2001; 2001WO-US030552.

XX 28-SEP-2000; 2000US-0236284P.

PR 28-SEP-2000; 2000US-0236286P.

PR 03-OCT-2000; 2000US-0237581P.

PR 06-OCT-2000; 2000US-0238735P.

PR 16-OCT-2000; 2000US-0240736P.

PR 05-JAN-2001; 2001US-0260019P.

PR 08-JAN-2001; 2001US-0260338P.

PR 17-JAN-2001; 2001US-0262156P.

PR 18-JAN-2001; 2001US-0262498P.

PR 19-JAN-2001; 2001US-0263133P.

PR 24-JAN-2001; 2001US-0263691P.

PR 02-FEB-2001; 2001US-0266109P.

PR 26-FEB-2001; 2001US-0271634P.

PR 27-SEP-2001; 2001US-00965422.

PI Spaderma SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;
 PI MacDougall JR, Smithson G, Li L, Malyankar UM, Taylor S, Gunther E;
 XX Tchernev VT;
 XX WPI; 2002-499868/53.
 XX Novel G-protein coupled-receptor polypeptides and nucleic acids for
 PT diagnosing, treating cardiomyopathy, atherosclerosis, cancer,
 PT neurodegenerative, autoimmune disorders, infectious diseases and
 PT diabetes.

PS Example 1; Page 158; 213pp; English.

XX ABN89112 to ABN89130 encoding the human G protein-coupled receptor
 CC (GPCR) proteins given in ABN81440 to ABN81458. GPCR proteins can have
 CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
 CC virucide, analgesic, cytostatic, immunomodulator, metabolic, hypotensive,
 CC antiasthmatic, antiparkinsonian, hypertensive, osteopathic, anti-HIV,
 CC antiinflammatory, antinfertility, neuroprotective, antianigmal,
 CC cardiant, antiulcer, antiallergic, nootropic, tranquiliser, neuroleptic,
 CC antidepressant, antimanic, anticonvulsant, haemostatic, hepatotropic,
 CC immunosuppressive, cerebroprotective, dermatological, antiaddictive,
 CC nephrotropic and gynaecological activities, and can be used in vaccines
 CC and gene therapy. GPCR proteins and polynucleotides can be used for
 CC treating or preventing a GPCR-associated disorder such as
 CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
 CC processing and metabolic pathway modulation, in a human. GPCR proteins
 CC and polynucleotides can also be used in the manufacture of a medicament
 CC for preventing or treating disorders or syndromes including developmental
 CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
 CC disorders, autoimmune disorders, infectious diseases and diabetes.
 CC ABN89131 to ABN89187 represent PCR primers and probes used in the
 CC exemplification of the present invention
 XX

SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 6; Length 22;
 Best Local Similarity 85.0%; Pred. No. 5.4e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
 ||||| ||||| ||||| |||||
 Db 21 TCCTTTCATCTCTCCTTC 2

RESULT 23

ABN89136/c

ID ABN89136 standard; DNA; 22 BP.

XX ABN89136;

XX 28-AUG-2002 (first entry)

DT Human GPCR2 reverse PCR primer SEQ ID NO:76.

XX Human; GPCR; GPCR; G protein-coupled receptor; antiatherosclerotic;
 KW anorectic; antibacterial; fungicide; protozoacide; virucide; analgesic;
 KW cytotatic; immunomodulator; metabolic; antiasthmatic; antiparkinsonian;
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
 KW antinfertility; neuroprotective; antianigmal; cardiant; antiulcer;
 KW antiallergic; nootropic; tranquiliser; neuroleptic; antidepressant;
 KW antimanic; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;
 KW autoimmune disorder; infectious disease; PCR primer; ss.

OS Homo sapiens.

OS Synthetic.

XX WO200226985-A2.

XX 04-APR-2002.

PI Spytek KA, Casman S, Padigar M, Dickson K, Vernet C;

```

XX PF 28-SEP-2001; 2001WO-US030552.
XX PR 28-SEP-2000; 2000US-0236284P.
XX PR 28-SEP-2000; 2000US-0236286P.
XX PR 03-OCT-2000; 2000US-0237581P.
XX PR 06-OCT-2000; 2000US-0238735P.
XX PR 16-OCT-2000; 2000US-0240736P.
XX PR 05-JAN-2001; 2001US-0260013P.
XX PR 08-JAN-2001; 2001US-0260338P.
XX PR 17-JAN-2001; 2001US-0262156P.
XX PR 18-JAN-2001; 2001US-0262498P.
XX PR 19-JAN-2001; 2001US-0263133P.
XX PR 02-FEB-2001; 2001US-0263691P.
XX PR 04-FEB-2001; 2001US-0266109P.
XX PR 26-FEB-2001; 2001US-0271634P.
XX PR 27-SEP-2001; 2001US-00965422.
XX (CURA-) CURAGEN CORP.
XX
XX Spytek KA, Casman S, Padigaru M, Dickson K, Vernet C;
PI Spaderna SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;
PI MacDougall JR, Smithson G, Li L, Malyankar UM, Taylor S, Gunther E;
PI Tchernev VT;
XX
XX WPI; 2002-499868/53.
XX
XX Novel G-protein coupled-receptor polypeptides and nucleic acids for
PT diagnosing, treating cardiomyopathy, atherosclerosis, cancer,
PT neurodegenerative, autoimmune disorders, infectious diseases and
PT diabetes.
XX
XX Example 1; Page 158; 213pp; English.
XX
XX ABN89112 to ABN89130 encoding the human G protein-coupled receptor
CC (GPCRX) proteins given in ABN81440 to ABN81458. GPCRX proteins can have
CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
CC virucide, analgesic, cytostatic, immunomodulator, metabolic, hypotensive,
CC antiasthmatic, antiparkinsonian, hypertensive, osteopathic, anti-HIV,
CC antiinflammatory, antifertility, neuroprotective, antiangiinal,
CC cardiant, antitumor, antiallergic, nootropic, tranquilizer, neuroleptic,
CC antidepressant, antinamic, anticonvulsant, haemostatic, hepatotropic,
CC immunosuppressive, cerebroprotective, dermatological, antiaddictive,
CC nephrotropic and gynaecological activities, and can be used in vaccines
CC and gene therapy. GPCRX proteins and polynucleotides can be used for
CC treating or preventing a GPCRX-associated disorder such as
CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
CC processing and metabolic pathway modulation, in a human. GPCRX proteins
CC and polynucleotides can also be used in the manufacture of a medicament
CC for preventing or treating disorders or syndromes including developmental
CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
CC disorders, autoimmune disorders, infectious diseases and diabetes.
CC ABN89111 to ABN89187 represent PCR primers and probes used in the
CC exemplification of the present invention
XX
XX Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;
SQ
Query Match 50.7%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCTTC 2
RESULT 24
ABT05749/c
ID ABT05749 standard; DNA; 22 BP.
XX
XX AC ABT05749;
XX
XX 16-OCT-2002 (first entry)
DT

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XX GPCR related reverse PCR primer SEQ ID No 202.
XX
XX Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX;
XX antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;
XX hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
XX anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
XX diabetes; metabolic disorder; diabetes; obesity; infectious disease;
XX Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
XX anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;
XX metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;
XX congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
XX congenital heart defect; aortic stenosis; congenital adrenal hyperplasia;
XX transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
XX prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
XX hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
XX graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
XX multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
XX gene therapy; transgenic animal; PCR; primer; ss.
XX
XX Unidentified.
XX
XX WO200246229-A2.
XX
XX 13-JUN-2002.
XX
XX 05-DEC-2001; 2001WO-US046530.
XX
XX 05-DEC-2000; 2000US-0251459P.
XX 29-DEC-2000; 2000US-0259007P.
XX 04-DEC-2001; 2001US-00005041.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Casman SJ, Padigaru M, Burgess CE, Shimkets RA, Spytek KA;
XX Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CM;
XX Dickinson KS, Ballinger RA, Wolenc AR;
XX
XX WPI; 2002-537559/57.
XX
XX Novel isolated G-protein coupled receptor polypeptide, designated NOVX,
XX useful for treating or preventing in human receptor-associated disorders
XX e.g. cardiomyopathy, atherosclerosis or diabetes.
XX
XX Example 2; Page 247; 264pp; English.
XX
XX The invention relates to a novel isolated G-protein coupled receptor X
XX (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide
XX and the antibody of the isolated protein is useful for treating or
XX preventing a GPCRX-associated disorder in a subject, preferably human,
XX where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
XX isolated protein, its encoding polynucleotide and the antibody of the
XX isolated protein is useful for treating or preventing metabolic
XX disorders, diabetes, obesity, infectious disease, anorexia,
XX neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
XX immune disorders, haematopoietic disorders, and various dyslipidaemias,
XX metabolic disturbances associated with obesity, the metabolic syndrome X,
XX wasting disorders associated with chronic diseases, and cancer. The
XX disorders also include cardiomyopathy, atherosclerosis, hypertension,
XX congenital heart defects, aortic stenosis, subaortic stenosis,
XX transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,
XX prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
XX fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
XX purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
XX asthma, Crohn's disease, and multiple sclerosis. The isolated protein,
XX its encoding polynucleotide and the antibody of the isolated protein is
XX useful in screening assays, detection assays (e.g., chromosomal mapping,
XX tissue typing, forensic biology). The isolated polynucleotide is useful
XX in gene therapy, to express the isolated protein, to detect GPCRX mRNA or
XX a genetic lesion in a GPCRX gene, and to modulate GPCRX activity. The
XX cell of the invention is useful for producing non-human transgenic
XX animals. This polynucleotide sequence represents a reverse PCR primer of
XX a GPCRX protein of the invention
XX

```

SQ Sequence 22 BP; 11 A; 0 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 6; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
Db 21 TCCTTTCATCTCTCTCTC 2
RESULT 25
AAV27123/c
ID AAV27123 standard; DNA; 24 BP.
XX
AC AAV27123;
XX
DT 28-SEP-1998 (first entry)
XX
DE Synthetic human prollyl-4-hydroxylase PCR primer.
XX
KW collagen III; yeast expression vector; production; prollyl-4-hydroxylase;
KW PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9818918-A1.
XX
PD 07-MAY-1998.
XX
PF 29-OCT-1997; 97WO-AU000721.
XX
PR 29-OCT-1996; 96AU-00003310.
XX
PR 19-DEC-1996; 96AU-00004306.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
PI Vaughan PR, Galanis M, Ramshaw JAM, Werkmeister JA;
XX WPI; 1998-272214/24.
XX
XX Stable expression of hydroxylated triple helical proteins - using yeast
PT transformed with nucleotide sequences encoding prollyl 4-hydroxylase
PT subunits and products such as collagen polypeptides.
XX
PS Example 1; Page 11; 45pp; English.
XX
CC The sequence is that of a PCR primer which was used in the construction
CC of a yeast vector for the co-ordinated co-expression of the alpha and
CC beta subunits of Prollyl-4-hydroxylase
XX
SQ Sequence 24 BP; 9 A; 4 C; 10 G; 1 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 2; Length 24;
Best Local Similarity 85.0%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 10 TCCTTGGTCATCTCACCTTC 29
Db 20 TCCTTGGTCATCTCACCTTC 1
RESULT 26
AAL56525/c
ID AAL56525 standard; DNA; 33 BP.
XX
AC AAL56525;
XX
DT 04-DEC-2003 (first entry)
XX
DE PCR primer 1b related to human clathrin light chain polypeptide 9-02.
XX

KW Human clathrin light chain polypeptide-9.02; cancer; HIV infection; PCR;
KW primer; ss.
XX
OS Homo sapiens.
XX
PN CN1381482-A.
XX
PD 27-NOV-2002.
XX
PF 18-APR-2001; 2001CN-00112630.
XX
PR 18-APR-2001; 2001CN-00112630.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-258235/26.
XX
PT Polypeptide-clathrin light chain -9.02 and polynucleotide for coding it.
XX
PS Disclosure; Page 31; Opp; Chinese.
XX
CC This invention relates to a clathrin light chain polypeptide-9.02 and the
CC nucleotide sequence encoding the polypeptide of the invention. The
CC polypeptide may be used to treat diseases such as cancer and HIV
CC infection. The present sequence is that of PCR primer 1b related to the
CC human clathrin light chain polypeptide-9.02 of the invention and used in
CC example 5 of the specification. Note: This sequence, assigned Seq ID 5 in
CC the sequence listing differs from Seq ID 5 in example 5 of the
CC specification. The alternative sequence is given in AAL56517
XX
SQ Sequence 33 BP; 12 A; 10 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 50.7%; Score 15.2; DB 10; Length 33;
Best Local Similarity 71.4%; Pred. No. 5.8e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 3 GACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 32 GAGTCAGTCCTTGGTCATCTCACCTAT 5
RESULT 27
AAZ32382/c
ID AAZ32382 standard; DNA; 37 BP.
XX
AC AAZ32382;
XX
DT 26-JAN-2000 (first entry)
XX
DE Receptor construct IR-Delta-685 sense PCR primer.
XX
KW Receptor construct; soluble insulin receptor; IgG; immunoglobulin G;
KW fusion protein; insulin binding protein; growth factor; PCR primer;
KW insulin specific tyrosine kinase; screening; mimetic; ss.
XX
OS Synthetic.
XX
PN EP957164-A1.
XX
PD 17-NOV-1999.
XX
PF 15-MAY-1998; 98EP-00201633.
XX
PR 15-MAY-1998; 98EP-00201633.
XX
PA (NOVO) NOVO-NORDISK AS.
XX
PI Kristensen C;
XX
DR WPI; 1999-621951/54.
XX

PT Polypeptides used for the screening of ligands capable of binding to an
 XX insulin specific tyrosine kinase.

PS Example 1; Page 7; 17pp; English.

XX The present invention describes a polypeptide (I), with a molecular
 CC weight of 40-100KD, which is capable of binding to insulin. Also
 CC described are: (1) a fusion polypeptide comprising (I) and another
 CC polypeptide capable of facilitating expression, purification and/or
 CC crystallisation of the polypeptide; (2) a process of producing a
 CC polypeptide, where a cell containing a recombinant expression vector
 CC comprising a DNA fragment encoding (I), is cultured to promote the
 CC expression of (I), (I) being recovered from the culture; and (3) an
 CC insulin mimetic which has insulin activity when bound to an insulin
 CC receptor in vivo, and which is capable of binding to (I). (I) is used for
 CC the screening of ligands binding to the polypeptide, and for screening
 CC for insulin mimetics. The insulin mimetics isolated may be oral insulin
 CC mimetics which can be formulated into tablets or other oral medicaments.
 CC The polypeptide due to its size, may be co-crystallised with insulin
 CC making it possible to obtain knowledge of the structure- activity
 CC relationship. The present sequence represents a PCR primer used in the
 CC construction of receptor constructs, which are expressed as soluble
 CC insulin receptor (IR) immunoglobulin G (IgG) fusion proteins, in the
 CC exemplification of the present invention

XX SQ Sequence 37 BP; 12 A; 11 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 2; Length 37;
 Best Local Similarity 71.4%; Pred. No. 6e+03;
 Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTACCTTCT 30
 |||||
 DB 29 GAGTCTGTCCTTGGACAGTAGCCTTGT 2

RESULT 28

AAT91980
 ID AAT91980 standard; DNA; 39 BP.

AC AAT91980;

XX 13-FEB-1998 (first entry)

DE Primer 8 for rat thrombomodulin DNA amplification.

KW rat; thrombomodulin; thrombin; activation; protein C;
 KW recombinant production; PCR primer; amplify; ss.

XX Synthetic.

PN JP09268200-A.

XX 14-OCT-1997.

PF 01-APR-1996; 96JP-00078494.

XX 01-APR-1996; 96JP-00078494.

PA (ASAH) ASAH KASEI KOGYO KK.

XX WPI; 1997-554712/51.

XX Recombinant production of rat thrombomodulin - which promotes thrombin
 PT activation of protein C.

PS Example 3; Page 22; 28pp; Japanese.

XX This PCR primer was used to amplify DNA encoding rat thrombomodulin (TM).
 CC TM upon binding thrombin, promotes thrombin activation of protein C. Host
 CC cells transformed with the DNA can be used for the large scale
 CC recombinant production of the peptide, or rat thrombomodulin

XX

SQ Sequence 39 BP; 11 A; 12 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 2; Length 39;
 Best Local Similarity 85.0%; Pred. No. 6e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 CAGTCCTTGGTCATCTACCC 26
 |||||
 DB 14 CAGTCCTTGGTCATCTGACC 33

RESULT 29

ADQ94820
 ID ADQ94820 standard; DNA; 50 BP.

AC ADQ94820;

XX 23-SEP-2004 (first entry)

DE Generic binding agent associated primer seqid 13.

XX binding agent; beta barrel conformation; replicable vector;
 KW binding agent library; machine-accessible medium; immunoassay; PCR;
 KW primer; ss.

XX Synthetic.

XX US2004126769-A1.

XX 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335181.

XX 30-DEC-2002; 2002US-00335181.

XX (QUIR/) QUIRK S.

XX Quirk S;

XX WPI; 2004-591378/57.

XX New isolated binding agents, useful for binding, detecting or identifying
 PT a target molecule (e.g. antigen or antigenic epitope), or for detecting
 PT or isolating a target in a sample suspected of containing the target.

PS Example 1; SEQ ID NO 13; 60pp; English.

XX The invention describes an isolated binding agent comprising a
 CC polypeptide: having an amino acid sequence selected from 2 sequences of
 CC 134 amino acids (SEQ ID NO: 2 and 4) given in the specification; or
 CC having a beta barrel conformation, where the polypeptide comprises a
 CC sequence of 134 amino acids (SEQ ID NO: 37) given in the specification.
 CC Also described are: an isolated nucleic acid encoding SEQ ID NO: 2 or 4,
 CC or comprising SEQ ID NO: 25, 26, 27, 28 or 29 (sequences not defined in
 CC the specification); an expression vector comprising a promoter and a
 CC nucleic acid encoding a polypeptide comprising SEQ ID NO: 2, 4 or 37; a
 CC library of binding agents where each binding agent in the library
 CC comprises a polypeptide comprising SEQ ID NO: 2 or 37; making a library
 CC of binding agent nucleic acids; making a library of replicable vectors
 CC that encode binding agent polypeptides; making a library of binding agent
 CC polypeptides; a computer implemented method of making a library of
 CC binding agents; a system for generating peptide sequences; and a machine-
 CC accessible medium. The specifically claimed binding agent comprises a
 CC sequence selected from 2 fully defined sequences of 134 amino acids (SEQ
 CC ID NO: 2 and 4) given in the specification. The binding agents can be
 CC used to bind, detect or identify a target molecule, such as an antigen or
 CC containing the target, in immunoassays where antibodies are commonly
 CC employed. This sequence represents a primer used in the creation of
 CC generic binding agent DNA ADQ94810.

XX Sequence 50 BP; 9 A; 13 C; 11 G; 17 T; 0 U; 0 Other;

Query Match 50.7%; Score 15.2; DB 12; Length 50;
Best Local Similarity 71.4%; Pred. No. 6.3e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCTGGTGCATCTCACCCTTCT 30
| | | | | | | | | | | | | | | | | | | | | |
Db 6 GACTCTGTAAAGGTCGTTTCCACCATCT 33
| | | | | | | | | | | | | | | | | | | | | |

RESULT 30
ACK06327
ID ACK06327 standard; DNA; 25 BP.
XX
AC ACK06327;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 106308.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 106308; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 3 A; 8 C; 4 G; 10 T; 0 U; 0 Other;

Query Match 50.0%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 6.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCTCTGTCATCTC 23
| | | | | | | | | | | | | | | | | | | | | |
Db 3 TGGACCCTCTACTTGGTCTTCTC 25
| | | | | | | | | | | | | | | | | | | | | |

RESULT 31
ACK06326
ID ACK06326 standard; DNA; 25 BP.
XX
AC ACK06326;
XX
DT 14-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 106307.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 106307; 9pp; English.
XX
CC The invention discloses a microarray comprising a plurality of nucleic
CC acid probes including one of 2,018,500 fully defined sequences, or its
CC perfect match, perfect mismatch, antisense match or antisense mismatch.
CC Also disclosed is a method of gene expression analysis. The array is used
CC in monitoring gene expression levels by hybridisation to a DNA library,
CC in analysis of genetic variation or in hybridisation of tag-labelled
CC compounds. The nucleic acid probes are specifically designed for analysis
CC of at least one target sequence. The method of analysis comprises
CC hybridising at least one or more nucleic acids to at least two or more
CC nucleic acid probes and detecting the hybridisation. The nucleic acid
CC probes are attached to a solid support. The analysis comprises monitoring
CC gene expression levels, identifying biallelic markers or polymorphisms,
CC or family members of a gene and a cross-species comparison. Each of the
CC nucleic acids further comprises a tag sequence. The array of nucleic acid
CC probes is useful in situ hybridisation, in Southern, Northern or dot-
CC blot hybridisation to identify or detect the sequence or specific
CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
CC primer extensions or in screening cDNA or genomic libraries or subclones
CC for additional subclones containing segments of DNA that have been
CC isolated and previously sequenced. The sequence presented is one of the
CC nucleic acid probes incorporated in the microarray. Note: The sequence
CC data for this patent can also be obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 25 BP; 2 A; 8 C; 4 G; 11 T; 0 U; 0 Other;

QY 1 TGGACTCAGTCTTGGTCATCTC 23
 DB 3 TGGACCCCTCTTCTGGTCTCTC 25

RESULT 32
 ACI99857
 ID ACI99857 standard; DNA; 25 BP.
 XX AC ACI99857;
 XX 14-OCT-2003 (first entry)
 XX Human microarray DNA oligonucleotide SEQ ID NO 99848.
 DE EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX Homo sapiens.
 OS US2003104410-A1.
 PN 05-JUN-2003.
 PD 15-MAR-2002; 2002US-00098263.
 XX 16-MAR-2001; 2001US-02767599.
 PR (APFY-) APFYMATRIX INC.
 XX Mittmann MP;
 PI WPI; 2003-567953/53.
 DR New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 PT sequence or specific mutations of any gene.
 XX Claim 1; SEQ ID NO 99848; 9pp; English.

CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one target sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX Sequence 25 BP; 4 A; 8 C; 6 G; 7 T; 0 U; 0 Other;
 SQ Query Match 50.0%; Score 15; DB 9; Length 25;
 Best Local Similarity 78.3%; Pred. No. 6.8e+03;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTAGGTCGTCTCTC 25
 DB 3 GACTCAGTCCTAGGTCGTCTCTC 25

RESULT 33
 ADM35884
 ID ADM35884 standard; DNA; 42 BP.
 XX AC ADM35884;
 XX 03-JUN-2004 (first entry)
 XX Human RANTES/ER retention signal PCR primer, SEQ ID NO:28.
 DE Human; RANTES; chemokine; chemokine receptor 5; CCR5;
 KW expression inhibition; intracellular immunisation; animal model;
 KW HIV-1 resistant phenotype; HIV-1 infection;
 KW chemokine receptor-related disease; anti-HIV; gene therapy;
 KW endoplasmic reticulum retention signal; PCR; primer; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2004013330-A1.
 PN 12-FEB-2004.
 PD 10-JUL-2003; 2003WO-ES000350.
 XX 26-JUL-2002; 2002ES-00001776.
 PR (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 XX (GENE-) GENETRIX SL.
 PI Gonzalez De La Pena MA, Serrano Gomez F, Abad Miquel J L;
 PI Bernard Miana A, Llorente Gomez MDLM, Martinez Alonso C;
 PI Garmendia Mendizabal C;
 XX WPI; 2004-157133/15.
 DR New genetic construct that inhibits expression of the CCR5 receptor,
 PT useful for preparing vectors for gene therapy of human immune deficiency
 PT virus infection and a murine model of immunization.
 XX Example 15; SEQ ID NO 28; 92pp; Spanish.

CC The invention relates to a genetic construct that, when expressed
 CC intracellularly, specifically inhibits expression of the human chemokine
 CC receptor CCR5. The genetic construct may encode a ribozyme directed
 CC against the CCR5 mRNA (ADM35860), or a multicatalytic ribozyme containing
 CC several consecutive functional units from one or more ribozymes
 CC (ADM35869). In addition to a ribozyme, the construct may also encode the
 CC chemokine RANTES which is modified to contain an endoplasmic reticulum
 CC retention signal (ADM35872) and which is preferably mutated to inactivate
 CC its signalling properties. Alternatively, the genetic construct of the
 CC invention may encode an N-terminal part of CCR5 (including 2-6
 CC transmembrane domains) with an endoplasmic reticulum retention signal and
 CC in which the region corresponding to the extracellular part is replaced
 CC with a domain which binds the N-terminal region of CCR5 (such as RANTES),
 CC and the construct may additionally encode an anti-CCR5 ribozyme in the
 CC 3'UTR. The invention also relates to a eukaryotic expression vector or a
 CC retroviral vector containing a genetic construct of the invention; a
 CC eukaryotic cell transformed with the vector; and an animal model of
 CC intracellular immunisation against HIV-1 developed from NOD/Scid mice
 CC using the vectors. The genetic constructs of the invention inhibit
 CC surface expression of CCR5, thereby mimicking the phenotype of HIV-1
 CC resistance in individuals where CCR5 is inactivated by mutation. The
 CC constructs are used to prepare expression or retroviral vectors for the
 CC establishment of a murine model of intracellular immunisation against HIV
 CC to test the effectiveness of the genetic constructs in restricting
 CC infection with macrophage-tropic strains of HIV-1. The vectors may also
 CC be used in gene therapy of humans who are seropositive for HIV-1,
 CC particularly in the early stages of infection, or who have a disease that
 CC involves chemokine receptors closely related, structurally and


```
XX Human; calmodulin 9.02; phosphatidylinositol signal pathway dysfunction;  
KW PCR; primer; ss.  
XX  
XX Homo sapiens.  
XX CN1333273-A.  
XX  
XX 30-JAN-2002.  
XX  
XX 07-JUL-2000; 2000CN-00117090.  
XX  
XX 07-JUL-2000; 2000CN-00117090.  
PR (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.  
XX  
XX Mao Y, Xie Y;  
XX WPI; 2002-305590/35.  
XX  
XX Novel polypeptide human calmodulin 9.02 and polynucleotide for encoding  
PT said polypeptide.  
XX  
XX Example 2; Page 18 (Disclosure); 33pp; Chinese.  
XX  
XX The invention relates to human calmodulin 9.02 (AB83796), the  
CC polynucleotide (ABN8528) encoding said polypeptide and the method for  
CC producing this polypeptide by recombinant DNA technology. The invention  
CC also discloses the method for curing several diseases, such as  
CC phosphatidylinositol signal pathway dysfunction related diseases by the  
CC polypeptide. The invention also discloses an antagonist for resisting the  
CC polypeptide and its therapeutic action and the application of  
CC polynucleotide coding this novel human calmodulin 9.02. The present  
CC sequence is that of a human calmodulin 9.02 PCR primer, useful in  
CC examples of the invention  
XX  
SQ Sequence 24 BP; 0 A; 10 C; 3 G; 11 T; 0 U; 0 Other;  
Query Match 49.3%; Score 14.8; DB 6; Length 24;  
Best Local Similarity 88.9%; Pred. No. 8.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 12 CTTGGTCATCTCACCTTC 29  
Db 1 CTTGGTCATCTCACCTTC 18  
RESULT 37  
ADN97703  
ID ADN97703 standard; DNA; 30 BP.  
XX  
XX ADN97703;  
XX  
XX 15-JUL-2004 (first entry)  
DE  
DE Primer KF43.  
XX  
XX antibacterial; immunosuppressive; antirheumatic; antiarthritic;  
KW anthelmintic; insecticide; biosynthesis; macrolide; antibiotic;  
KW spiramycin; veterinary medicine; immunosuppressant; transplant rejection;  
KW rheumatoid arthritis; autoimmune disease; insecticide; anthelmintic;  
KW avermectin; primer; ss.  
XX  
XX Streptomyces ambofaciens.  
XX  
XX WO2004033689-A2.  
PN  
XX  
XX 22-APR-2004.  
XX  
XX 08-OCT-2003; 2003WO-FR002962.  
PF  
XX 08-OCT-2002; 2002FR-00012489.  
PR 27-FEB-2003; 2003FR-00002439.  
XX
```

```
PR 07-AUG-2003; 2003US-0493490P.  
XX  
XX (AVET ) AVENTIS PHARMA SA.  
XX (CNRS.) CNRS.  
XX  
XX Blondelet-Rouault M, Dominguez H, Darbon-Rongere E, Gerbaud C;  
PI Gondran A, Karray F, Lacroix P, Oestreicher-Mermet- Bouvier N;  
PI Pernodet J, Tuppelle K;  
XX  
XX WPI; 2004-330455/30.  
XX  
XX New polynucleotides encoding proteins involved in spiramycin  
PT biosynthesis, useful for improving synthesis of macrolide antibiotics or  
PT for generating new hybrid macrolides.  
XX  
XX Example 28; SEQ ID NO 154; 480pp; French.  
XX  
XX The invention relates to polynucleotides that encode polypeptides  
CC involved in biosynthesis of the macrolide antibiotic spiramycin (A), or  
CC equivalents within the degeneracy of the genetic code. The  
CC polynucleotides and polypeptides are used: (a) to improve production  
CC (optionally also purity) of macrolides (M), especially spiramycins; and  
CC (b) to produce hybrid antibiotics. The macrolides are useful in human and  
CC veterinary medicine as antibiotics, but some are also immunosuppressants  
CC (e.g. FK506) useful for treating transplant rejection, rheumatoid  
CC arthritis and other autoimmune diseases; or insecticides and  
CC anthelmintics (e.g. avermectin). This sequence corresponds to a PCR  
CC primer to amplify the spiramycin biosynthetic genes from Streptomyces  
CC ambofaciens.  
XX  
SQ Sequence 30 BP; 5 A; 9 C; 6 G; 10 T; 0 U; 0 Other;  
Query Match 49.3%; Score 14.8; DB 12; Length 30;  
Best Local Similarity 88.9%; Pred. No. 8.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 11 CTTGGTCATCTCACCTT 28  
Db 13 CTTGGTCATCTCACCTT 30  
RESULT 38  
AAX55831/c  
ID AAX55831 standard; DNA; 46 BP.  
XX  
XX AAX55831;  
XX  
XX 09-JUL-1999 (first entry)  
XX  
XX PCR mutagenesis primer #914 from WO9918240 Example 6.  
XX  
XX Labelling; tag; molecular species; identification; property;  
KW characteristic; hybridisation; amplification; PCR primer; ss.  
XX  
XX Synthetic.  
XX  
XX WO9918240-A2.  
XX  
XX 15-APR-1999.  
XX  
XX 05-OCT-1998; 98WO-US020874.  
XX  
XX 06-OCT-1997; 97US-00944410.  
XX  
XX (STRA-) STRATAGENE.  
XX  
XX Sorge JA;  
XX  
XX WPI; 1999-264040/22.  
XX  
XX Uniquely tagged molecules identifiable by a unique property or  
PT characteristic.  
XX
```

```

PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention
XX
SQ Sequence 46 BP; 10 A; 13 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 46;
Best Local Similarity 73.1%; Pred. No. 9.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGTCATCTCACCTT 28
Db 41 GACTCAGACCTTGTCGACGTGACGTT 16

RESULT 39
AAXS5830/c
ID AAXS5830 standard; DNA; 46 BP.
XX
AC AAXS5830;
XX
DT 09-JUL-1999 (first entry)
XX
DE PCR mutagenesis primer #913 from WO9918240 Example 6.
XX
KW Labelling; tag; molecular species; identification; property;
KW characteristic; hybridisation; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9918240-A2.
XX
PD 15-APR-1999.
XX
PF 05-OCT-1998; 98WO-US020874.
XX
PR 06-OCT-1997; 97US-00944410.
XX
PA (STRA-) STRATAGENE.
XX
PI Sorge JA;
XX
DR WPI; 1999-264040/22.
XX
PT Uniquely tagged molecules identifiable by a unique property or
PT characteristic.
XX
PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or
CC probes or analytes for use in a liquid phase hybridisation method. Tagged
CC probes able to detect small changes or mutations in the target specimen.
CC Use of molecular tags overcomes difficulties of prior art methods, e.g.
CC the concentration of the probe would not be limited by the solid support,
CC both the target nucleic acids and the probes can diffuse toward each
CC other, and signal amplification through cycling reactions could occur.
CC Sequencing DNA with tags in combination with DNA amplification techniques
CC means that there is no need for traditional sequencing methods or
CC attaching to a solid phase, either the materials to be analysed or the
CC tags. The present sequence represents a PCR primer which is used in an
CC example from the present invention
XX
SQ Sequence 46 BP; 10 A; 13 C; 13 G; 10 T; 0 U; 0 Other;
Query Match 49.3%; Score 14.8; DB 2; Length 46;
Best Local Similarity 73.1%; Pred. No. 9.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGTCATCTCACCTT 28
Db 41 GACTCAGACCTTGTCGACGTGACGTT 16

RESULT 40
AAXS5832/c
ID AAXS5832 standard; DNA; 46 BP.
XX
AC AAXS5832;
XX
DT 09-JUL-1999 (first entry)
XX
DE PCR mutagenesis primer #915 from WO9918240 Example 6.
XX
KW Labelling; tag; molecular species; identification; property;
KW characteristic; hybridisation; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9918240-A2.
XX
PD 15-APR-1999.
XX
PF 05-OCT-1998; 98WO-US020874.
XX
PR 06-OCT-1997; 97US-00944410.
XX
PA (STRA-) STRATAGENE.
XX
PI Sorge JA;
XX
DR WPI; 1999-264040/22.
XX
PT Uniquely tagged molecules identifiable by a unique property or
PT characteristic.
XX
PS Example 6; Page 94; 138pp; English.
XX
CC The present invention describes a composition comprising a mixture of
CC different species of molecules where each species is linked to a tag that
CC is unique to that species and that encodes at least two variable
CC positions on that species, where the tags can be identified without the
CC need for first isolating each of the tags prior to identification. Liquid
CC phase hybridisation system may be used for simultaneous identification of
CC a large subset of targets out of a very large collection of similar of
CC dissimilar molecular species. It may also be used to create tagged
CC molecules that identify any collection of molecular species, e.g.
CC peptides, antibodies, nucleic acids. Method bar codes collections or

```

Sequence 46 BP; 10 A; 13 C; 12 G; 11 T; 0 U; 0 Other;

Query Match 49.3%; Score 14.8; DB 2; Length 46;

3 GACTCAGTCCTTGGTCATCTCACCTT 28

Search completed: November 23, 2004, 17:28:24

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:48 ; Search time 34.7191 Seconds
(without alignments)
614.177 Million cell updates/sec

Title: US-10-087-631B-4

Perfect score: 30

Sequence: 1 tggactcagtccttggtcatcctctct 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 905748

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	19	63.3	33	1	US-08-299-682-13
C 2	19	63.3	33	1	US-08-347-657-1
C 3	16.4	54.7	46	4	US-08-944-410-52
C 4	15.2	50.7	24	4	US-09-297-269-7
C 5	15.2	50.7	47	4	US-09-671-317-930
C 6	14.8	49.3	46	4	US-08-944-410-53
C 7	14.8	49.3	46	4	US-08-944-410-54
C 8	14.8	49.3	46	4	US-08-944-410-55
C 9	14.8	49.3	47	4	US-09-422-978-1893
C 10	14.6	48.7	36	4	US-09-916-510A-20
C 11	14.6	48.7	42	4	US-09-530-139-28
C 12	14.6	48.7	49	3	US-09-710-200-40
C 13	14.6	48.7	49	4	US-09-975-408-40
C 14	14.4	48.0	27	1	US-08-758-306-368
C 15	14.4	48.0	34	4	US-09-029-941-6
C 16	14.2	47.3	24	4	US-09-297-269-6
C 17	14.2	47.3	34	2	US-09-132-619-18
C 18	14.2	47.3	39	3	US-09-079-984A-13
C 19	14.2	47.3	39	4	US-09-390-729-13
C 20	14.2	47.3	45	1	US-08-221-816B-18
C 21	14.2	47.3	45	4	US-10-112-547-18
C 22	14.2	47.3	45	4	US-10-112-241-18
C 23	14.2	47.3	45	4	US-09-639-667-1
C 24	14.2	47.3	45	4	US-10-104-611-18
C 25	14.2	47.3	45	4	US-10-109-368-18
C 26	14.2	47.3	47	3	US-09-338-907-269
C 27	14.2	47.3	47	3	US-09-218-207-261
C 28	14.2	47.3	20	4	US-08-299-682-13
C 29	14.2	47.3	20	4	US-08-347-657-1
C 30	14.2	47.3	20	4	US-08-944-410-52
C 31	14.2	47.3	20	4	US-09-297-269-7
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C 65	14.2	47.3	20	4	US-09-530-139-28
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C 68	14.2	47.3	20	4	US-08-758-306-368
C 69	14.2	47.3	20	4	US-09-029-941-6
C 70	14.2	47.3	20	4	US-09-297-269-6
C 71	14.2	47.3	20	4	US-09-132-619-18
C 72	14.2	47.3	20	4	US-09-079-984A-13
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C 86	14.2	47.3	20	4	US-09-671-317-930
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3	US-08-591-492-20	48	47.3	14.2	47.3	30	14.2	47.3	48	1	US-08-591-492-20	Sequence 20, Appl
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6	US-08-591-492-23	48	47.3	14.2	47.3	33	14.2	47.3	48	1	US-08-591-492-23	Sequence 23, Appl
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9	US-08-591-492-26	48	47.3	14.2	47.3	36	14.2	47.3	48	1	US-08-591-492-26	Sequence 26, Appl
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11	US-08-591-492-28	48	47.3	14.2	47.3	38	14.2	47.3	48	1	US-08-591-492-28	Sequence 28, Appl
12	US-08-591-492-29	48	47.3	14.2	47.3	39	14.2	47.3	48	1	US-08-591-492-29	Sequence 29, Appl
13	US-08-591-492-30	48	47.3	14.2	47.3	40	14.2	47.3	48	1	US-08-591-492-30	Sequence 30, Appl
14	US-08-591-492-31	48	47.3	14.2	47.3	41	14.2	47.3	48	1	US-08-591-492-31	Sequence 31, Appl
15	US-08-591-492-32	48	47.3	14.2	47.3	42	14.2	47.3	48	1	US-08-591-492-32	Sequence 32, Appl
16	US-08-591-492-33	48	47.3	14.2	47.3	43	14.2	47.3	48	1	US-08-591-492-33	Sequence 33, Appl
17	US-08-591-492-34	48	47.3	14.2	47.3	44	14.2	47.3	48	1	US-08-591-492-34	Sequence 34, Appl
18	US-08-591-492-35	48	47.3	14.2	47.3	45	14.2	47.3	48	1	US-08-591-492-35	Sequence 35, Appl
19	US-08-591-492-36	48	47.3	14.2	47.3	46	14.2	47.3	48	1	US-08-591-492-36	Sequence 36, Appl
20	US-08-591-492-37	48	47.3	14.2	47.3	47	14.2	47.3	48	1	US-08-591-492-37	Sequence 37, Appl
21	US-08-591-492-38	48	47.3	14.2	47.3	48	14.2	47.3	48	1	US-08-591-492-38	Sequence 38, Appl
22	US-08-591-492-39	48	47.3	14.2	47.3	49	14.2	47.3	48	1	US-08-591-492-39	Sequence 39, Appl
23	US-08-591-492-40	48	47.3	14.2	47.3	50	14.2	47.3	48	1	US-08-591-492-40	Sequence 40, Appl
24	US-08-591-492-41	48	47.3	14.2	47.3	51	14.2	47.3	48	1	US-08-591-492-41	Sequence 41, Appl
25	US-08-591-492-42	48	47.3	14.2	47.3	52	14.2	47.3	48	1	US-08-591-492-42	Sequence 42, Appl
26	US-08-591-492-43	48	47.3	14.2	47.3	53	14.2	47.3	48	1	US-08-591-492-43	Sequence 43, Appl
27	US-08-591-492-44	48	47.3	14.2	47.3	54	14.2	47.3	48	1	US-08-591-492-44	Sequence 44, Appl
28	US-08-591-492-45	48	47.3	14.2	47.3	55	14.2	47.3	48	1	US-08-591-492-45	Sequence 45, Appl
29	US-08-591-492-46	48	47.3	14.2	47.3	56	14.2	47.3	48	1	US-08-591-492-46	Sequence 46, Appl
30	US-08-591-492-47	48	47.3	14.2	47.3	57	14.2	47.3	48	1	US-08-591-492-47	Sequence 47, Appl
31	US-08-591-492-48	48	47.3	14.2	47.3	58	14.2	47.3	48	1	US-08-591-492-48	Sequence 48, Appl
32	US-08-591-492-49	48	47.3	14.2	47.3	59	14.2	47.3	48	1	US-08-591-492-49	Sequence 49, Appl

c 101	13	43.3	50	1	US-08-171-389-393	Sequence 393, App	174	12.6	42.0	26	4	US-08-749-955-19	Sequence 19, Appl
c 102	13	43.3	50	1	US-08-123-936-393	Sequence 393, App	c 175	12.6	42.0	26	4	US-08-749-955-20	Sequence 20, Appl
c 103	13	43.3	50	2	US-08-475-228A-393	Sequence 393, App	176	12.6	42.0	29	4	US-09-915-815-18	Sequence 18, Appl
c 104	13	43.3	50	3	US-08-482-080A-393	Sequence 393, App	177	12.6	42.0	32	4	US-09-194-300A-7	Sequence 7, Appl
c 105	13	43.3	50	3	US-09-354-947-393	Sequence 393, App	178	12.6	42.0	33	4	US-09-207-388-84	Sequence 84, Appl
c 106	13	43.3	50	4	US-09-554-929-70	Sequence 70, Appl	179	12.6	42.0	37	3	US-09-161-241-70	Sequence 70, Appl
c 107	13	43.3	50	4	US-09-554-929-71	Sequence 71, Appl	c 180	12.6	42.0	41	1	US-08-464-531-63	Sequence 63, Appl
c 108	13	43.3	50	4	US-09-554-929-123	Sequence 123, App	c 181	12.6	42.0	41	2	US-08-461-598-63	Sequence 63, Appl
c 109	13	43.3	50	5	PCT-US93-12388-393	Sequence 393, App	c 182	12.6	42.0	41	3	US-08-323-137-63	Sequence 63, Appl
c 110	12.8	42.7	18	4	US-09-422-978-6022	Sequence 6022, App	c 183	12.6	42.0	41	3	US-08-936-632B-19	Sequence 19, Appl
c 111	12.8	42.7	20	3	US-09-124-238A-15	Sequence 15, Appl	c 184	12.6	42.0	41	3	US-08-582-333A-71	Sequence 71, Appl
c 112	12.8	42.7	20	4	US-09-721-975-15	Sequence 15, Appl	c 185	12.6	42.0	42	1	US-08-367-122-50	Sequence 50, Appl
c 113	12.8	42.7	20	4	US-09-986-621-15	Sequence 15, Appl	c 186	12.6	42.0	42	1	US-09-338-907-132	Sequence 192, App
c 114	12.8	42.7	21	3	US-09-124-238A-24	Sequence 24, Appl	c 187	12.6	42.0	47	3	US-09-338-907-193	Sequence 193, App
c 115	12.8	42.7	21	4	US-09-721-975-24	Sequence 24, Appl	c 188	12.6	42.0	47	3	US-09-218-207-132	Sequence 192, App
c 116	12.8	42.7	21	4	US-09-986-621-24	Sequence 24, Appl	c 189	12.6	42.0	47	3	US-09-218-207-193	Sequence 193, App
c 117	12.8	42.7	21	4	US-09-422-978-10245	Sequence 10245, A	c 190	12.6	42.0	47	4	US-09-641-638-803	Sequence 803, App
c 118	12.8	42.7	24	3	US-09-124-238A-27	Sequence 27, Appl	c 191	12.6	42.0	47	4	US-09-641-638-981	Sequence 981, App
c 119	12.8	42.7	24	4	US-09-721-975-27	Sequence 27, Appl	c 192	12.6	42.0	47	4	US-09-422-978-1198	Sequence 1198, App
c 120	12.8	42.7	24	4	US-09-986-621-27	Sequence 27, Appl	c 193	12.6	42.0	47	4	US-09-422-978-1547	Sequence 1547, App
c 121	12.8	42.7	27	1	US-08-758-306-1038	Sequence 1038, App	c 194	12.6	42.0	47	4	US-09-422-978-2807	Sequence 2807, App
c 122	12.8	42.7	27	3	US-08-584-048-371	Sequence 371, App	c 195	12.6	42.0	47	4	US-09-422-978-3752	Sequence 3752, App
c 123	12.8	42.7	34	3	US-09-027-998A-54	Sequence 54, Appl	c 196	12.6	42.0	47	4	US-10-170-097-803	Sequence 803, App
c 124	12.8	42.7	38	4	US-09-517-740-1	Sequence 1, Appl	c 197	12.6	42.0	47	4	US-10-170-097-981	Sequence 981, App
c 125	12.8	42.7	40	3	US-09-626-923-3	Sequence 3, Appl	c 198	12.6	42.0	48	1	US-08-411-796-166	Sequence 166, App
c 126	12.8	42.7	40	3	US-09-484-850-3	Sequence 3, Appl	c 199	12.6	42.0	48	1	US-08-411-796-170	Sequence 170, App
c 127	12.8	42.7	40	3	US-09-408-392-3	Sequence 3, Appl	c 200	12.6	42.0	48	3	US-08-471-039-166	Sequence 166, App
c 128	12.8	42.7	40	4	US-09-626-930-3	Sequence 3, Appl	c 201	12.6	42.0	48	3	US-08-471-039-170	Sequence 170, App
c 129	12.8	42.7	40	4	US-09-626-528-3	Sequence 3, Appl	c 202	12.6	42.0	48	3	US-08-864-473-72	Sequence 72, Appl
c 130	12.8	42.7	40	4	US-09-626-595-3	Sequence 3, Appl	c 203	12.6	42.0	48	3	US-09-440-523-72	Sequence 72, Appl
c 131	12.8	42.7	40	4	US-09-694-863-3	Sequence 3, Appl	c 204	12.6	42.0	48	4	US-08-559-390-166	Sequence 166, App
c 132	12.8	42.7	43	3	US-09-068-195-5	Sequence 5, Appl	c 205	12.6	42.0	48	4	US-08-559-390-170	Sequence 170, App
c 133	12.8	42.7	47	4	US-09-671-317-734	Sequence 734, App	c 206	12.6	42.0	48	4	US-09-181-156-72	Sequence 72, Appl
c 134	12.8	42.7	47	4	US-09-422-978-1322	Sequence 1322, App	c 207	12.6	42.0	48	5	PCT-US93-11198-166	Sequence 166, App
c 135	12.8	42.7	47	4	US-09-422-978-2336	Sequence 2336, App	c 208	12.6	42.0	48	5	PCT-US93-11198-170	Sequence 170, App
c 136	12.6	42.0	20	1	US-08-635-309-31	Sequence 31, Appl	c 209	12.6	42.0	50	2	US-08-933-749-7	Sequence 7, Appl
c 137	12.6	42.0	20	3	US-09-345-882-96	Sequence 96, Appl	c 210	12.6	42.0	50	3	US-09-235-583-7	Sequence 7, Appl
c 138	12.6	42.0	20	4	US-08-469-260A-711	Sequence 711, App	c 211	12.6	42.0	50	3	US-09-599-164-7	Sequence 7, Appl
c 139	12.6	42.0	20	4	US-08-488-446-711	Sequence 711, App	c 212	12.6	42.0	50	3	US-09-198-452A-4748	Sequence 4748, App
c 140	12.6	42.0	20	4	US-08-467-344A-711	Sequence 711, App	c 213	12.6	42.0	50	4	US-09-081-385-123	Sequence 123, App
c 141	12.6	42.0	20	4	US-08-424-550B-711	Sequence 711, App	c 214	12.6	42.0	50	4	US-09-657-472-454	Sequence 454, App
c 142	12.6	42.0	23	1	US-08-412-614-57	Sequence 57, Appl	c 215	12.6	42.0	50	4	US-09-657-472-970	Sequence 970, App
c 143	12.6	42.0	23	1	US-08-412-614-58	Sequence 58, Appl	c 216	12.6	42.0	50	4	US-09-687-637B-4	Sequence 4, Appl
c 144	12.6	42.0	23	1	US-08-412-614-59	Sequence 59, Appl	c 217	12.6	42.0	50	1	US-07-971-819A-27	Sequence 27, Appl
c 145	12.6	42.0	23	1	US-08-412-614-60	Sequence 60, Appl	c 218	12.6	42.0	50	1	US-08-475-231-27	Sequence 27, Appl
c 146	12.6	42.0	23	2	US-08-635-761-57	Sequence 57, Appl	c 219	12.6	42.0	50	1	US-08-758-306-370	Sequence 370, App
c 147	12.6	42.0	23	2	US-08-635-761-58	Sequence 58, Appl	c 220	12.6	42.0	50	3	US-08-584-040-6900	Sequence 6900, App
c 148	12.6	42.0	23	2	US-08-635-761-59	Sequence 59, Appl	c 221	12.6	42.0	50	3	US-09-044-718-30	Sequence 30, Appl
c 149	12.6	42.0	23	2	US-08-635-761-60	Sequence 60, Appl	c 222	12.6	42.0	50	3	US-09-044-718-31	Sequence 31, Appl
c 150	12.6	42.0	23	3	US-09-312-520-57	Sequence 57, Appl	c 223	12.6	42.0	50	4	US-10-062-848-30	Sequence 30, Appl
c 151	12.6	42.0	23	3	US-09-312-520-58	Sequence 58, Appl	c 224	12.6	42.0	50	4	US-10-062-848-31	Sequence 31, Appl
c 152	12.6	42.0	23	3	US-09-312-520-59	Sequence 59, Appl	c 225	12.6	42.0	50	1	US-08-081-539-8	Sequence 8, Appl
c 153	12.6	42.0	23	3	US-09-312-520-60	Sequence 60, Appl	c 226	12.6	42.0	50	1	US-08-466-647-8	Sequence 8, Appl
c 154	12.6	42.0	23	4	US-09-863-086-57	Sequence 57, Appl	c 227	12.6	42.0	50	1	US-08-411-795B-133	Sequence 133, App
c 155	12.6	42.0	23	4	US-09-863-086-58	Sequence 58, Appl	c 228	12.6	42.0	50	1	US-08-411-795B-400	Sequence 400, App
c 156	12.6	42.0	23	4	US-09-863-086-59	Sequence 59, Appl	c 229	12.6	42.0	50	1	US-08-411-796-133	Sequence 133, App
c 157	12.6	42.0	23	4	US-09-863-086-60	Sequence 60, Appl	c 230	12.6	42.0	50	1	US-08-469-319A-133	Sequence 133, App
c 158	12.6	42.0	25	4	US-09-866-108A-3476	Sequence 3476, App	c 231	12.6	42.0	50	1	US-08-469-319A-400	Sequence 400, App
c 159	12.6	42.0	25	4	US-09-866-108A-3477	Sequence 3477, App	c 232	12.6	42.0	50	3	US-08-471-039-133	Sequence 133, App
c 160	12.6	42.0	25	4	US-09-866-108A-3478	Sequence 3478, App	c 233	12.6	42.0	50	4	US-08-764-114-133	Sequence 133, App
c 161	12.6	42.0	25	4	US-09-866-108A-3479	Sequence 3479, App	c 234	12.6	42.0	50	4	US-08-764-114-400	Sequence 400, App
c 162	12.6	42.0	25	4	US-09-866-108A-3480	Sequence 3480, App	c 235	12.6	42.0	50	4	US-08-469-419-133	Sequence 133, App
c 163	12.6	42.0	25	4	US-09-866-108A-3481	Sequence 3481, App	c 236	12.6	42.0	50	4	US-08-469-419-400	Sequence 400, App
c 164	12.6	42.0	25	4	US-09-866-108A-3482	Sequence 3482, App	c 237	12.6	42.0	50	4	US-08-559-390-133	Sequence 133, App
c 165	12.6	42.0	25	4	US-09-866-108A-14154	Sequence 14154, A	c 238	12.6	42.0	50	4	US-08-559-390-133	Sequence 133, App
c 166	12.6	42.0	25	4	US-09-866-108A-14155	Sequence 14155, A	c 239	12.6	42.0	50	5	PCT-US93-11198-133	Sequence 133, App
c 167	12.6	42.0	25	4	US-09-866-108A-14156	Sequence 14156, A	c 240	12.6	42.0	50	4	US-09-672-725C-21	Sequence 21, Appl
c 168	12.6	42.0	25	4	US-09-866-108A-14157	Sequence 14157, A	c 241	12.6	42.0	50	3	US-09-894-799-16	Sequence 16, Appl
c 169	12.6	42.0	25	4	US-09-866-108A-14158	Sequence 14158, A	c 242	12.6	42.0	50	3	US-08-832-571-11	Sequence 11, Appl
c 170	12.6	42.0	25	4	US-09-866-108A-14159	Sequence 14159, A	c 243	12.6	42.0	50	3	US-09-345-882-45	Sequence 45, Appl
c 171	12.6	42.0	25	4	US-09-866-108A-14160	Sequence 14160, A	c 244	12.6	42.0	50	4	US-09-422-978-1776	Sequence 1776, App
c 172	12.6	42.0	26	4	US-08-749-955-17	Sequence 17, Appl	c 245	12.6	42.0	50	4	US-09-422-978-1988	Sequence 1988, App
c 173	12.6	42.0	26	4	US-08-749-955-18	Sequence 18, Appl	c 246	12.6	42.0	50	1	US-08-160-670A-46	Sequence 46, Appl

247	12.2	40.7	17	1	US-08-390-850-585	Sequence 585, Appl	320	12.2	40.7	39	4	US-09-390-729-7	Sequence 7, Appli
248	12.2	40.7	17	1	US-08-435-634-585	Sequence 585, Appl	321	12.2	40.7	46	3	US-09-262-773-182	Sequence 182, App
c 249	12.2	40.7	17	4	US-09-866-108A-547	Sequence 547, App	c 322	12.2	40.7	47	1	US-08-119-773-10	Sequence 10, Appl
c 250	12.2	40.7	17	4	US-09-404-912-109	Sequence 109, App	c 323	12.2	40.7	47	4	US-09-422-978-105	Sequence 105, App
251	12.2	40.7	18	4	US-08-117-952-204	Sequence 204, App	324	12.2	40.7	47	4	US-09-422-978-1042	Sequence 1042, Ap
252	12.2	40.7	19	4	US-09-696-791-803	Sequence 803, App	325	12.2	40.7	47	4	US-09-422-978-1459	Sequence 1459, Ap
253	12.2	40.7	20	3	US-09-359-757-17	Sequence 17, Appl	326	12.2	40.7	48	1	US-08-168-917-12	Sequence 12, Appl
254	12.2	40.7	20	3	US-09-359-757-18	Sequence 18, Appl	c 327	12.2	40.7	48	1	US-08-391-000-13	Sequence 13, Appl
255	12.2	40.7	20	3	US-09-428-584-22	Sequence 22, Appl	c 328	12.2	40.7	48	2	US-08-741-931-13	Sequence 13, Appl
c 256	12.2	40.7	20	3	US-09-622-543-3	Sequence 3, Appli	329	12.2	40.7	48	2	US-08-460-510-12	Sequence 12, Appl
c 257	12.2	40.7	20	4	US-09-929-486-3	Sequence 3, Appli	330	12.2	40.7	48	3	US-08-460-490-12	Sequence 12, Appl
c 258	12.2	40.7	20	4	US-10-259-903-3	Sequence 3, Appli	331	12.2	40.7	48	3	US-09-035-665-8	Sequence 8, Appli
259	12.2	40.7	20	4	US-10-259-903-4	Sequence 4, Appli	332	12.2	40.7	48	3	US-09-035-665-9	Sequence 9, Appli
c 260	12.2	40.7	20	6	5219727-55	Patent No. 5219727	333	12.2	40.7	48	5	US-09-035-665-9	Sequence 9, Appli
c 261	12.2	40.7	21	1	US-07-906-930E-22	Sequence 22, Appl	c 334	12.2	40.7	48	5	PCT-US92-10430-12	Sequence 12, Appl
c 262	12.2	40.7	21	1	US-07-906-930E-27	Sequence 27, Appl	335	12.2	40.7	49	1	US-08-171-389-118	Sequence 118, App
c 263	12.2	40.7	21	1	US-08-338-579A-80	Sequence 80, Appl	336	12.2	40.7	49	1	US-08-123-936-118	Sequence 118, App
c 264	12.2	40.7	21	3	US-09-301-978C-7	Sequence 7, Appli	337	12.2	40.7	49	2	US-08-475-228A-118	Sequence 118, App
c 265	12.2	40.7	21	5	PCT-US94-09851-80	Sequence 80, Appl	338	12.2	40.7	49	3	US-08-482-080A-118	Sequence 118, App
c 266	12.2	40.7	23	3	US-08-905-223-32	Sequence 32, Appl	339	12.2	40.7	49	3	US-09-354-947-118	Sequence 118, App
c 267	12.2	40.7	23	3	US-09-247-155-32	Sequence 32, Appl	340	12.2	40.7	49	5	PCT-US93-12388-118	Sequence 118, App
c 268	12.2	40.7	23	4	US-09-599-360B-18	Sequence 18, Appl	c 341	12.2	40.0	18	2	US-08-970-269A-8	Sequence 8, Appli
c 269	12.2	40.7	23	4	US-09-663-600A-32	Sequence 32, Appl	c 342	12.2	40.0	18	3	US-09-407-562-8	Sequence 8, Appli
c 270	12.2	40.7	23	4	US-09-621-976-18	Sequence 18, Appl	c 343	12.2	40.0	18	3	US-09-080-525-17	Sequence 17, Appl
c 271	12.2	40.7	23	4	US-09-533-999C-18	Sequence 18, Appl	c 344	12.2	40.0	18	4	US-09-695-782-17	Sequence 17, Appl
c 272	12.2	40.7	25	4	US-09-866-108A-3483	Sequence 3483, Ap	c 345	12.2	40.0	20	3	US-08-804-180C-12	Sequence 12, Appl
c 273	12.2	40.7	25	4	US-09-866-108A-3484	Sequence 3484, Ap	346	12.2	40.0	20	4	US-09-198-452A-2977	Sequence 2977, Ap
c 274	12.2	40.7	26	1	US-08-033-072-1	Sequence 1, Appli	c 347	12.2	40.0	20	4	US-09-544-398B-320	Sequence 320, App
275	12.2	40.7	26	1	US-08-479-852-4	Sequence 4, Appli	348	12.2	40.0	22	4	US-09-792-024-474	Sequence 474, App
c 276	12.2	40.7	26	1	US-08-479-852-56	Sequence 56, Appl	c 349	12.2	40.0	24	3	US-08-896-449A-10	Sequence 10, Appl
c 277	12.2	40.7	26	1	US-08-479-852-70	Sequence 70, Appl	c 350	12.2	40.0	24	3	US-09-132-652-10	Sequence 10, Appl
c 278	12.2	40.7	26	1	US-08-479-852-84	Sequence 84, Appl	351	12.2	40.0	24	4	US-09-177-650-81	Sequence 81, Appl
c 279	12.2	40.7	26	1	US-08-479-852-84	Sequence 84, Appl	c 352	12.2	40.0	24	4	US-09-886-900A-10	Sequence 10, Appl
c 280	12.2	40.7	26	2	US-08-462-646-4	Sequence 4, Appli	c 353	12.2	40.0	24	4	US-09-662-478C-10	Sequence 10, Appl
c 281	12.2	40.7	26	2	US-08-462-646-56	Sequence 56, Appl	c 354	12.2	40.0	24	4	US-09-551-161-3	Sequence 3, Appli
c 282	12.2	40.7	26	2	US-08-462-646-70	Sequence 70, Appl	355	12.2	40.0	25	2	US-08-632-787-35	Sequence 35, Appl
c 283	12.2	40.7	26	2	US-08-462-646-84	Sequence 84, Appl	c 356	12.2	40.0	25	3	US-09-047-199-35	Sequence 35, Appl
c 284	12.2	40.7	26	3	US-07-695-201B-12	Sequence 12, Appl	c 357	12.2	40.0	27	3	US-08-985-162-872	Sequence 872, App
c 285	12.2	40.7	26	3	US-08-470-532-12	Sequence 12, Appl	c 358	12.2	40.0	27	3	US-08-985-162-901	Sequence 901, App
c 286	12.2	40.7	26	3	US-09-013-406-4	Sequence 4, Appli	c 359	12.2	40.0	27	3	US-09-105-839D-17	Sequence 17, Appl
c 287	12.2	40.7	26	3	US-09-013-406-56	Sequence 56, Appl	c 360	12.2	40.0	27	3	US-08-584-040-4727	Sequence 4727, Ap
c 288	12.2	40.7	26	3	US-09-013-406-70	Sequence 70, Appl	c 361	12.2	40.0	27	4	US-09-344-040C-17	Sequence 17, Appl
c 289	12.2	40.7	26	4	US-09-168-947-10	Sequence 10, Appl	c 362	12.2	40.0	27	4	US-09-401-063-872	Sequence 872, App
c 290	12.2	40.7	26	4	US-08-968-208-12	Sequence 12, Appl	c 363	12.2	40.0	27	4	US-09-401-063-901	Sequence 901, App
c 291	12.2	40.7	26	4	US-09-766-095-4	Sequence 4, Appli	c 364	12.2	40.0	28	1	US-08-833-039A-17	Sequence 17, Appl
c 292	12.2	40.7	26	4	US-09-766-095-56	Sequence 56, Appl	365	12.2	40.0	28	1	US-08-485-107-6	Sequence 6, Appli
c 293	12.2	40.7	26	4	US-09-766-095-70	Sequence 70, Appl	366	12.2	40.0	28	2	US-08-472-719-5	Sequence 6, Appli
c 294	12.2	40.7	26	4	US-09-766-095-84	Sequence 84, Appl	c 367	12.2	40.0	28	4	US-09-304-232-551	Sequence 551, App
c 295	12.2	40.7	27	3	US-08-584-040-6616	Sequence 6616, Ap	368	12.2	40.0	30	3	US-08-876-078-9	Sequence 9, Appli
c 296	12.2	40.7	28	3	US-09-327-681-1	Sequence 1, Appli	369	12.2	40.0	30	3	US-08-831-823-9	Sequence 9, Appli
c 297	12.2	40.7	28	4	US-09-091-134-7	Sequence 7, Appli	370	12.2	40.0	33	1	US-08-752-238-10	Sequence 10, Appl
c 298	12.2	40.7	29	1	US-08-345-505A-7	Sequence 7, Appli	c 371	12.2	40.0	33	3	US-09-085-603B-10	Sequence 10, Appl
c 299	12.2	40.7	29	3	US-08-913-778-2	Sequence 2, Appli	c 372	12.2	40.0	34	4	US-09-551-161-5	Sequence 5, Appli
c 300	12.2	40.7	29	3	US-08-646-265A-67	Sequence 67, Appl	373	12.2	40.0	37	3	US-09-363-939A-213	Sequence 213, App
c 301	12.2	40.7	29	3	US-08-646-265A-83	Sequence 83, Appl	374	12.2	40.0	37	4	US-09-791-301-213	Sequence 213, App
c 302	12.2	40.7	30	3	US-09-178-869-11	Sequence 11, Appl	c 375	12.2	40.0	39	3	US-09-052-995-4	Sequence 4, Appli
c 303	12.2	40.7	30	4	US-09-761-413-11	Sequence 11, Appl	c 376	12.2	40.0	39	4	US-09-535-008-25	Sequence 25, Appl
c 304	12.2	40.7	31	1	US-07-940-652-15	Sequence 15, Appl	c 377	12.2	40.0	39	4	US-09-220-557-16	Sequence 16, Appl
c 305	12.2	40.7	31	1	US-08-255-553-15	Sequence 15, Appl	c 378	12.2	40.0	40	3	US-09-262-773-91	Sequence 91, Appl
c 306	12.2	40.7	33	1	US-08-538-875-8	Sequence 8, Appli	c 379	12.2	40.0	42	2	US-08-343-443B-60	Sequence 60, Appl
c 307	12.2	40.7	33	2	US-08-600-783-6	Sequence 6, Appli	380	12.2	40.0	42	4	US-09-359-304B-23	Sequence 23, Appl
c 308	12.2	40.7	33	3	US-09-079-984A-3	Sequence 3, Appli	c 381	12.2	40.0	42	6	5231166-15	Patent No. 5231166
c 309	12.2	40.7	34	4	US-09-390-729-3	Sequence 3, Appli	c 382	12.2	40.0	44	2	US-08-441-887A-20	Sequence 20, Appl
c 310	12.2	40.7	34	6	5182196-15	Patent No. 5182196	c 383	12.2	40.0	44	3	US-08-544-381B-117	Sequence 117, App
c 311	12.2	40.7	34	6	5182196-15	Patent No. 5182196	384	12.2	40.0	45	3	US-09-312-285-6	Sequence 6, Appli
c 312	12.2	40.7	36	3	US-09-446-504-81	Sequence 81, Appl	385	12.2	40.0	45	3	US-09-312-286-6	Sequence 6, Appli
c 313	12.2	40.7	36	3	US-09-712-266-81	Sequence 81, Appl	386	12.2	40.0	45	3	US-09-312-038-6	Sequence 6, Appli
c 314	12.2	40.7	39	2	US-08-857-946-42	Sequence 42, Appl	387	12.2	40.0	45	3	US-09-554-511-13	Sequence 13, Appl
c 315	12.2	40.7	39	2	US-08-857-946-46	Sequence 46, Appl	388	12.2	40.0	45	4	US-09-728-764-6	Sequence 6, Appli
c 316	12.2	40.7	39	3	US-08-970-740-46	Sequence 46, Appl	389	12.2	40.0	45	4	US-09-312-304B-4	Sequence 4, Appli
c 317	12.2	40.7	39	3	US-08-970-740-46	Sequence 46, Appl	390	12.2	40.0	45	4	US-09-728-792-6	Sequence 6, Appli
c 318	12.2	40.7	39	3	US-09-262-773-74	Sequence 74, Appl	391	12.2	40.0	45	4	US-09-850-964-6	Sequence 6, Appli
319	12.2	40.7	39	3	US-09-079-984A-7	Sequence 7, Appli	392	12.2	40.0	45	4	US-09-532-806-7	Sequence 7, Appli

C 393	12	40.0	47	1	US-08-171-389-15	Sequence 15, Appl	466	11.8	39.3	33	4	US-09-758-282B-45	Sequence 45, Appl
C 394	12	40.0	47	1	US-08-123-936-15	Sequence 15, Appl	467	11.8	39.3	33	4	US-09-577-304A-45	Sequence 45, Appl
C 395	12	40.0	47	1	US-08-475-228A-15	Sequence 15, Appl	468	11.8	39.3	34	2	US-08-577-492-15	Sequence 15, Appl
C 396	12	40.0	47	3	US-08-482-080A-15	Sequence 15, Appl	469	11.8	39.3	34	3	US-09-073-630-15	Sequence 15, Appl
C 397	12	40.0	47	3	US-08-961-083-391	Sequence 391, Appl	c 470	11.8	39.3	35	3	US-08-902-632-12	Sequence 12, Appl
C 398	12	40.0	47	3	US-09-354-947-15	Sequence 15, Appl	c 471	11.8	39.3	36	2	US-08-418-085-31	Sequence 31, Appl
C 399	12	40.0	47	4	US-09-641-638-775	Sequence 775, Appl	472	11.8	39.3	36	3	US-09-099-011A-31	Sequence 31, Appl
C 400	12	40.0	47	4	US-09-422-978-575	Sequence 575, Appl	473	11.8	39.3	36	4	US-09-098-877B-31	Sequence 31, Appl
C 401	12	40.0	47	4	US-09-422-978-1243	Sequence 1243, Appl	c 474	11.8	39.3	38	4	US-09-474-432B-1264	Sequence 1264, Appl
C 402	12	40.0	47	4	US-09-422-978-2137	Sequence 2137, Appl	c 475	11.8	39.3	38	4	US-09-476-387-1263	Sequence 1263, Appl
C 403	12	40.0	47	4	US-09-422-978-2424	Sequence 2424, Appl	476	11.8	39.3	39	2	US-08-857-946-52	Sequence 52, Appl
C 404	12	40.0	47	4	US-09-536-784-391	Sequence 391, Appl	477	11.8	39.3	39	3	US-08-970-740-52	Sequence 52, Appl
C 405	12	40.0	47	4	US-10-170-097-775	Sequence 775, Appl	478	11.8	39.3	39	4	US-09-517-871-16	Sequence 16, Appl
C 406	12	40.0	47	5	PCT-US93-12388-15	Sequence 15, Appl	479	11.8	39.3	39	4	US-09-517-439-16	Sequence 16, Appl
C 407	12	40.0	49	3	US-08-535-057A-8	Sequence 8, Appl	480	11.8	39.3	40	1	US-08-171-389-166	Sequence 166, Appl
C 408	12	40.0	49	4	US-09-503-252-8	Sequence 8, Appl	481	11.8	39.3	40	1	US-08-123-936-166	Sequence 166, Appl
C 409	12	40.0	50	4	US-09-443-199C-986	Sequence 986, Appl	482	11.8	39.3	40	1	US-08-436-463-12	Sequence 12, Appl
C 410	12	40.0	50	4	US-09-443-199C-988	Sequence 988, Appl	483	11.8	39.3	40	2	US-08-475-228A-166	Sequence 166, Appl
C 411	11.8	39.3	17	2	US-08-844-525A-63	Sequence 63, Appl	484	11.8	39.3	40	3	US-08-482-080A-166	Sequence 166, Appl
C 412	11.8	39.3	17	4	US-08-389-423-33	Sequence 33, Appl	485	11.8	39.3	40	3	US-09-354-947-166	Sequence 166, Appl
C 413	11.8	39.3	18	3	US-09-189-028-33	Sequence 33, Appl	486	11.8	39.3	40	5	PCT-US93-12388-166	Sequence 166, Appl
C 414	11.8	39.3	19	4	US-09-448-176-8	Sequence 8, Appl	487	11.8	39.3	42	3	US-08-454-098-17	Sequence 17, Appl
C 415	11.8	39.3	20	1	US-09-647-504-6	Sequence 6, Appl	488	11.8	39.3	43	4	US-09-647-390-6	Sequence 6, Appl
C 416	11.8	39.3	20	1	US-08-441-430-67	Sequence 67, Appl	489	11.8	39.3	45	4	US-09-517-871-15	Sequence 15, Appl
C 417	11.8	39.3	20	4	US-09-844-525A-63	Sequence 63, Appl	c 490	11.8	39.3	45	4	US-09-517-439-15	Sequence 15, Appl
C 418	11.8	39.3	21	4	US-09-657-472-480	Sequence 480, Appl	c 491	11.8	39.3	47	4	US-09-422-978-1087	Sequence 1087, Appl
C 419	11.8	39.3	21	4	US-09-696-791-4479	Sequence 4479, Appl	c 492	11.8	39.3	47	4	US-09-422-978-1204	Sequence 1204, Appl
C 420	11.8	39.3	22	4	US-09-755-665-113	Sequence 113, Appl	c 493	11.8	39.3	47	4	US-09-422-978-3052	Sequence 3052, Appl
C 421	11.8	39.3	23	3	US-08-781-891-13	Sequence 114, Appl	c 494	11.8	39.3	47	4	US-09-422-978-3864	Sequence 3864, Appl
C 422	11.8	39.3	23	4	US-09-618-166-13	Sequence 13, Appl	c 495	11.8	39.3	47	4	US-09-422-978-3901	Sequence 3901, Appl
C 423	11.8	39.3	23	4	US-09-618-166-13	Sequence 13, Appl	c 496	11.8	39.3	50	1	US-07-994-469A-27	Sequence 27, Appl
C 424	11.8	39.3	24	4	US-09-904-389-6	Sequence 6, Appl	c 497	11.6	38.7	18	1	US-08-390-850-1131	Sequence 1131, Appl
C 425	11.8	39.3	25	3	US-08-776-971-91	Sequence 91, Appl	c 498	11.6	38.7	18	1	US-08-435-634-1131	Sequence 1131, Appl
C 426	11.8	39.3	25	4	US-09-866-108A-4970	Sequence 4970, Appl	c 499	11.6	38.7	20	3	US-09-358-683-11	Sequence 11, Appl
C 427	11.8	39.3	25	4	US-09-866-108A-4971	Sequence 4971, Appl	c 500	11.6	38.7	20	4	US-09-487-792-42	Sequence 42, Appl
C 428	11.8	39.3	25	4	US-09-866-108A-4972	Sequence 4972, Appl	c 501	11.6	38.7	20	4	US-09-791-211-78	Sequence 78, Appl
C 429	11.8	39.3	25	4	US-09-576-290-91	Sequence 91, Appl	c 502	11.6	38.7	20	4	US-09-908-594-42	Sequence 42, Appl
C 430	11.8	39.3	26	2	US-08-859-998-778	Sequence 778, Appl	c 503	11.6	38.7	20	4	US-09-423-978-10056	Sequence 10056, A
C 431	11.8	39.3	26	3	US-09-225-928-778	Sequence 778, Appl	c 504	11.6	38.7	20	4	US-09-614-614-34	Sequence 34, Appl
C 432	11.8	39.3	26	4	US-09-225-201B-778	Sequence 778, Appl	c 505	11.6	38.7	20	4	US-09-198-452A-6076	Sequence 6076, Appl
C 433	11.8	39.3	26	4	US-09-665-615B-89	Sequence 89, Appl	c 506	11.6	38.7	20	4	US-09-356-806-11	Sequence 11, Appl
C 434	11.8	39.3	27	1	US-08-229-284A-3	Sequence 3, Appl	c 507	11.6	38.7	21	3	US-08-803-085-13	Sequence 13, Appl
C 435	11.8	39.3	27	1	US-08-640-517A-85	Sequence 85, Appl	c 508	11.6	38.7	21	3	US-09-231-227-6	Sequence 6, Appl
C 436	11.8	39.3	27	3	US-08-985-162-1111	Sequence 1111, Appl	c 509	11.6	38.7	21	3	US-08-943-731-541	Sequence 541, Appl
C 437	11.8	39.3	27	3	US-08-985-162-1396	Sequence 1396, Appl	c 510	11.6	38.7	21	4	US-09-768-585-6	Sequence 6, Appl
C 438	11.8	39.3	27	3	US-08-584-040-222	Sequence 222, Appl	c 511	11.6	38.7	21	4	US-09-814-351-32	Sequence 32, Appl
C 439	11.8	39.3	27	3	US-08-584-040-435	Sequence 435, Appl	c 512	11.6	38.7	21	4	US-09-657-472-1582	Sequence 1582, Appl
C 440	11.8	39.3	27	3	US-08-584-040-4637	Sequence 4637, Appl	c 513	11.6	38.7	22	4	US-09-680-420A-8	Sequence 8, Appl
C 441	11.8	39.3	27	3	US-08-584-040-6284	Sequence 6284, Appl	c 514	11.6	38.7	23	4	US-09-207-388-101	Sequence 101, Appl
C 442	11.8	39.3	27	3	US-08-584-040-6301	Sequence 6301, Appl	c 515	11.6	38.7	24	4	US-10-006-611-10	Sequence 10, Appl
C 443	11.8	39.3	27	3	US-08-679-645-908	Sequence 908, Appl	c 516	11.6	38.7	25	4	US-09-538-709-323	Sequence 323, Appl
C 444	11.8	39.3	27	4	US-09-401-063-1111	Sequence 1111, Appl	c 517	11.6	38.7	25	4	US-09-866-108A-3475	Sequence 3475, Appl
C 445	11.8	39.3	27	4	US-09-401-063-1396	Sequence 1396, Appl	c 518	11.6	38.7	25	4	US-09-866-108A-14153	Sequence 14153, A
C 446	11.8	39.3	28	3	US-09-162-021B-17	Sequence 17, Appl	c 519	11.6	38.7	26	3	US-09-245-041-74	Sequence 74, Appl
C 447	11.8	39.3	28	4	US-09-687-477-22	Sequence 22, Appl	c 520	11.6	38.7	26	4	US-09-060-482-6	Sequence 6, Appl
C 448	11.8	39.3	28	4	US-09-687-476-22	Sequence 22, Appl	c 521	11.6	38.7	26	4	US-09-358-055B-75	Sequence 75, Appl
C 449	11.8	39.3	28	4	US-09-687-373-22	Sequence 22, Appl	c 522	11.6	38.7	26	4	US-09-893-238-74	Sequence 74, Appl
C 450	11.8	39.3	28	4	US-09-975-553-22	Sequence 22, Appl	c 523	11.6	38.7	27	1	US-08-478-039-50	Sequence 50, Appl
C 451	11.8	39.3	28	4	US-10-270-793-22	Sequence 22, Appl	c 524	11.6	38.7	27	1	US-08-478-039-50	Sequence 50, Appl
C 452	11.8	39.3	28	4	US-10-270-876-22	Sequence 22, Appl	c 525	11.6	38.7	27	3	US-08-476-349A-50	Sequence 50, Appl
C 453	11.8	39.3	28	4	US-10-268-051-12	Sequence 12, Appl	c 526	11.6	38.7	27	3	US-08-523-894-43	Sequence 43, Appl
C 454	11.8	39.3	29	1	US-07-977-284A-225	Sequence 225, Appl	c 527	11.6	38.7	27	3	US-08-341-560B-15	Sequence 15, Appl
C 455	11.8	39.3	29	2	US-08-256-426B-225	Sequence 225, Appl	c 528	11.6	38.7	27	5	PCT-US93-03605-15	Sequence 15, Appl
C 456	11.8	39.3	30	1	US-09-636-771-9	Sequence 9, Appl	c 529	11.6	38.7	29	2	US-08-761-277A-77	Sequence 77, Appl
C 457	11.8	39.3	30	2	US-08-535-243-9	Sequence 9, Appl	c 530	11.6	38.7	29	4	US-09-304-232-214	Sequence 214, Appl
C 458	11.8	39.3	30	2	US-08-859-998-341	Sequence 341, Appl	c 531	11.6	38.7	29	4	US-09-304-232-726	Sequence 726, Appl
C 459	11.8	39.3	30	3	US-09-225-928-341	Sequence 341, Appl	c 532	11.6	38.7	29	4	US-09-304-232-809	Sequence 809, Appl
C 460	11.8	39.3	30	4	US-09-486-241-32	Sequence 32, Appl	c 533	11.6	38.7	30	2	US-08-373-130-59	Sequence 59, Appl
C 461	11.8	39.3	30	4	US-09-225-201B-341	Sequence 341, Appl	c 534	11.6	38.7	30	2	US-08-438-130A-59	Sequence 59, Appl
C 462	11.8	39.3	30	4	US-09-270-957-48	Sequence 48, Appl	c 535	11.6	38.7	30	2	US-09-100-388-16	Sequence 16, Appl
C 463	11.8	39.3	30	6	5466586-1	Patent No. 5466586	c 536	11.6	38.7	30	3	US-08-803-085-14	Sequence 14, Appl
C 464	11.8	39.3	32	2	US-08-512-129A-88	Sequence 88, Appl	c 537	11.6	38.7	30	3	US-09-287-145A-59	Sequence 59, Appl
C 465	11.8	39.3	33	2	US-08-731-272A-23	Sequence 23, Appl	c 538	11.6	38.7	30	3	US-09-556-111-59	Sequence 59, Appl

539	11.6	38.7	31	4	US-08-887-497A-63	Sequence 63, Appl	c 612	11.6	38.7	50	4	US-08-880-865-9	Sequence 9, Appli
540	11.6	38.7	31	4	US-08-887-497A-65	Sequence 65, Appl	613	11.4	38.0	17	3	US-08-584-040-5983	Sequence 5983, Ap
541	11.6	38.7	32	3	US-09-232-477-4	Sequence 4, Appli	614	11.4	38.0	17	4	US-09-371-772B-2820	Sequence 2820, Ap
542	11.6	38.7	32	4	US-09-784-982-4	Sequence 4, Appli	c 615	11.4	38.0	17	4	US-09-371-772B-6276	Sequence 6276, Ap
543	11.6	38.7	32	4	US-09-581-070-6	Sequence 6, Appli	c 616	11.4	38.0	17	4	US-09-371-772B-6277	Sequence 6277, Ap
544	11.6	38.7	32	4	US-09-818-733-3	Sequence 3, Appli	c 617	11.4	38.0	19	1	US-07-977-284A-21	Sequence 21, Appl
545	11.6	38.7	33	2	US-08-636-602A-8	Sequence 8, Appli	c 618	11.4	38.0	19	2	US-08-256-426B-21	Sequence 21, Appl
546	11.6	38.7	33	3	US-09-263-314-8	Sequence 8, Appli	619	11.4	38.0	19	3	US-08-851-843A-90	Sequence 90, Appl
547	11.6	38.7	33	4	US-08-755-592A-10	Sequence 10, Appl	620	11.4	38.0	19	3	US-08-974-549A-382	Sequence 382, App
548	11.6	38.7	33	4	US-10-006-611-4	Sequence 4, Appli	621	11.4	38.0	19	3	US-08-854-050-90	Sequence 90, Appl
549	11.6	38.7	34	1	US-08-411-796-448	Sequence 41, Appl	622	11.4	38.0	19	3	US-09-430-323-90	Sequence 90, Appl
550	11.6	38.7	34	2	US-08-596-387B-41	Sequence 41, Appl	623	11.4	38.0	19	4	US-08-912-951-149	Sequence 149, App
551	11.6	38.7	34	3	US-08-471-039-448	Sequence 448, App	624	11.4	38.0	19	4	US-09-422-978-5040	Sequence 5040, Ap
552	11.6	38.7	34	3	US-08-960-190A-3	Sequence 3, Appli	625	11.4	38.0	19	4	US-09-402-181B-382	Sequence 382, App
553	11.6	38.7	34	3	US-09-067-615-41	Sequence 41, Appl	626	11.4	38.0	19	4	US-09-721-456-382	Sequence 382, App
554	11.6	38.7	34	4	US-08-559-390-448	Sequence 448, App	627	11.4	38.0	19	4	US-09-696-791-2023	Sequence 2023, Ap
555	11.6	38.7	34	5	PCT-US93-11198-448	Sequence 448, App	628	11.4	38.0	20	2	US-08-117-952-253	Sequence 253, App
556	11.6	38.7	34	5	PCT-US95-09816A-41	Sequence 41, Appl	629	11.4	38.0	20	4	US-09-446-754-14	Sequence 14, Appl
557	11.6	38.7	35	1	US-07-985-110-10	Sequence 10, Appl	630	11.4	38.0	20	4	US-09-446-754-15	Sequence 15, Appl
558	11.6	38.7	35	1	US-08-099-053-10	Sequence 10, Appl	631	11.4	38.0	20	4	US-09-733-294A-55	Sequence 55, Appl
559	11.6	38.7	35	1	US-08-135-611-9	Sequence 9, Appli	632	11.4	38.0	20	6	5487993-6	Patent No. 5487993
560	11.6	38.7	35	1	US-08-452-823-10	Sequence 10, Appl	633	11.4	38.0	21	2	US-09-211-930-9	Sequence 9, Appli
561	11.6	38.7	35	1	US-08-187-453-9	Sequence 9, Appli	634	11.4	38.0	21	3	US-09-340-993-9	Sequence 9, Appli
562	11.6	38.7	35	1	US-08-613-743-2	Sequence 2, Appli	635	11.4	38.0	21	3	US-09-254-023B-38	Sequence 38, Appl
563	11.6	38.7	35	4	US-10-153-063-126	Sequence 126, App	636	11.4	38.0	21	3	US-09-468-442-9	Sequence 9, Appli
564	11.6	38.7	35	4	US-10-153-064-128	Sequence 128, App	637	11.4	38.0	22	5	PCT-US92-00282-35	Sequence 35, Appl
565	11.6	38.7	36	3	US-08-692-922-7	Sequence 7, Appli	c 638	11.4	38.0	22	5	PCT-US92-00282-35	Sequence 35, Appl
566	11.6	38.7	36	3	US-08-688-908-1	Sequence 1, Appli	639	11.4	38.0	23	3	US-09-087-232A-7	Sequence 7, Appli
567	11.6	38.7	36	4	US-09-813-781-25	Sequence 25, Appl	640	11.4	38.0	23	3	US-09-014-241-16	Sequence 16, Appl
568	11.6	38.7	36	4	US-09-813-781-26	Sequence 26, Appl	c 641	11.4	38.0	24	1	US-08-219-633-3	Sequence 3, Appli
569	11.6	38.7	38	1	US-08-197-770-17	Sequence 17, Appl	c 642	11.4	38.0	24	1	US-08-515-236-3	Sequence 3, Appli
570	11.6	38.7	38	1	US-07-744-282C-47	Sequence 47, Appl	c 643	11.4	38.0	24	1	US-08-761-950-3	Sequence 3, Appli
571	11.6	38.7	38	5	PCT-US92-06821A-90	Sequence 90, Appl	c 644	11.4	38.0	24	2	US-08-632-575B-33	Sequence 33, Appli
572	11.6	38.7	40	3	US-08-951-923-30	Sequence 30, Appl	645	11.4	38.0	24	2	US-08-690-184-3	Sequence 3, Appli
573	11.6	38.7	41	2	US-08-343-443B-43	Sequence 43, Appl	c 646	11.4	38.0	24	3	US-08-933-358-12	Sequence 12, Appl
574	11.6	38.7	43	1	US-07-985-110-9	Sequence 9, Appli	c 647	11.4	38.0	24	3	US-08-938-830-60	Sequence 60, Appl
575	11.6	38.7	43	1	US-08-099-053-9	Sequence 9, Appli	648	11.4	38.0	24	3	US-09-327-229-5	Sequence 5, Appli
576	11.6	38.7	43	1	US-08-452-823-9	Sequence 9, Appli	c 649	11.4	38.0	24	4	US-09-553-690-42	Sequence 42, Appl
577	11.6	38.7	43	3	US-08-832-985-68	Sequence 68, Appl	c 650	11.4	38.0	24	4	US-09-199-542B-33	Sequence 33, Appli
578	11.6	38.7	43	3	US-08-732-708C-1	Sequence 1, Appli	c 651	11.4	38.0	24	4	PCT-US95-12608-5	Sequence 5, Appli
579	11.6	38.7	43	4	US-09-410-903-49	Sequence 49, Appl	c 652	11.4	38.0	24	5	US-09-866-108A-4968	Sequence 4968, Ap
580	11.6	38.7	43	4	US-08-835-159-68	Sequence 68, Appl	c 653	11.4	38.0	25	4	US-09-866-108A-4969	Sequence 4969, Ap
581	11.6	38.7	44	1	US-08-023-757-8	Sequence 8, Appli	c 654	11.4	38.0	25	4	US-09-866-108A-4973	Sequence 4973, Ap
582	11.6	38.7	44	1	US-08-177-507-8	Sequence 8, Appli	c 655	11.4	38.0	25	4	US-09-866-108A-4974	Sequence 4974, Ap
583	11.6	38.7	44	1	US-08-054-650A-2	Sequence 2, Appli	c 656	11.4	38.0	26	2	US-08-480-473B-64	Sequence 64, Appl
584	11.6	38.7	44	2	US-08-411-796-449	Sequence 449, App	c 657	11.4	38.0	26	2	US-08-915-213-64	Sequence 64, Appl
585	11.6	38.7	44	2	US-08-383-621-11	Sequence 11, Appl	c 658	11.4	38.0	26	3	US-09-235-217-64	Sequence 64, Appl
586	11.6	38.7	44	3	US-08-459-906-11	Sequence 11, Appl	c 659	11.4	38.0	26	3	US-09-245-041-65	Sequence 65, Appl
587	11.6	38.7	44	3	US-08-471-033-449	Sequence 449, App	660	11.4	38.0	26	3	US-09-358-055B-66	Sequence 66, Appl
588	11.6	38.7	44	4	US-08-559-390-449	Sequence 449, App	661	11.4	38.0	26	4	US-09-893-238-65	Sequence 65, Appl
589	11.6	38.7	44	5	PCT-US93-11198-449	Sequence 449, App	662	11.4	38.0	26	4	PCT-US92-08094-36	Sequence 36, Appl
590	11.6	38.7	46	1	US-08-089-755A-14	Sequence 14, Appl	c 663	11.4	38.0	26	5	US-08-261-304-12	Sequence 12, Appl
591	11.6	38.7	46	1	US-08-421-754-14	Sequence 14, Appl	664	11.4	38.0	27	1	US-08-758-306-52	Sequence 52, Appl
592	11.6	38.7	46	2	US-08-421-791-14	Sequence 14, Appl	c 665	11.4	38.0	27	1	US-08-257-584-14	Sequence 14, Appl
593	11.6	38.7	47	4	US-09-641-638-919	Sequence 919, App	666	11.4	38.0	27	3	US-08-485-611A-6	Sequence 6, Appli
594	11.6	38.7	47	4	US-09-641-638-1158	Sequence 1158, Ap	c 667	11.4	38.0	29	2	US-08-859-998-148	Sequence 148, App
595	11.6	38.7	47	4	US-09-671-317-735	Sequence 735, App	c 668	11.4	38.0	31	2	US-08-694-869-9	Sequence 9, Appli
596	11.6	38.7	47	4	US-09-422-978-118	Sequence 118, App	c 669	11.4	38.0	31	2	US-09-349-546-9	Sequence 9, Appli
597	11.6	38.7	47	4	US-09-422-978-897	Sequence 897, App	670	11.4	38.0	31	3	US-09-223-928-148	Sequence 148, App
598	11.6	38.7	47	4	US-09-422-978-1665	Sequence 1665, Ap	c 671	11.4	38.0	31	3	US-09-225-201B-148	Sequence 148, App
599	11.6	38.7	47	4	US-09-422-978-1961	Sequence 1961, Ap	c 672	11.4	38.0	31	4	US-09-502-831-9	Sequence 9, Appli
600	11.6	38.7	47	4	US-09-422-978-3780	Sequence 3780, Ap	c 673	11.4	38.0	32	1	US-08-591-070A-32	Sequence 32, Appl
601	11.6	38.7	47	4	US-09-422-978-3993	Sequence 3993, Ap	c 674	11.4	38.0	32	1	US-08-927-855-32	Sequence 32, Appl
602	11.6	38.7	47	4	US-10-170-097-919	Sequence 919, App	c 675	11.4	38.0	32	2	US-08-647-924-22	Sequence 22, Appl
603	11.6	38.7	47	4	US-08-472-194A-29	Sequence 1158, Ap	c 676	11.4	38.0	32	3	US-09-603-185-7	Sequence 7, Appli
604	11.6	38.7	48	1	US-08-472-194A-29	Sequence 29, Appl	c 677	11.4	38.0	32	3	US-09-862-844-10	Sequence 10, Appl
605	11.6	38.7	48	3	US-08-849-567A-29	Sequence 29, Appl	c 678	11.4	38.0	32	4	US-09-862-844-12	Sequence 12, Appl
606	11.6	38.7	48	3	US-08-381-572-2	Sequence 2, Appli	c 679	11.4	38.0	33	1	US-08-343-785-11	Sequence 11, Appl
607	11.6	38.7	49	1	US-08-592-820-2	Sequence 2, Appli	c 680	11.4	38.0	33	1	US-08-067-160-2	Sequence 2, Appli
608	11.6	38.7	49	1	US-08-416-756A-9	Sequence 9, Appli	c 681	11.4	38.0	33	2	US-08-462-221-11	Sequence 11, Appl
609	11.6	38.7	50	1	US-08-690-184-4	Sequence 4, Appli	c 682	11.4	38.0	33	2	US-08-717-394-2	Sequence 2, Appli
610	11.6	38.7	50	3	US-09-291-823-4	Sequence 4, Appli	c 683	11.4	38.0	33	2	US-08-487-110-2	Sequence 2, Appli
611	11.6	38.7	50	3			c 684	11.4	38.0	33	2		

685	11.4	38.0	33	2	US-08-646-367-19	Sequence 19, Appl	758	11.4	38.0	47	1	US-08-411-796-53	Sequence 53, Appl
686	11.4	38.0	33	2	US-08-690-184-7	Sequence 7, Appl	c 759	11.4	38.0	47	1	US-08-123-936-237	Sequence 237, App
687	11.4	38.0	33	3	US-09-028-648A-2	Sequence 2, Appl	c 760	11.4	38.0	47	2	US-08-475-228A-237	Sequence 237, App
688	11.4	38.0	33	3	US-08-523-373-12	Sequence 12, Appl	c 761	11.4	38.0	47	3	US-08-482-080A-237	Sequence 237, App
689	11.4	38.0	33	3	US-08-946-405-11	Sequence 11, Appl	c 762	11.4	38.0	47	3	US-08-471-039-53	Sequence 53, Appl
690	11.4	38.0	33	3	US-08-379-850-10	Sequence 10, Appl	c 763	11.4	38.0	47	3	US-09-354-947-237	Sequence 237, App
691	11.4	38.0	33	3	US-09-028-587-2	Sequence 2, Appl	c 764	11.4	38.0	47	4	US-08-559-390-53	Sequence 53, Appl
692	11.4	38.0	33	3	US-09-048-129-10	Sequence 10, Appl	c 765	11.4	38.0	47	4	US-09-671-317-551	Sequence 551, App
693	11.4	38.0	33	3	US-08-511-759B-8	Sequence 8, Appl	c 766	11.4	38.0	47	4	US-09-671-317-840	Sequence 840, App
694	11.4	38.0	33	3	US-09-028-652-2	Sequence 2, Appl	c 767	11.4	38.0	47	4	US-09-671-317-862	Sequence 862, App
695	11.4	38.0	33	3	US-08-487-107-2	Sequence 2, Appl	c 768	11.4	38.0	47	4	US-09-422-978-1106	Sequence 1106, App
696	11.4	38.0	33	3	US-09-048-079-10	Sequence 10, Appl	c 769	11.4	38.0	47	4	US-09-422-978-1646	Sequence 1646, App
697	11.4	38.0	33	3	US-09-291-823-7	Sequence 7, Appl	c 770	11.4	38.0	47	4	US-09-422-978-2772	Sequence 2772, App
698	11.4	38.0	33	3	US-09-592-197-8	Sequence 8, Appl	c 771	11.4	38.0	47	4	US-09-422-978-3131	Sequence 3131, App
699	11.4	38.0	33	3	US-08-892-704-8	Sequence 8, Appl	c 772	11.4	38.0	47	4	US-09-422-978-3225	Sequence 3225, App
700	11.4	38.0	33	3	US-08-793-410-19	Sequence 19, Appl	c 773	11.4	38.0	47	4	US-09-422-978-721	Sequence 721, App
701	11.4	38.0	34	2	US-09-915-060A-13	Sequence 13, Appl	c 774	11.4	38.0	47	4	US-09-422-978-938	Sequence 938, App
702	11.4	38.0	35	4	US-08-383-743A-21	Sequence 21, Appl	c 775	11.4	38.0	47	4	PCT-US93-11638-11	Sequence 11, Appl
703	11.4	38.0	37	1	US-08-808-881-21	Sequence 21, Appl	c 776	11.4	38.0	47	5	PCT-US93-12388-237	Sequence 237, App
704	11.4	38.0	37	3	US-09-017-631-21	Sequence 21, Appl	c 777	11.4	38.0	47	5	US-08-411-796-167	Sequence 167, App
705	11.4	38.0	37	3	US-09-455-960-22	Sequence 22, Appl	c 778	11.4	38.0	48	1	US-08-411-796-168	Sequence 168, App
706	11.4	38.0	37	4	US-09-520-118-21	Sequence 21, Appl	c 779	11.4	38.0	48	1	US-08-518-878B-6	Sequence 6, Appl
707	11.4	38.0	37	4	US-10-051-325-22	Sequence 22, Appl	c 780	11.4	38.0	48	1	US-08-518-878B-39	Sequence 39, Appl
708	11.4	38.0	37	5	PCT-US93-07116-21	Sequence 21, Appl	c 781	11.4	38.0	48	1	US-08-294-522B-6	Sequence 6, Appl
709	11.4	38.0	38	3	US-08-851-843A-108	Sequence 108, App	c 782	11.4	38.0	48	1	US-08-294-522B-39	Sequence 39, Appl
710	11.4	38.0	38	3	US-08-974-549A-595	Sequence 595, App	c 783	11.4	38.0	48	1	US-08-807-861A-6	Sequence 6, Appl
711	11.4	38.0	38	3	US-08-854-050-108	Sequence 108, App	c 784	11.4	38.0	48	2	US-08-807-861A-39	Sequence 39, Appl
712	11.4	38.0	38	3	US-09-430-323-108	Sequence 108, App	c 785	11.4	38.0	48	2	US-08-470-868A-6	Sequence 6, Appl
713	11.4	38.0	38	4	US-09-402-181B-595	Sequence 595, App	c 786	11.4	38.0	48	2	US-08-470-868A-39	Sequence 39, Appl
714	11.4	38.0	38	4	US-09-721-456-595	Sequence 595, App	c 787	11.4	38.0	48	2	US-08-470-868A-39	Sequence 39, Appl
715	11.4	38.0	40	3	US-09-277-016-11	Sequence 11, Appl	c 788	11.4	38.0	48	2	US-08-676-279-9	Sequence 9, Appl
716	11.4	38.0	40	4	US-10-153-064-108	Sequence 108, App	c 789	11.4	38.0	48	3	US-08-471-039-167	Sequence 167, App
717	11.4	38.0	41	1	US-07-931-473B-104	Sequence 104, App	c 790	11.4	38.0	48	3	US-08-471-039-168	Sequence 168, App
718	11.4	38.0	41	1	US-07-931-473B-156	Sequence 156, App	c 791	11.4	38.0	48	3	US-09-210-681-6	Sequence 6, Appl
719	11.4	38.0	41	1	US-07-931-473B-158	Sequence 158, App	c 792	11.4	38.0	48	3	US-09-210-681-39	Sequence 39, Appl
720	11.4	38.0	41	1	US-07-714-131C-104	Sequence 104, App	c 793	11.4	38.0	48	3	US-08-946-719A-6	Sequence 6, Appl
721	11.4	38.0	41	1	US-07-714-131C-156	Sequence 156, App	c 794	11.4	38.0	48	3	US-08-946-719A-39	Sequence 39, Appl
722	11.4	38.0	41	1	US-07-714-131C-158	Sequence 158, App	c 795	11.4	38.0	48	4	US-08-559-390-167	Sequence 167, App
723	11.4	38.0	41	1	US-08-412-110-104	Sequence 104, App	c 796	11.4	38.0	48	4	US-08-559-390-168	Sequence 168, App
724	11.4	38.0	41	1	US-08-412-110-156	Sequence 156, App	c 797	11.4	38.0	48	4	US-09-547-983-6	Sequence 6, Appl
725	11.4	38.0	41	1	US-08-412-110-158	Sequence 158, App	c 798	11.4	38.0	48	4	US-09-547-983-39	Sequence 39, Appl
726	11.4	38.0	41	1	US-08-409-442A-104	Sequence 104, App	c 799	11.4	38.0	48	5	PCT-US93-11198-167	Sequence 167, App
727	11.4	38.0	41	1	US-08-409-442A-156	Sequence 156, App	c 800	11.4	38.0	48	5	PCT-US93-11198-168	Sequence 168, App
728	11.4	38.0	41	1	US-08-409-442A-158	Sequence 158, App	c 801	11.4	38.0	48	5	US-08-955-138-74	Sequence 74, Appl
729	11.4	38.0	41	2	US-08-469-609A-104	Sequence 104, App	c 802	11.4	38.0	49	5	PCT-US94-08052-8	Sequence 8, Appl
730	11.4	38.0	41	2	US-08-469-609A-156	Sequence 156, App	c 803	11.4	38.0	50	1	US-08-171-389-360	Sequence 360, App
731	11.4	38.0	41	2	US-08-469-609A-158	Sequence 158, App	c 804	11.4	38.0	50	1	US-08-171-389-582	Sequence 582, App
732	11.4	38.0	41	3	US-09-143-190-104	Sequence 104, App	c 805	11.4	38.0	50	1	US-08-207-901-63	Sequence 63, Appl
733	11.4	38.0	41	3	US-09-143-190-156	Sequence 156, App	c 806	11.4	38.0	50	1	US-08-123-936-360	Sequence 360, App
734	11.4	38.0	41	3	US-09-143-190-158	Sequence 158, App	c 807	11.4	38.0	50	1	US-08-123-936-582	Sequence 582, App
735	11.4	38.0	41	3	US-09-502-344-104	Sequence 104, App	c 808	11.4	38.0	50	2	US-08-475-228A-360	Sequence 360, App
736	11.4	38.0	41	3	US-09-502-344-156	Sequence 156, App	c 809	11.4	38.0	50	2	US-08-475-228A-582	Sequence 582, App
737	11.4	38.0	41	3	US-09-502-344-158	Sequence 158, App	c 810	11.4	38.0	50	3	US-08-482-080A-360	Sequence 360, App
738	11.4	38.0	41	3	US-09-564-805-102	Sequence 102, App	c 811	11.4	38.0	50	3	US-08-482-080A-582	Sequence 582, App
739	11.4	38.0	42	1	US-08-233-009-53	Sequence 53, Appl	c 812	11.4	38.0	50	3	US-09-043-233-7	Sequence 7, Appl
740	11.4	38.0	42	1	US-08-233-009-54	Sequence 54, Appl	c 813	11.4	38.0	50	3	US-09-354-947-360	Sequence 360, App
741	11.4	38.0	42	3	US-08-864-357F-13	Sequence 13, Appl	c 814	11.4	38.0	50	3	US-09-354-947-582	Sequence 582, App
742	11.4	38.0	42	4	US-09-475-947A-324	Sequence 324, App	c 815	11.4	38.0	50	4	PCT-US93-12388-360	Sequence 360, App
743	11.4	38.0	42	4	US-09-475-947A-325	Sequence 325, App	c 816	11.4	38.0	50	5	PCT-US93-12388-582	Sequence 582, App
744	11.4	38.0	43	2	US-08-686-599A-14	Sequence 14, Appl	c 817	11.4	38.0	50	5	US-08-390-850-584	Sequence 584, App
745	11.4	38.0	43	3	US-09-061-702-13	Sequence 13, Appl	c 818	11.2	37.3	17	1	US-08-435-634-584	Sequence 584, App
746	11.4	38.0	43	3	US-09-748-451-13	Sequence 7, Appl	c 819	11.2	37.3	17	3	US-08-584-040-5991	Sequence 5991, App
747	11.4	38.0	45	3	US-09-312-285-7	Sequence 7, Appl	c 820	11.2	37.3	17	3	US-08-584-040-6042	Sequence 6042, App
748	11.4	38.0	45	3	US-09-312-266-7	Sequence 7, Appl	c 821	11.2	37.3	17	3	US-08-584-040-7634	Sequence 7634, App
749	11.4	38.0	45	3	US-08-987-943-7	Sequence 7, Appl	c 822	11.2	37.3	17	3	US-09-371-772B-2879	Sequence 2879, App
750	11.4	38.0	45	3	US-08-312-038-7	Sequence 7, Appl	c 823	11.2	37.3	17	4	US-09-371-772B-3426	Sequence 3426, App
751	11.4	38.0	45	4	US-09-728-764-7	Sequence 7, Appl	c 824	11.2	37.3	17	4	US-09-371-772B-3426	Sequence 3426, App
752	11.4	38.0	45	4	US-09-312-304B-5	Sequence 5, Appl	c 825	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
753	11.4	38.0	45	4	US-09-728-792-7	Sequence 7, Appl	c 826	11.2	37.3	17	4	US-09-866-108A-548	Sequence 548, App
754	11.4	38.0	45	4	US-09-850-964-7	Sequence 7, Appl	c 827	11.2	37.3	17	4	US-09-866-108A-9259	Sequence 9259, App
755	11.4	38.0	45	4	US-09-532-806-7	Sequence 8, Appl	c 828	11.2	37.3	17	4	US-09-866-108A-9260	Sequence 9260, App
756	11.4	38.0	46	2	US-09-381-691-12	Sequence 12, Appl	c 829	11.2	37.3	17	4	US-09-866-108A-9262	Sequence 9262, App
c 757	11.4	38.0	47	1	US-08-171-389-237	Sequence 237, App	830	11.2	37.3	17	4		

831	11.2	37.3	17	4	US-09-866-108A-9263	Sequence 9263, Ap	904	11.2	37.3	28	2	US-08-859-998-1212	Sequence 1212, Ap
c 832	11.2	37.3	18	3	US-09-630-708-91	Sequence 91, Appl	c 905	11.2	37.3	28	3	US-08-648-263-15	Sequence 15, Appl
833	11.2	37.3	18	4	US-09-422-978-4787	Sequence 4787, Ap	906	11.2	37.3	28	3	US-09-397-238A-14	Sequence 14, Appl
834	11.2	37.3	18	4	US-09-422-978-9660	Sequence 9660, Ap	907	11.2	37.3	28	3	US-09-225-928-1212	Sequence 1212, Ap
c 835	11.2	37.3	19	3	US-08-072-064-11	Sequence 11, Appl	c 908	11.2	37.3	28	3	US-09-468-265-9	Sequence 9, Appl
836	11.2	37.3	19	4	US-09-060-295-54	Sequence 54, Appl	909	11.2	37.3	28	4	US-09-225-201B-1212	Sequence 1212, Ap
837	11.2	37.3	19	4	US-09-402-923A-54	Sequence 54, Appl	910	11.2	37.3	28	1	US-07-931-473B-125	Sequence 125, App
c 838	11.2	37.3	20	1	US-08-198-779-13	Sequence 13, Appl	911	11.2	37.3	29	1	US-07-714-131C-125	Sequence 125, App
c 839	11.2	37.3	20	3	US-08-578-615A-115	Sequence 115, Appl	912	11.2	37.3	29	1	US-08-409-442A-125	Sequence 125, App
840	11.2	37.3	20	3	US-09-359-757-19	Sequence 19, Appl	913	11.2	37.3	29	1	US-08-412-110-125	Sequence 125, App
841	11.2	37.3	20	4	US-09-428-584-21	Sequence 21, Appl	914	11.2	37.3	29	2	US-08-469-609A-125	Sequence 125, App
842	11.2	37.3	20	4	US-09-780-175-23	Sequence 23, Appl	c 915	11.2	37.3	29	2	US-08-787-902A-5	Sequence 5, Appl
843	11.2	37.3	20	4	US-09-676-610B-49	Sequence 49, Appl	916	11.2	37.3	29	3	US-09-143-130-125	Sequence 125, App
844	11.2	37.3	20	4	US-09-422-978-11629	Sequence 11629, A	917	11.2	37.3	29	3	US-09-502-344-125	Sequence 125, App
845	11.2	37.3	20	4	US-09-198-452A-5613	Sequence 5613, Ap	918	11.2	37.3	29	4	US-09-304-232-214	Sequence 214, App
846	11.2	37.3	20	4	US-09-495-714C-95	Sequence 95, Appl	919	11.2	37.3	29	4	US-10-119-466-2	Sequence 2, Appl
c 847	11.2	37.3	20	4	US-10-215-448-25	Sequence 25, Appl	c 920	11.2	37.3	30	1	US-07-955-718-38	Sequence 38, Appl
c 848	11.2	37.3	20	5	PCT-US94-07770-115	Sequence 115, Appl	921	11.2	37.3	30	2	US-08-629-001A-30	Sequence 30, Appl
849	11.2	37.3	21	2	US-08-798-738-9	Sequence 9, Appl	c 922	11.2	37.3	30	3	US-08-297-395-31	Sequence 31, Appl
c 850	11.2	37.3	21	2	US-08-738-922-6	Sequence 6, Appl	923	11.2	37.3	30	3	US-08-627-907A-8	Sequence 8, Appl
c 851	11.2	37.3	21	4	US-08-951-0348-4	Sequence 4, Appl	c 924	11.2	37.3	30	3	US-09-178-869-12	Sequence 12, Appl
c 852	11.2	37.3	23	1	US-08-211-202-81	Sequence 81, Appl	925	11.2	37.3	30	3	US-08-642-274D-109	Sequence 109, App
853	11.2	37.3	23	1	US-08-308-949A-11	Sequence 11, Appl	c 926	11.2	37.3	30	4	US-09-761-413-12	Sequence 12, Appl
c 854	11.2	37.3	23	1	US-08-307-619-52	Sequence 52, Appl	c 927	11.2	37.3	30	5	PCT-US91-05742-38	Sequence 38, Appl
c 855	11.2	37.3	23	1	US-08-299-187-3	Sequence 3, Appl	c 928	11.2	37.3	30	6	5217891-16	Patent No. 5217891
c 856	11.2	37.3	23	1	US-08-685-764-26	Sequence 26, Appl	c 929	11.2	37.3	31	3	US-08-951-923-45	Sequence 45, Appl
c 857	11.2	37.3	23	2	US-08-350-260A-98	Sequence 98, Appl	c 930	11.2	37.3	31	3	US-08-679-645-455	Sequence 455, Appl
c 858	11.2	37.3	23	2	US-08-350-260A-571	Sequence 571, Appl	c 931	11.2	37.3	32	1	US-08-021-623C-15	Sequence 15, Appl
c 859	11.2	37.3	23	3	US-09-050-783-52	Sequence 52, Appl	c 932	11.2	37.3	32	2	US-08-859-998-386	Sequence 386, Appl
c 860	11.2	37.3	23	4	US-09-104-337A-98	Sequence 98, Appl	c 933	11.2	37.3	32	3	US-08-535-057A-10	Sequence 10, Appl
c 861	11.2	37.3	23	4	US-09-104-337A-571	Sequence 571, Appl	c 934	11.2	37.3	32	3	US-09-225-928-386	Sequence 386, App
c 862	11.2	37.3	23	4	US-10-067-443-53	Sequence 53, Appl	c 935	11.2	37.3	32	4	US-09-225-201B-386	Sequence 386, App
c 863	11.2	37.3	23	4	US-10-067-443-65	Sequence 65, Appl	c 936	11.2	37.3	32	4	US-09-503-252-10	Sequence 10, Appl
c 864	11.2	37.3	23	4	US-10-153-064-53	Sequence 53, Appl	c 937	11.2	37.3	33	4	US-09-948-495A-9	Sequence 9, Appl
c 865	11.2	37.3	23	4	US-10-153-064-65	Sequence 65, Appl	938	11.2	37.3	34	1	US-07-796-106-8	Sequence 8, Appl
c 866	11.2	37.3	23	5	PCT-US95-11114-3	Sequence 3, Appl	c 939	11.2	37.3	35	2	US-08-850-049-27	Sequence 27, Appl
c 867	11.2	37.3	24	2	US-08-318-157B-50	Sequence 50, Appl	c 940	11.2	37.3	35	2	US-08-050-478-27	Sequence 27, Appl
c 868	11.2	37.3	24	2	US-08-687-080-129	Sequence 129, Appl	c 941	11.2	37.3	35	3	US-09-414-117-27	Sequence 27, Appl
c 869	11.2	37.3	24	3	US-08-646-861-34	Sequence 34, Appl	c 942	11.2	37.3	35	4	US-08-613-743-3	Sequence 3, Appl
c 870	11.2	37.3	24	4	US-09-253-794-50	Sequence 50, Appl	c 943	11.2	37.3	35	4	US-09-678-437-27	Sequence 27, Appl
c 871	11.2	37.3	25	1	US-08-394-210-3	Sequence 3, Appl	c 944	11.2	37.3	35	4	US-09-964-895-8	Sequence 8, Appl
872	11.2	37.3	25	1	US-08-394-210-16	Sequence 16, Appl	c 945	11.2	37.3	35	4	US-09-943-722-27	Sequence 27, Appl
c 873	11.2	37.3	25	2	US-08-273-402B-4	Sequence 4, Appl	946	11.2	37.3	36	2	US-09-375-257-9	Sequence 9, Appl
c 874	11.2	37.3	25	4	US-09-866-108A-3485	Sequence 3485, Ap	c 947	11.2	37.3	36	4	US-09-375-257-9	Sequence 9, Appl
875	11.2	37.3	25	4	US-09-866-108A-14151	Sequence 14151, A	c 948	11.2	37.3	37	1	US-08-399-696-61	Sequence 61, Appl
876	11.2	37.3	25	4	US-09-866-108A-14152	Sequence 14152, A	c 949	11.2	37.3	37	1	US-08-961-083-284	Sequence 284, App
877	11.2	37.3	25	4	US-09-866-108A-14162	Sequence 14162, A	950	11.2	37.3	37	4	US-09-536-784-284	Sequence 284, App
878	11.2	37.3	25	4	US-09-866-108A-14163	Sequence 14163, A	c 951	11.2	37.3	38	1	US-08-328-314-11	Sequence 11, Appl
879	11.2	37.3	25	4	US-09-142-108C-38	Sequence 38, Appl	c 952	11.2	37.3	38	1	US-08-731-045-11	Sequence 11, Appl
880	11.2	37.3	26	1	US-08-062-022-5	Sequence 5, Appl	c 953	11.2	37.3	38	3	US-08-535-057A-9	Sequence 9, Appl
881	11.2	37.3	26	1	US-08-495-743-5	Sequence 5, Appl	c 954	11.2	37.3	38	3	US-09-262-773-126	Sequence 126, App
882	11.2	37.3	26	1	US-08-495-739-5	Sequence 5, Appl	c 955	11.2	37.3	38	4	US-09-503-252-9	Sequence 9, Appl
883	11.2	37.3	26	1	US-08-495-741-5	Sequence 5, Appl	956	11.2	37.3	39	1	US-07-759-568-5	Sequence 5, Appl
884	11.2	37.3	26	1	US-08-257-073-123	Sequence 123, Appl	957	11.2	37.3	39	3	US-08-961-083-275	Sequence 275, App
c 885	11.2	37.3	26	3	US-08-062-023-5	Sequence 5, Appl	958	11.2	37.3	39	4	US-09-536-784-275	Sequence 275, App
c 886	11.2	37.3	26	4	US-07-955-726A-38	Sequence 38, Appl	959	11.2	37.3	40	4	US-09-313-221A-78	Sequence 78, Appl
c 887	11.2	37.3	26	4	US-08-062-021A-11	Sequence 11, Appl	960	11.2	37.3	41	1	US-07-931-473B-157	Sequence 157, App
c 888	11.2	37.3	27	1	US-08-758-306-456	Sequence 456, Appl	961	11.2	37.3	41	1	US-07-714-131C-157	Sequence 157, App
c 889	11.2	37.3	27	3	US-08-985-162-858	Sequence 858, App	c 962	11.2	37.3	41	1	US-08-211-202-91	Sequence 91, Appl
c 890	11.2	37.3	27	3	US-08-985-162-959	Sequence 959, App	963	11.2	37.3	41	1	US-08-412-110-157	Sequence 157, App
c 891	11.2	37.3	27	3	US-08-985-162-976	Sequence 976, App	964	11.2	37.3	41	1	US-08-409-442A-157	Sequence 157, App
c 892	11.2	37.3	27	3	US-08-584-040-695	Sequence 695, App	965	11.2	37.3	41	1	US-08-409-442A-361	Sequence 361, App
c 893	11.2	37.3	27	3	US-08-584-040-773	Sequence 773, App	c 966	11.2	37.3	41	1	US-08-307-619-60	Sequence 60, Appl
c 894	11.2	37.3	27	3	US-08-584-040-7710	Sequence 7710, Ap	967	11.2	37.3	41	2	US-08-469-609A-157	Sequence 157, App
c 895	11.2	37.3	27	3	US-08-584-040-4748	Sequence 4748, Ap	968	11.2	37.3	41	2	US-08-469-609A-361	Sequence 361, App
c 896	11.2	37.3	27	3	US-08-584-040-4948	Sequence 4948, Ap	c 969	11.2	37.3	41	2	US-08-350-260A-106	Sequence 106, App
c 897	11.2	37.3	27	3	US-08-584-040-5266	Sequence 5266, Ap	c 970	11.2	37.3	41	2	US-08-350-260A-207	Sequence 207, App
c 898	11.2	37.3	27	3	US-08-584-040-6910	Sequence 6910, Ap	971	11.2	37.3	41	2	US-08-576-626A-24	Sequence 24, Appl
c 899	11.2	37.3	27	4	US-09-401-063-858	Sequence 858, App	972	11.2	37.3	41	3	US-09-143-190-157	Sequence 157, App
c 900	11.2	37.3	27	4	US-09-401-063-959	Sequence 959, App	973	11.2	37.3	41	3	US-09-143-190-361	Sequence 361, App
c 901	11.2	37.3	27	4	US-09-401-063-976	Sequence 976, App	c 974	11.2	37.3	41	3	US-09-050-783-60	Sequence 60, Appl
902	11.2	37.3	28	2	US-08-948-569A-14	Sequence 14, Appl	975	11.2	37.3	41	3	US-09-502-344-157	Sequence 157, App
903	11.2	37.3	28	2	US-09-188-469-14	Sequence 14, Appl	976	11.2	37.3	41	3	US-09-502-344-361	Sequence 361, App


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; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-52

Query Match          54.7%; Score 16.4; DB 4; Length 46;
Best Local Similarity 76.9%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
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Db 41 GACTCAGACCTTGTGCGATCTGACGTT 16

RESULT 4
US-09-297-269-7/c
; Sequence 7, Application US/09297269
; Patent No. 6451557
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; APPLICANT: WERKMEISTER, Jerome A.
; TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
; TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
; TITLE OF INVENTION: METHOD (As Amended)
; FILE REFERENCE: Q54094
; CURRENT APPLICATION NUMBER: US/09/297,269
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: P03310
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: P04306
; EARLIER FILING DATE: 1996-12-19
; EARLIER APPLICATION NUMBER: PCT/AU97/00721
; EARLIER FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-297-269-7

Query Match          50.7%; Score 15.2; DB 4; Length 24;
Best Local Similarity 85.0%; Pred. No. 8.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| ||||| |||||
Db 20 TCCTTGGTGACCTCCCTTC 1

RESULT 5
US-09-317-930-3/c
; Sequence 930, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
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; SOFTWARE: Patent.pm
; SEQ ID NO 930
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 21
; OTHER INFORMATION: 12-442-133 : insertion C
US-09-671-317-930

Query Match          50.7%; Score 15.2; DB 4; Length 47;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 TCCTTGGTCATCTCACCTTC 29
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Db 21 TCCCTGATCATTCACCTTC 2

RESULT 6
US-08-944-410-53/c
; Sequence 53, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorige, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-53

Query Match          49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
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Db 41 GACTCAGACCTTGTGCGAGCTGACCTT 16

RESULT 7
US-08-944-410-54/c
; Sequence 54, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: Sorige, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-54

Query Match          49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
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Db 41 GACTCAGCTTGTGCACTGACGTT 16

RESULT 8

US-08-944-410-55/c
; Sequence 55, Application US/08944410
; Patent No. 6607878
; GENERAL INFORMATION:
; APPLICANT: SORGE, JOSEPH A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-55

Query Match 49.3%; Score 14.8; DB 4; Length 46;
Best Local Similarity 73.1%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTT 28
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Db 41 GACTCAGCTTGTGCACTGACGTT 16

RESULT 9

US-09-422-978-1893
; Sequence 1893, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: COHEN, DANIEL
; APPLICANT: CHUMAKOV, ILIYA
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1893
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7144-261 : polymorphic base C or T
US-09-422-978-1893

Query Match 49.3%; Score 14.8; DB 4; Length 47;
Best Local Similarity 67.9%; Pred. No. 1.4e+03;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCTCACCTTCT 30
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Db 14 GTCTCAGTTCYGTGGAACCCACCTTCT 41

RESULT 10

US-09-916-510A-20
; Sequence 20, Application US/09916510A
; Patent No. 6544507
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; APPLICANT: BRUNORI, MICHELE A.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-20

Query Match 48.7%; Score 14.6; DB 4; Length 36;
Best Local Similarity 69.0%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
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Db 2 TGGCCCGCTATTGGTCATCTGACCTTC 30

RESULT 11

US-09-530-139-28/c
; Sequence 28, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOOT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 28
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-28

Query Match 48.7%; Score 14.6; DB 4; Length 42;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
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Db 41 GGACCCAGGTCCACCGTCTCTCCACCGTCT 13

RESULT 12

US-09-710-200-40/c
; Sequence 40, Application US/09710200
; Patent No. 6379897
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.

```
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICROARRAYS
; FILE REFERENCE: 256/262 Patrick S. Egleman
; CURRENT APPLICATION NUMBER: US/09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-710-200-40

Query Match      48.7%; Score 14.6; DB 3; Length 49;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACTCAGTCCTTGTCATCTCACCTTCT 30
Db 43 GCACTCAGTCCTAGTCACCTTCCTAT 15

RESULT 13
US-09-975-408-40/c
; Sequence 40, Application US/09975408
; Patent No. 6492122
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC MICROARRAYS
; FILE REFERENCE: 267/174 Patrick S. Egleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; PRIOR FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-975-408-40

Query Match      48.7%; Score 14.6; DB 4; Length 49;
Best Local Similarity 69.0%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 2 GCACTCAGTCCTTGTCATCTCACCTTCT 30
Db 43 GCACTCAGTCCTAGTCACCTTCCTAT 15

RESULT 14
US-08-758-306-368/c
; Sequence 368, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwiggen, James A.
```

```
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF DISEASES ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; TITLE OF INVENTION: ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; TITLE OF INVENTION: ASSOCIATED WITH INTERLEUKIN-2 RECEPTOR GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The letter "N" stands for the stem II
; OTHER INFORMATION: region of a HH ribozyme.
US-08-758-306-368

Query Match      48.0%; Score 14.4; DB 1; Length 27;
Best Local Similarity 72.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGTCATCTCACCT 27
Db 26 GTCTCATTTCTCATCTCACCT 2

RESULT 15
US-09-029-941-6
; Sequence 6, Application US/09029941
; Patent No. 6657106
; GENERAL INFORMATION:
; APPLICANT: SMITH, JAMES ANDREW CHARLES
; TITLE OF INVENTION: REMOVAL OF METALS FROM CONTAMINATED SUBSTRATES BY PLANTS
; FILE REFERENCE: SMITH ET AL.
; CURRENT APPLICATION NUMBER: US/09/029,941
; CURRENT FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
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OTHER INFORMATION: Description of Unknown Organism:SYNTHETIC DNA
OTHER INFORMATION: PRIMER
US-09-029-941-6
Query Match 48.0%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TGGACTCAGTCTCTGGTCA 19
Db 12 TGGACTTAGTCTTGCCCA 30
RESULT 18
US-09-079-984A-13
; Sequence 13, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyooshi, Satoh, Masashihiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1500 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other DNA; synthetic DNA
US-09-079-984A-13
Query Match 47.3%; Score 14.2; DB 3; Length 39;
US-09-132-619-18
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 5 CTCAGTCCTTGGTCACTC 23
Db 17 CTCAGCAGTGGTCACTC 35
RESULT 19
US-09-190-729-13
; Sequence 13, Application US/09390729
; Patent No. 6562334
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyooshi, Satoh, Masashihiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property

OTHER INFORMATION: Description of Unknown Organism:SYNTHETIC DNA
OTHER INFORMATION: PRIMER
US-09-029-941-6
Query Match 48.0%; Score 14.4; DB 4; Length 34;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 TGGACTCAGTCTCTGGTCACTCA 24
Db 6 TGGACTCACTCCATCATCTCTCA 29
RESULT 16
US-09-297-269-6
; Sequence 6, Application US/09297269
; Patent No. 6451557
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
; TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
; TITLE OF INVENTION: METHOD (As Amended)
; FILE REFERENCE: Q54094
; CURRENT APPLICATION NUMBER: US/09/297,269
; CURRENT FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: P03310
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: P04306
; EARLIER FILING DATE: 1996-12-19
; EARLIER APPLICATION NUMBER: PCT/AU97/00721
; EARLIER FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-297-269-6
Query Match 47.3%; Score 14.2; DB 4; Length 24;
US-09-132-619-18
Best Local Similarity 84.2%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 10 TCCTTGGTCACTCTCCTT 28
Db 6 TCCTTGGTCACTCTCCTT 24
RESULT 17
US-09-132-619-18
; Sequence 18, Application US/09132619B
; Patent No. 5958697
; GENERAL INFORMATION:
; APPLICANT: Shan, Bei
; APPLICANT: Nitta, Masahiro
; TITLE OF INVENTION: CYP7 Promoter-Binding Factors
; FILE REFERENCE: T97-013
; CURRENT APPLICATION NUMBER: US/09/132,619B
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 60/067,708
; EARLIER FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 34
; TYPE: DNA
; ORGANISM: human
US-09-132-619-18
Query Match 47.3%; Score 14.2; DB 2; Length 34;


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; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/390,729
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/079,984
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other DNA; synthetic DNA
; US-09-390-729-13

Query Match 47.3%; Score 14.2; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTC 23
Db 17 CTCAGTCAGTGGTCATCTC 35

RESULT 20
US-08-221-816B-18/c
; Sequence 18, Application US/08221816B
; Patent No. 5738985
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Withereil, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A

US-10-112-547-18/c
; Sequence 18, Application US/10112547
; Patent No. 6579674
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Withereil, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,547
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-112-547-18
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; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; US-08-221-816B-18

Query Match 47.3%; Score 14.2; DB 1; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4 ACTCAGTCCTTGGTCATCTCACCCTTCT 30
Db 33 ACTCAGTCAGTGATTATCTACCTGCT 7

RESULT 21
US-10-112-547-18/c
; Sequence 18, Application US/10112547
; Patent No. 6579674
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Withereil, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,547
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-112-547-18
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Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTGAGTGATTATCTACCTGCT 7

RESULT 22
US-10-112-241-18/c
; Sequence 18, Application US/10112241
; Patent No. 6623961
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Withereff, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,241
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-112-241-18

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTGAGTGATTATCTACCTGCT 7

RESULT 23
US-09-639-667-1/c
; Sequence 1, Application US/09639667
; Patent No. 6632800
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```
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen James
; APPLICANT: Peng, Kah Whye
; TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
; TRANSGENES
; FILE REFERENCE: 07039-292001
; CURRENT APPLICATION NUMBER: US/09/639,667
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 45
; TYPE: RNA
; ORGANISM: Influenza virus
; US-09-639-667-1

Query Match      47.3%; Score 14.2; DB 4; Length 45;
Best Local Similarity 70.4%; Pred. No. 2.5e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
   ||||| ||||| ||||| ||||| |||||
Db 33 ACTCAGTGAGTGATTATCTACCTGCT 7

RESULT 24
US-10-104-611-18/c
; Sequence 18, Application US/10104611
; Patent No. 6667152
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Withereff, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/104,611
; FILING DATE: 22-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-104-611-18
    Query Match      47.3%; Score 14.2; DB 4; Length 45;
    Best Local Similarity 70.4%; Pred. No. 2.5e+03;
    Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 33 ACTCAGTGAGTGATTCTACCTGCT 7

RESULT 25
US-10-109-368-18/c
; Sequence 18, Application US/10109368
; Patent No. 6777179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 27-Mar-2002
; APPLICATION NUMBER: US/10/109,368
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-109-368-18
    Query Match      47.3%; Score 14.2; DB 4; Length 45;
    Best Local Similarity 70.4%; Pred. No. 2.5e+03;
    Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 33 ACTCAGTGAGTGATTCTACCTGCT 7

RESULT 26
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US-09-338-907-269/c
; Sequence 269, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: PROSTATE CANCER GENE
; FILE REFERENCE: GENSET.18CPI
; CURRENT APPLICATION NUMBER: US/09/338,907
; CURRENT FILING DATE: 1999-06-23
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; EARLIER APPLICATION NUMBER: 09/218,207
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 269
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1..47
; OTHER INFORMATION: polymorphic fragment 4-26-60, variant version of SEQ ID192
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: base G ; A in SEQ ID192
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..23
; OTHER INFORMATION: potential microsequencing oligo 4-26-60.mis1
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 25..47
; OTHER INFORMATION: complement potential microsequencing oligo 4-26-60.mis2
US-09-338-907-269
    Query Match      47.3%; Score 14.2; DB 3; Length 47;
    Best Local Similarity 70.4%; Pred. No. 2.6e+03;
    Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 46 AGTCGCTCCTTGGCGCTGCTAACCGTCT 20

RESULT 27
US-09-218-207-269/c
; Sequence 269, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Ilya, Chumakov
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate cancer gene
; FILE REFERENCE: GENSET.018CPI
; CURRENT APPLICATION NUMBER: US/09/218,207
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 08/996,306
; EARLIER FILING DATE: 1997-12-22
; EARLIER APPLICATION NUMBER: 60/099,658
; EARLIER FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: Patent.pm
; SEQ ID NO 269
; LENGTH: 47
; TYPE: DNA
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```

Query Match          47.3%; Score 14.2; DB 1; Length 48;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 TGGACTCAGTCCTTGGTCATCTCACCT 27
      ||||| ||||| ||||| |||||
DB      30 TGGACCGACTCCATTCCTCCCAACTCACCT 4

RESULT 29
US-08-591-492-19
; Sequence 19, Application US/08591492
; Patent No. 5756086
; GENERAL INFORMATION:
; APPLICANT: McClelland, Alan
; APPLICANT: Stevenson, Susan C.
; TITLE OF INVENTION: Adenoviruses Having Modified
; TITLE OF INVENTION: Fiber Proteins
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,492
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/106,078
; FILING DATE: 13-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 271010-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: PCR DNA primer
US-08-591-492-19

Query Match          47.3%; Score 14.2; DB 1; Length 48;
Best Local Similarity 70.4%; Pred. No. 2.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 TGGACTCAGTCCTTGGTCATCTCACCT 27
      ||||| ||||| ||||| |||||
DB      19 TGGACCGACTCCATTCCTCCCAACTCACCT 45

RESULT 30
US-08-859-998-670
; Sequence 670, Application US/08859998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert

```

```
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 670:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; US-08-859-998-670

Query Match 46.7%; Score 14; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGGTCAT 20
Db 9 CAGTCCTTGGTCAT 22

RESULT 31
US-09-225-928-670
; Sequence 670, Application US/09235928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 670:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 670:
US-09-225-928-670

Query Match 46.7%; Score 14; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGGTCAT 20
Db 9 CAGTCCTTGGTCAT 22

RESULT 32
US-09-225-2018-670
; Sequence 670, Application US/09225201B
; Patent No. 6489455
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; Jokhadze, George
; Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,201B
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 670:
; SEQUENCE CHARACTERISTICS:
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LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 670;
US-09-225-201B-670
Query Match 46.7%; Score 14; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+03; Indels 0;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;
QY 7 CAGTCCTTGGTCAT 20
DB 9 CAGTCCTTGGTCAT 22
RESULT 33
PCT-US94-08052-9
Sequence 9, Application PC/TUS9408052
GENERAL INFORMATION:
APPLICANT: Schering Corporation
TITLE OF INVENTION: Agonists and Antagonists
TITLE OF INVENTION: Of Human Interleukin-10
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/08052
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/098,943
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul, G.
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-08052-9
Query Match 46.7%; Score 14; DB 5; Length 40;
Best Local Similarity 66.7%; Pred. No. 3.1e+03;
Matches 20; Conservative 0; Mismatches 10; Indels 0;
Gaps 0;
QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
DB 4 TGAATTCACCTTCAATGTCATGAGGCTTCT 33
RESULT 34
US-08-401-068-9/c
Sequence 9, Application US/08401068
Patent No. 5859335
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Enhanced Biotin Biosynthesis in Plant Tissue
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,068
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/351,970
FILING DATE: 08-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide primer for
DESCRIPTION: PCR of bioA gene"
HYPOTHETICAL: NO
US-08-401-068-9
Query Match 46.7%; Score 14; DB 2; Length 44;
Best Local Similarity 77.3%; Pred. No. 3.1e+03; Indels 0;
Matches 17; Conservative 0; Mismatches 5; Gaps 0;
QY 9 GTCCTTGGTCATCTCACCTTCT 30
DB 29 GTCCTTGGTCATCTCACCTTCT 8
RESULT 35
US-08-846-338-9/c
Sequence 9, Application US/08846338
Patent No. 5869719
GENERAL INFORMATION:
APPLICANT: Patton, David
TITLE OF INVENTION: Transgenic Plants Having Increased Biotin Content
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5869719artis Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,338
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucleotide primer for
HYPOTHETICAL: NO
US-08-846-338-9

Query Match 46.7%; Score 14; DB 2; Length 44;
Best Local Similarity 77.3%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 9 GTCCCTTGTCATCTCACCTTCT 30
Db 29 GTCCCTTGTCATCTCACCTTCT 8

RESULT 36
US-09-422-978-2989
Sequence 2989, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CPI
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2989
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-21448-361 : polymorphic base A or G
US-09-422-978-2989

Query Match 46.7%; Score 14; DB 4; Length 47;
Best Local Similarity 66.7%; Pred. No. 3.1e+03;
Matches 20; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGTCATCTCACCTTCT 30
Db 15 TGCCCTCTGCGCTGTCACCCACCACTT 44

RESULT 37
US-09-006-636-6/c
Sequence 6, Application US/09006636
Patent No. 6005092
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-
GLUCANASE GENE, PROMOTER AND PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,636
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-006-636-6

Query Match 46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TTGGTCATCTCACCTTC 29
Db 27 TTGGTCCTATCACCTTC 11

RESULT 38
US-09-006-632-6/c
Sequence 6, Application US/09006632
Patent No. 6184440
GENERAL INFORMATION:
APPLICANT: Shoseyov, Oded
APPLICANT: Shani, Ziv
APPLICANT: Shpigel, Etai
TITLE OF INVENTION: TRANSGENIC PLANTS OF ALTERED
MORPHOLOGY
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,632
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 7809-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

```

; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-006-632-6

Query Match          46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TTGGTCATCTCACCTTC 29
    ||||| |||||
Db 27 TTGGTCCTATCACCTTC 11

RESULT 39
US-09-325-274-6/c
; Sequence 6, Application US/09325274
; Patent No. 6323023
; GENERAL INFORMATION:
; APPLICANT: Shoseyov, Oded
; APPLICANT: Shani, Ziv
; TITLE OF INVENTION: ARABIDOPSIS THALIANA ENDO-1,4-BETA-
; TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/325,274
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/006,636
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Baldwin, Geraldine F.
; REGISTRATION NUMBER: 31,232
; REFERENCE/DOCKET NUMBER: 7809-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-325-274-6

Query Match          46.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TTGGTCATCTCACCTTC 29
    ||||| |||||
Db 27 TTGGTCCTATCACCTTC 11
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```

RESULT 40
US-09-416-756A-14
; Sequence 14, Application US/09416756A
; Patent No. 6171845
; GENERAL INFORMATION:
; APPLICANT: Degussa-Huls AG
; TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF PANTOTHENIC ACID BY
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEOTIDE SEQUENCES WHICH CODE FOR
; TITLE OF INVENTION: KETOPANTOATE REDUCTASE
; FILE REFERENCE: Elischewski
; CURRENT APPLICATION NUMBER: US/09/416,756A
; CURRENT FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: DB 19846499.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer
US-09-416-756A-14

Query Match          46.0%; Score 13.8; DB 3; Length 36;
Best Local Similarity 72.0%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCAC 25
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Db 12 TGCAGTCAGTCCTTTCTCCAGTCAC 36

Search completed: November 23, 2004, 22:26:22
Job time : 43.7191 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 18:47:33 ; Search time 140.674 Seconds
(without alignments)
; 1152.370 Million cell updates/sec

Title: US-10-087-631B-4
Perfect score: 30
Sequence: 1 tggactcagtccttggatccactctct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3627888 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 1987578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications NA:*

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4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	30	14	US-10-087-631B-4
2	30	100.0	30	15	US-10-419-022-4
3	30	100.0	30	16	US-10-337-190-2
4	19	63.3	31	15	US-10-147-679A-22
5	16.6	55.3	25	15	US-10-098-263B-99847
6	16.4	54.7	46	8	US-08-944-410-52
7	16.2	54.0	25	15	US-10-098-263B-123322
8	16.2	53.3	25	15	US-10-098-263B-101913
9	15.8	52.7	26	15	US-10-038-835-56
10	15.6	52.0	50	16	US-10-131-827-405
11	15.6	52.0	50	16	US-10-131-827-4918
12	15.4	51.3	25	15	US-10-098-263B-112496

c 13	15.2	50.7	22	10	US-09-912-976-93	Sequence 93, Appl
c 14	15.2	50.7	22	10	US-09-965-422-76	Sequence 76, Appl
c 15	15.2	50.7	22	10	US-09-965-422-82	Sequence 82, Appl
c 16	15.2	50.7	22	14	US-10-005-041A-202	Sequence 202, Appl
c 17	15.2	50.7	24	14	US-10-023-831A-7	Sequence 7, Appl
c 18	15.2	50.7	24	14	US-10-294-934-930	Sequence 930, Appl
c 19	15.2	50.7	47	16	US-10-335-181-13	Sequence 13, Appl
c 20	15.0	50.0	25	15	US-10-098-263B-99848	Sequence 99848, A
c 21	15.0	50.0	25	15	US-10-098-263B-106307	Sequence 106307, A
c 22	15.0	50.0	25	15	US-10-098-263B-106308	Sequence 106308, A
c 23	15.0	50.0	31	9	US-09-801-274-1484	Sequence 1484, Ap
c 24	15.0	50.0	50	16	US-10-131-827-4195	Sequence 4195, Ap
c 25	14.8	49.3	20	15	US-10-038-835-27	Sequence 27, Appl
c 26	14.8	49.3	25	18	US-10-427-696-311	Sequence 311, Appl
c 27	14.8	49.3	41	16	US-10-035-833A-347	Sequence 347, Appl
c 28	14.8	49.3	41	16	US-10-035-833A-6498	Sequence 6498, Ap
c 29	14.8	49.3	46	8	US-08-944-410-53	Sequence 53, Appl
c 30	14.8	49.3	46	8	US-08-944-410-54	Sequence 54, Appl
c 31	14.8	49.3	46	8	US-08-944-410-55	Sequence 55, Appl
c 32	14.8	49.3	47	16	US-10-349-143-1893	Sequence 1893, Ap
c 33	14.6	48.7	25	15	US-10-098-263B-102519	Sequence 102519, A
c 34	14.6	48.7	25	15	US-10-098-263B-123321	Sequence 123321, A
c 35	14.6	48.7	26	16	US-10-210-130-295	Sequence 295, Appl
c 36	14.6	48.7	36	9	US-09-916-510A-20	Sequence 20, Appl
c 37	14.6	48.7	36	16	US-10-376-630-20	Sequence 20, Appl
c 38	14.6	48.7	38	16	US-10-453-827-1043	Sequence 1043, Ap
c 39	14.6	48.7	38	16	US-10-453-827-1190	Sequence 1190, Ap
c 40	14.6	48.7	42	10	US-09-530-139-28	Sequence 28, Appl
c 41	14.6	48.7	49	9	US-09-975-408-40	Sequence 40, Appl
c 42	14.6	48.7	49	13	US-10-075-579-40	Sequence 40, Appl
c 43	14.6	48.7	50	16	US-10-416-122-11	Sequence 11, Appl
c 44	14.4	48.0	25	15	US-10-098-263B-66485	Sequence 66485, A
c 45	14.4	48.0	25	15	US-10-098-263B-101914	Sequence 101914, A
c 46	14.4	48.0	34	9	US-09-029-941-6	Sequence 6, Appl
c 47	14.4	48.0	45	10	US-09-791-153A-26	Sequence 26, Appl
c 48	14.4	48.0	47	16	US-10-333-429-6	Sequence 6, Appl
c 49	14.2	47.3	24	14	US-10-023-831A-6	Sequence 6, Appl
c 50	14.2	47.3	34	18	US-10-721-997A-1	Sequence 1, Appl
c 51	14.2	47.3	34	18	US-10-721-997A-2	Sequence 2, Appl
c 52	14.2	47.3	37	9	US-09-917-265-99	Sequence 99, Appl
c 53	14.2	47.3	45	13	US-10-104-611-18	Sequence 18, Appl
c 54	14.2	47.3	45	13	US-10-112-547-18	Sequence 18, Appl
c 55	14.2	47.3	45	13	US-10-112-241-18	Sequence 18, Appl
c 56	14.2	47.3	45	18	US-10-109-368-18	Sequence 18, Appl
c 57	14.2	47.3	45	18	US-10-641-834-1	Sequence 1, Appl
c 58	14.2	47.3	47	9	US-09-901-484A-269	Sequence 269, Appl
c 59	14.2	47.3	47	9	US-09-853-526-269	Sequence 269, Appl
c 60	14.0	46.7	19	15	US-10-038-835-25	Sequence 25, Appl
c 61	14.0	46.7	24	15	US-10-411-954-61	Sequence 61, Appl
c 62	14.0	46.7	24	15	US-10-411-954-293	Sequence 293, Appl
c 63	14.0	46.7	24	16	US-10-617-070-61	Sequence 61, Appl
c 64	14.0	46.7	24	16	US-10-617-070-293	Sequence 293, Appl
c 65	14.0	46.7	24	15	US-10-617-070-448	Sequence 448, Appl
c 66	14.0	46.7	25	15	US-10-098-263B-13236	Sequence 13236, A
c 67	14.0	46.7	25	15	US-10-098-263B-80490	Sequence 80490, A
c 68	14.0	46.7	25	15	US-10-098-263B-127582	Sequence 127582, A
c 69	14.0	46.7	41	16	US-10-035-833A-4865	Sequence 4865, Ap
c 70	14.0	46.7	47	16	US-10-349-143-2989	Sequence 2989, Ap
c 71	14.0	46.7	50	15	US-10-131-827-885	Sequence 885, Appl
c 72	13.8	46.0	24	15	US-10-032-585-4184	Sequence 4184, Appl
c 73	13.8	46.0	25	15	US-10-098-263B-96195	Sequence 96195, A
c 74	13.8	46.0	25	15	US-10-098-263B-112495	Sequence 112495, A
c 75	13.8	46.0	37	16	US-10-671-403-159	Sequence 159, Appl
c 76	13.8	46.0	37	16	US-10-671-419-159	Sequence 159, Appl
c 77	13.8	46.0	37	16	US-10-670-844-159	Sequence 159, Appl
c 78	13.8	46.0	37	16	US-10-671-134-159	Sequence 159, Appl
c 79	13.8	46.0	37	16	US-10-673-098-159	Sequence 159, Appl
c 80	13.8	46.0	37	16	US-10-672-638-159	Sequence 159, Appl
c 81	13.8	46.0	37	16	US-10-673-127-159	Sequence 159, Appl
c 82	13.8	46.0	37	17	US-10-670-817-159	Sequence 159, Appl
c 83	13.8	46.0	37	17	US-10-673-119-159	Sequence 159, Appl
c 84	13.8	46.0	37	17	US-10-673-127-159	Sequence 159, Appl
c 85	13.8	46.0	50	16	US-10-131-827-4500	Sequence 4500, Ap

C 86	13.6	45.3	20	17	US-10-480-276-18	Sequence 18, Appl	C 159	13.2	44.0	23	15	US-10-094-466-113	Sequence 113, App
C 87	13.6	45.3	21	18	US-10-786-720-8259	Sequence 8259, Ap	C 160	13.2	44.0	25	15	US-10-098-263B-346	Sequence 346, App
C 88	13.6	45.3	21	18	US-10-786-720-10491	Sequence 10491, A	C 161	13.2	44.0	25	15	US-10-098-263B-29149	Sequence 29149, A
C 89	13.6	45.3	24	10	US-09-940-185-2392	Sequence 2392, Ap	C 162	13.2	44.0	25	15	US-10-098-263B-29150	Sequence 29150, A
C 90	13.6	45.3	25	15	US-10-098-263B-242	Sequence 242, App	C 163	13.2	44.0	25	15	US-10-098-263B-110822	Sequence 110822, A
C 91	13.6	45.3	25	15	US-10-098-263B-12999	Sequence 12999, A	C 164	13.2	44.0	25	17	US-10-717-597-952	Sequence 952, App
C 92	13.6	45.3	25	15	US-10-098-263B-42188	Sequence 42188, A	C 165	13.2	44.0	25	17	US-10-775-159-581	Sequence 581, App
C 93	13.6	45.3	25	15	US-10-098-263B-73505	Sequence 73505, A	C 166	13.2	44.0	26	15	US-10-243-581B-7	Sequence 7, Appli
C 94	13.6	45.3	25	15	US-10-098-263B-93212	Sequence 93212, A	C 167	13.2	44.0	26	17	US-10-741-601-26211	Sequence 26211, A
C 95	13.6	45.3	29	16	US-10-093-463-204	Sequence 204, App	C 168	13.2	44.0	34	9	US-09-086-118-19	Sequence 19, Appl
C 96	13.6	45.3	29	16	US-10-072-012-1238	Sequence 1238, Ap	C 169	13.2	44.0	34	15	US-10-387-806-19	Sequence 19, Appl
C 97	13.6	45.3	31	17	US-09-961-077-437	Sequence 437, App	C 170	13.2	44.0	36	9	US-09-765-272-291	Sequence 291, App
C 98	13.6	45.3	31	17	US-10-772-656-69	Sequence 69, Appl	C 171	13.2	44.0	37	13	US-10-027-632-178427	Sequence 178427, App
C 99	13.6	45.3	39	10	US-09-093-972C-989	Sequence 989, App	C 172	13.2	44.0	37	15	US-10-027-632-178427	Sequence 87, Appl
C 100	13.6	45.3	43	16	US-10-260-238-6023	Sequence 6023, Ap	C 173	13.2	44.0	37	15	US-10-612-779-87	Sequence 49, Appl
C 101	13.4	44.7	17	14	US-10-060-756A-1888	Sequence 1888, Ap	C 174	13.2	44.0	46	8	US-08-944-410-49	Sequence 50, Appl
C 102	13.4	44.7	17	14	US-10-060-756A-1889	Sequence 1889, Ap	C 175	13.2	44.0	46	8	US-08-944-410-51	Sequence 51, Appl
C 103	13.4	44.7	17	14	US-10-060-756A-1890	Sequence 1890, Ap	C 176	13.2	44.0	46	8	US-08-944-410-56	Sequence 56, Appl
C 104	13.4	44.7	20	9	US-09-754-167-22	Sequence 22, Appl	C 177	13.2	44.0	46	8	US-08-944-410-57	Sequence 57, Appl
C 105	13.4	44.7	20	12	US-09-745-167A-22	Sequence 22, Appl	C 178	13.2	44.0	46	8	US-08-944-410-57	Sequence 57, Appl
C 106	13.4	44.7	21	18	US-10-786-720-6553	Sequence 6553, Ap	C 179	13.2	44.0	47	15	US-10-367-438-42	Sequence 42, Appl
C 107	13.4	44.7	21	18	US-10-786-720-6554	Sequence 6554, Ap	C 180	13.2	44.0	47	15	US-10-349-143-1615	Sequence 1615, Ap
C 108	13.4	44.7	21	18	US-10-786-720-6555	Sequence 6555, Ap	C 181	13.2	44.0	47	16	US-10-349-143-2521	Sequence 2521, Ap
C 109	13.4	44.7	21	18	US-10-786-720-7888	Sequence 7888, Ap	C 182	13.2	44.0	47	16	US-10-294-934-802	Sequence 802, App
C 110	13.4	44.7	21	18	US-10-786-720-8257	Sequence 8257, Ap	C 183	13.2	44.0	47	16	US-10-294-934-945	Sequence 945, App
C 111	13.4	44.7	21	18	US-10-786-720-8258	Sequence 8258, Ap	C 184	13.2	44.0	50	16	US-10-131-827-1516	Sequence 1516, Ap
C 112	13.4	44.7	21	18	US-10-786-720-8260	Sequence 8260, Ap	C 185	13	43.3	20	10	US-09-998-009-2	Sequence 2, Appli
C 113	13.4	44.7	21	18	US-10-786-720-8261	Sequence 8261, Ap	C 186	13	43.3	22	9	US-09-814-777A-62	Sequence 62, Appl
C 114	13.4	44.7	21	18	US-10-786-720-8262	Sequence 8262, Ap	C 187	13	43.3	22	9	US-09-814-777A-66	Sequence 66, Appl
C 115	13.4	44.7	21	18	US-10-786-720-8845	Sequence 8845, Ap	C 188	13	43.3	22	14	US-10-137-290-2	Sequence 2, Appli
C 116	13.4	44.7	21	18	US-10-786-720-8846	Sequence 8846, Ap	C 189	13	43.3	22	15	US-10-141-541-12	Sequence 12, Appl
C 117	13.4	44.7	21	18	US-10-786-720-8847	Sequence 8847, Ap	C 190	13	43.3	22	15	US-10-388-263-158	Sequence 158, App
C 118	13.4	44.7	21	18	US-10-786-720-10138	Sequence 10138, A	C 191	13	43.3	25	15	US-10-098-263B-41815	Sequence 41815, A
C 119	13.4	44.7	21	18	US-10-786-720-10489	Sequence 10489, A	C 192	13	43.3	25	15	US-10-098-263B-42654	Sequence 42654, A
C 120	13.4	44.7	21	18	US-10-786-720-10490	Sequence 10490, A	C 193	13	43.3	25	15	US-10-098-263B-81526	Sequence 81526, A
C 121	13.4	44.7	21	18	US-10-786-720-10492	Sequence 10492, A	C 194	13	43.3	25	15	US-10-098-263B-93072	Sequence 93072, A
C 122	13.4	44.7	21	18	US-10-786-720-10493	Sequence 10493, A	C 195	13	43.3	25	15	US-10-098-263B-102520	Sequence 102520, A
C 123	13.4	44.7	21	18	US-10-786-720-10494	Sequence 10494, A	C 196	13	43.3	25	15	US-10-098-263B-117000	Sequence 117000, A
C 124	13.4	44.7	25	14	US-10-060-756A-3885	Sequence 3885, Ap	C 197	13	43.3	25	15	US-10-061-201-2402	Sequence 2402, Ap
C 125	13.4	44.7	25	14	US-10-060-756A-3886	Sequence 3886, Ap	C 198	13	43.3	25	15	US-10-061-201-2403	Sequence 2403, Ap
C 126	13.4	44.7	25	14	US-10-060-756A-3887	Sequence 3887, Ap	C 199	13	43.3	25	15	US-10-061-201-2404	Sequence 2404, Ap
C 127	13.4	44.7	25	14	US-10-060-756A-3888	Sequence 3888, Ap	C 200	13	43.3	25	15	US-10-061-201-2405	Sequence 2405, Ap
C 128	13.4	44.7	25	14	US-10-060-756A-3889	Sequence 3889, Ap	C 201	13	43.3	25	15	US-10-061-201-2406	Sequence 2406, Ap
C 129	13.4	44.7	25	14	US-10-060-756A-3890	Sequence 3890, Ap	C 202	13	43.3	27	10	US-09-940-227-61	Sequence 61, Appl
C 130	13.4	44.7	25	14	US-10-060-756A-3891	Sequence 3891, Ap	C 203	13	43.3	29	16	US-10-451-942-21	Sequence 21, Appl
C 131	13.4	44.7	25	14	US-10-060-756A-3892	Sequence 3892, Ap	C 204	13	43.3	30	13	US-10-139-262-37	Sequence 37, Appl
C 132	13.4	44.7	25	14	US-10-060-756A-3893	Sequence 3893, Ap	C 205	13	43.3	31	14	US-10-255-969-37	Sequence 37, Appl
C 133	13.4	44.7	25	14	US-10-060-756A-3894	Sequence 3894, Ap	C 206	13	43.3	31	10	US-09-912-263-269	Sequence 269, App
C 134	13.4	44.7	25	14	US-10-060-756A-3895	Sequence 3895, Ap	C 207	13	43.3	32	9	US-09-334-477-45	Sequence 45, Appl
C 135	13.4	44.7	25	14	US-10-215-112-3767	Sequence 3767, Ap	C 208	13	43.3	32	15	US-10-327-592-1	Sequence 1, Appli
C 136	13.4	44.7	25	14	US-10-215-112-4702	Sequence 4702, Ap	C 209	13	43.3	33	17	US-10-679-620-49	Sequence 49, Appl
C 137	13.4	44.7	25	15	US-10-098-263B-94375	Sequence 94375, A	C 210	13	43.3	34	17	US-10-475-970-57	Sequence 57, Appl
C 138	13.4	44.7	27	16	US-10-401-520-113	Sequence 113, App	C 211	13	43.3	35	15	US-10-280-261-7	Sequence 7, Appli
C 139	13.4	44.7	27	16	US-10-401-520-130	Sequence 130, App	C 212	13	43.3	36	9	US-09-932-2548-2	Sequence 2, Appli
C 140	13.4	44.7	30	15	US-10-197-844-3	Sequence 3, Appli	C 213	13	43.3	36	14	US-10-118-495-17	Sequence 17, Appl
C 141	13.4	44.7	31	9	US-09-801-274-1749	Sequence 1749, Ap	C 214	13	43.3	36	14	US-10-118-495-18	Sequence 18, Appl
C 142	13.4	44.7	32	14	US-10-118-783-8	Sequence 8, Appli	C 215	13	43.3	36	16	US-10-620-914-17	Sequence 17, Appl
C 143	13.4	44.7	36	15	US-10-182-268A-2	Sequence 2, Appli	C 216	13	43.3	36	16	US-10-620-914-18	Sequence 18, Appl
C 144	13.4	44.7	37	14	US-10-187-339-3	Sequence 3, Appli	C 217	13	43.3	39	9	US-09-749-831-33	Sequence 33, Appl
C 145	13.4	44.7	39	16	US-10-453-827-311	Sequence 311, App	C 218	13	43.3	41	15	US-10-005-956-246	Sequence 246, App
C 146	13.4	44.7	41	16	US-10-035-833A-1851	Sequence 1851, Ap	C 219	13	43.3	41	16	US-10-035-833A-6033	Sequence 6033, Ap
C 147	13.4	44.7	41	16	US-10-035-833A-4446	Sequence 4446, Ap	C 220	13	43.3	44	15	US-10-270-071-49	Sequence 49, Appl
C 148	13.4	44.7	42	8	US-08-944-410-80	Sequence 80, Appl	C 221	13	43.3	46	15	US-10-411-954-65	Sequence 65, Appl
C 149	13.4	44.7	44	16	US-10-377-134-24	Sequence 24, Appl	C 222	13	43.3	46	16	US-10-617-070-65	Sequence 65, Appl
C 150	13.4	44.7	44	16	US-10-377-134-36	Sequence 36, Appl	C 223	13	43.3	46	16	US-10-617-070-297	Sequence 297, App
C 151	13.4	44.7	47	16	US-10-349-143-1446	Sequence 1446, Ap	C 224	13	43.3	46	16	US-10-617-070-452	Sequence 452, App
C 152	13.4	44.7	49	9	US-09-771-425-16	Sequence 16, Appl	C 225	13	43.3	47	15	US-10-411-954-64	Sequence 64, Appl
C 153	13.4	44.7	50	16	US-10-131-827-520	Sequence 520, App	C 226	13	43.3	47	15	US-10-411-954-64	Sequence 296, App
C 154	13.2	44.0	19	16	US-10-206-705-77	Sequence 77, Appl	C 227	13	43.3	47	16	US-10-349-143-2988	Sequence 2988, Ap
C 155	13.2	44.0	19	16	US-10-206-705-262	Sequence 262, App	C 228	13	43.3	47	16	US-10-617-070-64	Sequence 64, Appl
C 156	13.2	44.0	20	16	US-09-865-866-93	Sequence 93, Appl	C 229	13	43.3	47	16	US-10-617-070-296	Sequence 296, App
C 157	13.2	44.0	20	16	US-10-444-206-336	Sequence 336, App	C 230	13	43.3	47	16	US-10-617-070-296	Sequence 296, App
C 158	13.2	44.0	22	13	US-10-021-509-14	Sequence 14, Appl	C 231	13	43.3	47	16	US-10-617-070-451	Sequence 451, App

378	12.6	42.0	30	17	US-10-723-955-123	Sequence 123, App	C 451	12.4	41.3	25	15	US-10-098-263B-130954	Sequence 103954,
C 379	12.6	42.0	30	17	US-10-723-955-124	Sequence 124, App	C 452	12.4	41.3	25	15	US-10-098-263B-111664	Sequence 111664,
380	12.6	42.0	31	9	US-09-801-274-992	Sequence 992, App	C 433	12.4	41.3	25	15	US-10-098-263B-124876	Sequence 124876,
381	12.6	42.0	32	16	US-10-312-273-407	Sequence 407, App	C 434	12.4	41.3	25	15	US-10-098-263B-127581	Sequence 127581,
382	12.6	42.0	33	14	US-10-269-557-84	Sequence 84, App	C 455	12.4	41.3	25	15	US-10-098-263B-128603	Sequence 128603,
383	12.6	42.0	33	18	US-10-784-880-161	Sequence 161, App	C 456	12.4	41.3	25	15	US-10-230-026-83	Sequence 83, Appl
384	12.6	42.0	35	14	US-10-784-880-161	Sequence 3, Appl	C 457	12.4	41.3	25	15	US-10-061-201-4101	Sequence 4101, Ap
385	12.6	42.0	35	15	US-10-127-746-3	Sequence 3, Appl	C 458	12.4	41.3	25	15	US-10-061-201-4102	Sequence 4102, Ap
C 386	12.6	42.0	36	15	US-10-150-165-3	Sequence 3, Appl	C 459	12.4	41.3	25	15	US-10-440-066-4	Sequence 4, Appl
387	12.6	42.0	37	9	US-10-067-449-17	Sequence 17, Appl	C 460	12.4	41.3	25	17	US-10-717-597-1738	Sequence 1738, Ap
388	12.6	42.0	37	9	US-09-917-265-87	Sequence 87, Appl	C 461	12.4	41.3	25	17	US-10-717-597-1739	Sequence 1739, Ap
C 389	12.6	42.0	37	9	US-09-976-736-70	Sequence 70, Appl	C 462	12.4	41.3	25	17	US-10-717-597-1740	Sequence 1740, Ap
C 390	12.6	42.0	41	9	US-09-747-774A-71	Sequence 71, Appl	C 463	12.4	41.3	25	17	US-10-717-597-1741	Sequence 1741, Ap
C 391	12.6	42.0	41	10	US-09-309-196-63	Sequence 63, Appl	C 464	12.4	41.3	25	17	US-10-775-169-835	Sequence 835, App
C 392	12.6	42.0	41	15	US-09-953-354-71	Sequence 71, Appl	C 465	12.4	41.3	25	17	US-10-062-848-30	Sequence 30, Appl
C 393	12.6	42.0	41	15	US-10-263-341-63	Sequence 63, Appl	C 466	12.4	41.3	25	17	US-10-062-848-31	Sequence 31, Appl
C 394	12.6	42.0	41	16	US-10-035-833A-1565	Sequence 1565, Ap	C 467	12.4	41.3	25	17	US-10-776-104-30	Sequence 30, Appl
C 395	12.6	42.0	41	16	US-10-035-833A-4060	Sequence 4060, Ap	C 468	12.4	41.3	25	17	US-10-776-104-31	Sequence 31, Appl
C 396	12.6	42.0	41	16	US-10-035-833A-7096	Sequence 7096, Ap	C 469	12.4	41.3	25	15	US-10-090-182A-133	Sequence 133, App
C 397	12.6	42.0	41	18	US-10-600-003-63	Sequence 63, Appl	C 470	12.4	41.3	25	15	US-10-090-182A-400	Sequence 400, App
C 398	12.6	42.0	45	15	US-10-156-995-224	Sequence 224, App	C 471	12.4	41.3	25	15	US-10-336-638-798	Sequence 798, App
C 399	12.6	42.0	47	9	US-09-901-484A-192	Sequence 192, App	C 472	12.4	41.3	25	15	US-10-078-113-133	Sequence 133, App
C 400	12.6	42.0	47	9	US-09-901-484A-193	Sequence 193, App	C 473	12.4	41.3	25	15	US-10-078-113-400	Sequence 400, App
C 401	12.6	42.0	47	9	US-09-853-526-192	Sequence 192, App	C 474	12.4	41.3	25	16	US-10-179-940-133	Sequence 133, App
C 402	12.6	42.0	47	15	US-10-076-802-63	Sequence 63, Appl	C 475	12.4	41.3	25	16	US-09-801-274-406	Sequence 406, App
C 403	12.6	42.0	47	15	US-10-170-097-803	Sequence 803, App	C 476	12.4	41.3	31	9	US-10-312-273-403	Sequence 403, App
C 404	12.6	42.0	47	15	US-10-170-097-803	Sequence 803, App	C 477	12.4	41.3	32	16	US-09-894-799-16	Sequence 16, Appl
C 405	12.6	42.0	47	15	US-10-367-169-63	Sequence 63, Appl	C 478	12.4	41.3	33	10	US-10-387-943-41	Sequence 41, Appl
C 406	12.6	42.0	47	16	US-10-349-143-1198	Sequence 1198, Ap	C 479	12.4	41.3	33	16	US-10-648-884-16	Sequence 16, Appl
C 407	12.6	42.0	47	16	US-10-349-143-1547	Sequence 1547, Ap	C 480	12.4	41.3	33	16	US-10-770-668-54	Sequence 54, Appl
C 408	12.6	42.0	47	16	US-10-349-143-2807	Sequence 2807, Ap	C 481	12.4	41.3	36	18	US-10-622-240-12	Sequence 12, Appl
C 409	12.6	42.0	47	16	US-10-349-143-3752	Sequence 3752, Ap	C 482	12.4	41.3	38	16	US-10-035-833A-14	Sequence 14, Appl
C 410	12.6	42.0	48	10	US-09-918-156-72	Sequence 72, Appl	C 483	12.4	41.3	41	16	US-10-035-833A-1669	Sequence 1669, Ap
C 411	12.6	42.0	48	16	US-10-179-940-166	Sequence 166, App	C 484	12.4	41.3	41	16	US-10-035-833A-1742	Sequence 1742, Ap
C 412	12.6	42.0	48	16	US-10-179-940-170	Sequence 170, App	C 485	12.4	41.3	41	16	US-10-035-833A-3889	Sequence 3889, Ap
C 413	12.6	42.0	48	18	US-10-843-720-72	Sequence 72, Appl	C 486	12.4	41.3	41	16	US-10-035-833A-5936	Sequence 5936, Ap
C 414	12.6	42.0	48	18	US-10-852-283-72	Sequence 72, Appl	C 487	12.4	41.3	41	16	US-09-276-455-5	Sequence 5, Appl
C 415	12.6	42.0	50	16	US-10-131-827-3448	Sequence 3448, Ap	C 488	12.4	41.3	42	10	US-10-361-208-34	Sequence 34, Appl
C 416	12.6	42.0	50	16	US-10-131-827-8136	Sequence 8136, Ap	C 489	12.4	41.3	42	16	US-10-361-208-35	Sequence 35, Appl
C 417	12.4	41.3	17	14	US-10-060-756A-1887	Sequence 1887, Ap	C 490	12.4	41.3	42	16	US-10-361-208-47	Sequence 47, Appl
C 418	12.4	41.3	17	14	US-10-060-756A-1891	Sequence 1891, Ap	C 491	12.4	41.3	42	16	US-10-361-208-48	Sequence 48, Appl
C 419	12.4	41.3	17	15	US-10-338-777-247	Sequence 247, App	C 492	12.4	41.3	42	16	US-10-601-610-11	Sequence 11, Appl
C 420	12.4	41.3	20	9	US-09-752-639-123	Sequence 123, App	C 493	12.4	41.3	46	16	US-10-071-179-46	Sequence 46, Appl
C 421	12.4	41.3	20	9	US-09-984-198-123	Sequence 123, App	C 494	12.4	41.3	46	15	US-10-126-704-46	Sequence 46, Appl
C 422	12.4	41.3	20	16	US-10-289-762-4748	Sequence 4748, Ap	C 495	12.4	41.3	47	15	US-10-126-704-46	Sequence 46, Appl
C 423	12.4	41.3	21	16	US-10-188-186-178	Sequence 178, App	C 496	12.4	41.3	47	16	US-10-349-143-1776	Sequence 1776, Ap
C 424	12.4	41.3	21	18	US-10-786-720-6232	Sequence 6232, App	C 497	12.4	41.3	47	16	US-10-349-143-1988	Sequence 1988, Ap
C 425	12.4	41.3	21	18	US-10-786-720-7890	Sequence 7890, Ap	C 498	12.4	41.3	47	16	US-09-864-785-3416	Sequence 3416, Ap
C 426	12.4	41.3	21	18	US-10-786-720-10140	Sequence 10140, A	C 499	12.4	41.3	48	9	US-10-103-597A-16	Sequence 16, Appl
C 427	12.4	41.3	21	18	US-10-786-720-13415	Sequence 13415, A	C 500	12.4	41.3	49	14	US-10-188-444-16	Sequence 16, Appl
C 428	12.4	41.3	22	16	US-10-114-270-338	Sequence 338, App	C 501	12.4	41.3	49	15	US-10-131-827-537	Sequence 537, App
C 429	12.4	41.3	22	16	US-10-092-900A-523	Sequence 523, App	C 502	12.4	41.3	50	16	US-10-131-827-2103	Sequence 2103, Ap
C 430	12.4	41.3	25	14	US-10-060-756A-3884	Sequence 3884, App	C 503	12.4	41.3	50	16	US-10-131-827-3321	Sequence 3321, Ap
C 431	12.4	41.3	25	14	US-10-060-756A-3896	Sequence 3896, App	C 504	12.4	41.3	50	16	US-10-131-827-4056	Sequence 4056, Ap
C 432	12.4	41.3	25	15	US-10-098-263B-767	Sequence 767, App	C 505	12.4	41.3	50	16	US-10-131-827-4056	Sequence 4056, Ap
C 433	12.4	41.3	25	15	US-10-098-263B-6401	Sequence 6401, App	C 506	12.4	41.3	50	16	US-10-131-827-4706	Sequence 4706, Ap
C 434	12.4	41.3	25	15	US-10-098-263B-7774	Sequence 7774, App	C 507	12.4	41.3	50	16	US-10-131-827-4933	Sequence 4933, Ap
C 435	12.4	41.3	25	15	US-10-098-263B-11738	Sequence 11738, A	C 508	12.4	41.3	50	16	US-10-131-827-5055	Sequence 5055, Ap
C 436	12.4	41.3	25	15	US-10-098-263B-12325	Sequence 12325, A	C 509	12.2	40.7	17	9	US-09-866-108-547	Sequence 547, App
C 437	12.4	41.3	25	15	US-10-098-263B-36574	Sequence 36574, A	C 510	12.2	40.7	17	10	US-09-818-875-3526	Sequence 3526, Ap
C 438	12.4	41.3	25	15	US-10-098-263B-46701	Sequence 46701, A	C 511	12.2	40.7	17	10	US-09-818-875-3527	Sequence 3527, Ap
C 439	12.4	41.3	25	15	US-10-098-263B-49081	Sequence 49081, A	C 512	12.2	40.7	17	10	US-09-818-875-3534	Sequence 3534, Ap
C 440	12.4	41.3	25	15	US-10-098-263B-58754	Sequence 58754, A	C 513	12.2	40.7	17	10	US-10-209-787-3526	Sequence 3526, Ap
C 441	12.4	41.3	25	15	US-10-098-263B-64671	Sequence 64671, A	C 514	12.2	40.7	17	15	US-10-209-787-3527	Sequence 3527, Ap
C 442	12.4	41.3	25	15	US-10-098-263B-64672	Sequence 64672, A	C 515	12.2	40.7	17	15	US-10-209-787-3527	Sequence 3527, Ap
C 443	12.4	41.3	25	15	US-10-098-263B-80489	Sequence 80489, A	C 516	12.2	40.7	17	15	US-10-209-787-3534	Sequence 3534, Ap
C 444	12.4	41.3	25	15	US-10-098-263B-86326	Sequence 86326, A	C 517	12.2	40.7	17	15	US-10-209-787-3535	Sequence 3535, Ap
C 445	12.4	41.3	25	15	US-10-098-263B-86815	Sequence 86815, A	C 518	12.2	40.7	17	16	US-10-261-185-3526	Sequence 3526, Ap
C 446	12.4	41.3	25	15	US-10-098-263B-88209	Sequence 88209, A	C 519	12.2	40.7	17	16	US-10-261-185-3534	Sequence 3534, Ap
C 447	12.4	41.3	25	15	US-10-098-263B-88210	Sequence 88210, A	C 520	12.2	40.7	17	16	US-10-261-185-3535	Sequence 3535, Ap
C 448	12.4	41.3	25	15	US-10-098-263B-97500	Sequence 97500, A	C 521	12.2	40.7	17	16	US-10-676-154-109	Sequence 109, App
C 449	12.4	41.3	25	15	US-10-098-263B-99849	Sequence 99849, A	C 522	12.2	40.7	17	16	US-10-723-361-547	Sequence 547, App
C 450	12.4	41.3	25	15	US-10-098-263B-99850	Sequence 99850, A	C 523	12.2	40.7	17	17		

C 524	12.2	40.7	17	17	US-10-681-074-3526	Sequence 3526, Ap	597	12.2	40.7	26	9	US-09-766-095-4	Sequence 4, Appli
C 525	12.2	40.7	17	17	US-10-681-074-3527	Sequence 3527, Ap	C 598	12.2	40.7	26	9	US-09-766-095-56	Sequence 56, Appl
C 526	12.2	40.7	17	17	US-10-681-074-3528	Sequence 3528, Ap	C 599	12.2	40.7	26	9	US-09-766-095-70	Sequence 70, Appl
C 527	12.2	40.7	17	17	US-10-681-074-3529	Sequence 3529, Ap	C 600	12.2	40.7	26	9	US-09-766-095-84	Sequence 84, Appl
C 528	12.2	40.7	19	15	US-10-225-023-297	Sequence 297, App	C 601	12.2	40.7	26	15	US-10-244-490-10	Sequence 10, Appl
C 529	12.2	40.7	19	15	US-10-225-023-301	Sequence 301, App	C 602	12.2	40.7	27	15	US-10-214-419-50	Sequence 50, Appl
C 530	12.2	40.7	19	15	US-10-225-023-313	Sequence 313, App	C 603	12.2	40.7	27	15	US-09-091-134-7	Sequence 7, Appli
C 531	12.2	40.7	19	15	US-10-225-023-1035	Sequence 1035, App	C 604	12.2	40.7	28	16	US-10-615-518-7	Sequence 7, Appli
C 532	12.2	40.7	19	15	US-10-225-023-1039	Sequence 1039, Ap	C 605	12.2	40.7	28	17	US-10-772-272A-1	Sequence 1, Appli
C 533	12.2	40.7	19	15	US-10-225-023-1351	Sequence 1351, Ap	C 606	12.2	40.7	29	10	US-09-749-873-67	Sequence 67, Appl
C 534	12.2	40.7	20	9	US-09-929-486-3	Sequence 3, Appli	C 607	12.2	40.7	29	10	US-09-749-873-83	Sequence 83, Appl
C 535	12.2	40.7	20	10	US-09-973-853-1	Sequence 1, Appli	C 608	12.2	40.7	30	9	US-09-761-413-11	Sequence 11, Appl
C 536	12.2	40.7	20	15	US-10-259-903-3	Sequence 3, Appli	C 609	12.2	40.7	30	15	US-10-341-836-11	Sequence 11, Appl
C 537	12.2	40.7	20	15	US-10-259-903-4	Sequence 4, Appli	C 610	12.2	40.7	30	15	US-10-310-734-73	Sequence 73, Appl
C 538	12.2	40.7	20	15	US-10-144-140-59	Sequence 59, Appl	C 611	12.2	40.7	30	15	US-10-310-734-74	Sequence 74, Appl
C 539	12.2	40.7	20	16	US-10-318-970-20	Sequence 20, Appl	C 612	12.2	40.7	31	10	US-09-801-274-1004	Sequence 1004, Ap
C 540	12.2	40.7	20	16	US-10-399-083-1	Sequence 1, Appli	C 613	12.2	40.7	31	10	US-09-912-263-123	Sequence 123, App
C 541	12.2	40.7	20	16	US-10-398-988-1	Sequence 1, Appli	C 614	12.2	40.7	33	15	US-10-338-411-42	Sequence 42, Appl
C 542	12.2	40.7	21	9	US-09-301-978C-7	Sequence 7, Appli	C 615	12.2	40.7	33	16	US-10-389-640-42	Sequence 42, Appl
C 543	12.2	40.7	21	13	US-10-090-378-7	Sequence 7, Appli	C 616	12.2	40.7	33	16	US-10-800-197-44	Sequence 44, Appl
C 544	12.2	40.7	21	18	US-10-786-720-12010	Sequence 12010, A	C 617	12.2	40.7	33	18	US-10-800-197-45	Sequence 45, Appl
C 545	12.2	40.7	21	18	US-10-786-720-12011	Sequence 12011, A	C 618	12.2	40.7	35	10	US-09-765-061B-56	Sequence 56, Appl
C 546	12.2	40.7	21	18	US-10-786-720-12012	Sequence 12012, A	C 619	12.2	40.7	35	10	US-09-948-747-21	Sequence 21, Appl
C 547	12.2	40.7	21	18	US-10-786-720-13492	Sequence 13492, A	C 620	12.2	40.7	35	18	US-10-719-895-40	Sequence 40, Appl
C 548	12.2	40.7	23	10	US-09-903-190-32	Sequence 32, Appl	C 621	12.2	40.7	36	9	US-09-971-309-81	Sequence 81, Appl
C 549	12.2	40.7	23	15	US-10-127-816-34	Sequence 34, Appl	C 622	12.2	40.7	36	15	US-10-202-896-32	Sequence 32, Appl
C 550	12.2	40.7	23	15	US-10-127-816-51	Sequence 51, Appl	C 623	12.2	40.7	41	15	US-10-224-683-14	Sequence 14, Appl
C 551	12.2	40.7	23	15	US-10-319-763-32	Sequence 32, Appl	C 624	12.2	40.7	41	16	US-10-035-833A-1009	Sequence 1009, Ap
C 552	12.2	40.7	23	15	US-10-315-664-18	Sequence 18, Appl	C 625	12.2	40.7	41	16	US-10-035-833A-3367	Sequence 3367, Ap
C 553	12.2	40.7	25	9	US-09-866-108-3483	Sequence 3483, Ap	C 626	12.2	40.7	41	16	US-10-035-833A-5321	Sequence 5321, Ap
C 554	12.2	40.7	25	9	US-09-866-108-3484	Sequence 3484, Ap	C 627	12.2	40.7	47	16	US-10-349-143-105	Sequence 105, App
C 555	12.2	40.7	25	10	US-09-770-107-48	Sequence 48, Appl	C 628	12.2	40.7	47	16	US-10-349-143-1042	Sequence 1042, Ap
C 556	12.2	40.7	25	10	US-09-848-107-18	Sequence 18, Appl	C 629	12.2	40.7	47	16	US-10-349-143-1459	Sequence 1459, Ap
C 557	12.2	40.7	25	10	US-09-848-107-19	Sequence 19, Appl	C 630	12.2	40.7	48	16	US-10-440-932-1	Sequence 1, Appli
C 558	12.2	40.7	25	14	US-10-109-498-13	Sequence 13, Appl	C 631	12.2	40.7	49	10	US-09-993-346-118	Sequence 118, App
C 559	12.2	40.7	25	14	US-10-109-498-14	Sequence 14, Appl	C 632	12.2	40.7	50	16	US-10-131-827-2927	Sequence 2927, Ap
C 560	12.2	40.7	25	14	US-10-215-112-4029	Sequence 4029, Ap	C 633	12.2	40.7	50	16	US-10-131-827-4858	Sequence 4858, Ap
C 561	12.2	40.7	25	15	US-10-255-032-2	Sequence 2, Appli	C 634	12.2	40.7	50	18	US-10-690-487-235	Sequence 235, App
C 562	12.2	40.7	25	15	US-10-255-032-3	Sequence 3, Appli	C 635	12	40.0	20	9	US-09-825-414-73	Sequence 73, Appl
C 563	12.2	40.7	25	15	US-10-098-263B-4369	Sequence 4369, Ap	C 636	12	40.0	20	14	US-10-010-802-331	Sequence 331, App
C 564	12.2	40.7	25	15	US-10-098-263B-12536	Sequence 12536, A	C 637	12	40.0	20	15	US-10-227-596-2	Sequence 2, Appli
C 565	12.2	40.7	25	15	US-10-098-263B-39284	Sequence 39284, A	C 638	12	40.0	20	15	US-10-164-863-9	Sequence 9, Appli
C 566	12.2	40.7	25	15	US-10-098-263B-41117	Sequence 41117, A	C 639	12	40.0	20	16	US-10-185-035-46	Sequence 46, Appl
C 567	12.2	40.7	25	15	US-10-098-263B-44049	Sequence 44049, A	C 640	12	40.0	20	16	US-10-185-035-107	Sequence 107, App
C 568	12.2	40.7	25	15	US-10-098-263B-48032	Sequence 48032, A	C 641	12	40.0	20	16	US-10-289-762-2977	Sequence 2977, Ap
C 569	12.2	40.7	25	15	US-10-098-263B-48568	Sequence 48568, A	C 642	12	40.0	20	17	US-10-342-311-2	Sequence 2, Appli
C 570	12.2	40.7	25	15	US-10-098-263B-51018	Sequence 51018, A	C 643	12	40.0	20	17	US-10-731-739-320	Sequence 320, App
C 571	12.2	40.7	25	15	US-10-098-263B-52725	Sequence 52725, A	C 644	12	40.0	20	18	US-10-477-238A-320	Sequence 320, App
C 572	12.2	40.7	25	15	US-10-098-263B-62212	Sequence 62212, A	C 645	12	40.0	21	18	US-10-786-720-7600	Sequence 7600, Ap
C 573	12.2	40.7	25	15	US-10-098-263B-65528	Sequence 65528, A	C 646	12	40.0	21	18	US-10-786-720-7602	Sequence 7602, Ap
C 574	12.2	40.7	25	15	US-10-098-263B-65922	Sequence 65922, A	C 647	12	40.0	21	18	US-10-786-720-9850	Sequence 9850, Ap
C 575	12.2	40.7	25	15	US-10-098-263B-75387	Sequence 75387, A	C 648	12	40.0	21	18	US-10-786-720-9852	Sequence 9852, Ap
C 576	12.2	40.7	25	15	US-10-098-263B-75388	Sequence 75388, A	C 649	12	40.0	21	18	US-10-786-720-13354	Sequence 13354, A
C 577	12.2	40.7	25	15	US-10-098-263B-78002	Sequence 78002, A	C 650	12	40.0	21	18	US-10-786-720-13355	Sequence 13355, A
C 578	12.2	40.7	25	15	US-10-098-263B-78572	Sequence 78572, A	C 651	12	40.0	21	18	US-10-786-720-13356	Sequence 13356, A
C 579	12.2	40.7	25	15	US-10-098-263B-80598	Sequence 80598, A	C 652	12	40.0	21	18	US-10-786-720-13357	Sequence 13357, A
C 580	12.2	40.7	25	15	US-10-098-263B-84844	Sequence 84844, A	C 653	12	40.0	21	18	US-10-786-720-13358	Sequence 13358, A
C 581	12.2	40.7	25	15	US-10-098-263B-87704	Sequence 87704, A	C 654	12	40.0	21	18	US-10-786-720-13359	Sequence 13359, A
C 582	12.2	40.7	25	15	US-10-098-263B-92657	Sequence 92657, A	C 655	12	40.0	21	18	US-10-786-720-13414	Sequence 13414, A
C 583	12.2	40.7	25	15	US-10-098-263B-96196	Sequence 96196, A	C 656	12	40.0	21	18	US-10-786-720-13416	Sequence 13416, A
C 584	12.2	40.7	25	15	US-10-098-263B-105046	Sequence 105046, A	C 657	12	40.0	21	18	US-10-786-720-13489	Sequence 13489, A
C 585	12.2	40.7	25	15	US-10-098-263B-106787	Sequence 106787, A	C 658	12	40.0	21	18	US-10-786-720-13490	Sequence 13490, A
C 586	12.2	40.7	25	15	US-10-098-263B-107251	Sequence 107251, A	C 659	12	40.0	22	15	US-10-032-585-5004	Sequence 5004, Ap
C 587	12.2	40.7	25	15	US-10-098-263B-114086	Sequence 114086, A	C 660	12	40.0	24	9	US-09-886-900-10	Sequence 10, Appl
C 588	12.2	40.7	25	15	US-10-098-263B-115799	Sequence 115799, A	C 661	12	40.0	24	10	US-09-940-185-3845	Sequence 3845, Ap
C 589	12.2	40.7	25	15	US-10-098-263B-125811	Sequence 125811, A	C 662	12	40.0	24	15	US-10-096-578-81	Sequence 81, Appl
C 590	12.2	40.7	25	17	US-10-717-597-4815	Sequence 4815, Ap	C 663	12	40.0	24	15	US-10-032-585-4814	Sequence 4814, Ap
C 591	12.2	40.7	25	17	US-10-717-597-4816	Sequence 4816, Ap	C 664	12	40.0	24	15	US-10-032-585-4879	Sequence 4879, Ap
C 592	12.2	40.7	25	17	US-10-723-361-3483	Sequence 3483, Ap	C 665	12	40.0	24	16	US-10-617-038-112	Sequence 112, App
C 593	12.2	40.7	25	17	US-10-723-361-3484	Sequence 3484, Ap	C 666	12	40.0	25	10	US-09-974-546-35	Sequence 35, Appl
C 594	12.2	40.7	25	17	US-10-669-537-2	Sequence 2, Appli	C 667	12	40.0	25	14	US-10-215-112-4039	Sequence 4039, Ap
C 595	12.2	40.7	25	18	US-10-669-537-3	Sequence 3, Appli	C 668	12	40.0	25	14	US-10-215-112-4040	Sequence 4040, Ap
C 596	12.2	40.7	25	18	US-10-669-537-4	Sequence 4, Appli	C 669	12	40.0	25	14	US-10-215-112-8243	Sequence 8243, Ap

c 670	12	40.0	25	14	US-10-215-112-6369	Sequence 8369, Ap	c 743	12	40.0	41	15	US-10-286-549A-34	Sequence 34, Appl
c 671	12	40.0	25	15	US-10-098-263B-241	Sequence 241, Appl	c 744	12	40.0	41	16	US-10-035-833A-431	Sequence 431, Appl
c 672	12	40.0	25	15	US-10-098-263B-3113	Sequence 3113, Ap	c 745	12	40.0	41	16	US-10-035-833A-2485	Sequence 2485, Ap
c 673	12	40.0	25	15	US-10-098-263B-4070	Sequence 4070, Ap	c 746	12	40.0	41	16	US-10-035-833A-2550	Sequence 2550, Ap
c 674	12	40.0	25	15	US-10-098-263B-5301	Sequence 5301, Ap	c 747	12	40.0	41	16	US-10-035-833A-3057	Sequence 3057, Ap
c 675	12	40.0	25	15	US-10-098-263B-9639	Sequence 9639, Ap	c 748	12	40.0	41	16	US-10-035-833A-5270	Sequence 5270, Ap
c 676	12	40.0	25	15	US-10-098-263B-10275	Sequence 10275, A	c 749	12	40.0	41	16	US-10-035-833A-5270	Sequence 5270, Ap
c 677	12	40.0	25	15	US-10-098-263B-13000	Sequence 13000, A	c 750	12	40.0	41	16	US-10-035-833A-5367	Sequence 5367, Ap
c 678	12	40.0	25	15	US-10-098-263B-17500	Sequence 17500, A	c 751	12	40.0	41	16	US-10-035-833A-6584	Sequence 6584, Ap
c 679	12	40.0	25	15	US-10-098-263B-27036	Sequence 27036, A	c 752	12	40.0	42	13	US-10-057-558-28	Sequence 28, Appl
c 680	12	40.0	25	15	US-10-098-263B-27984	Sequence 27984, A	c 753	12	40.0	42	18	US-10-858-775-28	Sequence 28, Appl
c 681	12	40.0	25	15	US-10-098-263B-28537	Sequence 28537, A	c 754	12	40.0	43	9	US-09-423-800-15	Sequence 15, Appl
c 682	12	40.0	25	15	US-10-098-263B-29222	Sequence 29222, A	c 755	12	40.0	43	14	US-10-182-018-15	Sequence 15, Appl
c 683	12	40.0	25	15	US-10-098-263B-34105	Sequence 34105, A	c 756	12	40.0	43	15	US-10-169-003-15	Sequence 15, Appl
c 684	12	40.0	25	15	US-10-098-263B-41114	Sequence 41114, A	c 757	12	40.0	43	15	US-10-337-981-15	Sequence 15, Appl
c 685	12	40.0	25	15	US-10-098-263B-42187	Sequence 42187, A	c 758	12	40.0	43	16	US-10-344-733-15	Sequence 15, Appl
c 686	12	40.0	25	15	US-10-098-263B-43957	Sequence 43957, A	c 759	12	40.0	44	10	US-09-510-378-117	Sequence 117, Appl
c 687	12	40.0	25	15	US-10-098-263B-55555	Sequence 55555, A	c 760	12	40.0	45	9	US-09-850-964-6	Sequence 6, Appl
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c 689	12	40.0	25	15	US-10-098-263B-61694	Sequence 61694, A	c 762	12	40.0	47	10	US-09-993-346-15	Sequence 15, Appl
c 690	12	40.0	25	15	US-10-098-263B-62681	Sequence 62681, A	c 763	12	40.0	47	15	US-10-076-802-59	Sequence 59, Appl
c 691	12	40.0	25	15	US-10-098-263B-68272	Sequence 68272, A	c 764	12	40.0	47	15	US-10-211-160-26	Sequence 26, Appl
c 692	12	40.0	25	15	US-10-098-263B-72261	Sequence 72261, A	c 765	12	40.0	47	15	US-10-051-681A-26	Sequence 26, Appl
c 693	12	40.0	25	15	US-10-098-263B-73506	Sequence 73506, A	c 766	12	40.0	47	15	US-10-170-077-775	Sequence 775, Appl
c 694	12	40.0	25	15	US-10-098-263B-76831	Sequence 76831, A	c 767	12	40.0	47	15	US-10-367-169-59	Sequence 59, Appl
c 695	12	40.0	25	15	US-10-098-263B-78612	Sequence 78612, A	c 768	12	40.0	47	16	US-10-349-143-575	Sequence 575, Appl
c 696	12	40.0	25	15	US-10-098-263B-89562	Sequence 89562, A	c 769	12	40.0	47	16	US-10-349-143-1243	Sequence 1243, Ap
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c 699	12	40.0	25	15	US-10-098-263B-96711	Sequence 96711, A	c 772	12	40.0	47	16	US-10-333-429-105	Sequence 105, Appl
c 700	12	40.0	25	15	US-10-098-263B-103946	Sequence 103946, A	c 773	12	40.0	47	16	US-10-617-070-487	Sequence 487, Appl
c 701	12	40.0	25	15	US-10-098-263B-103945	Sequence 103945, A	c 774	12	40.0	47	17	US-10-467-639-52	Sequence 52, Appl
c 702	12	40.0	25	15	US-10-098-263B-105592	Sequence 105592, A	c 775	12	40.0	48	10	US-09-927-046-5317	Sequence 5317, Ap
c 703	12	40.0	25	15	US-10-098-263B-111285	Sequence 111285, A	c 776	12	40.0	48	10	US-09-792-818-1981	Sequence 1981, Ap
c 704	12	40.0	25	15	US-10-098-263B-123180	Sequence 123180, A	c 777	12	40.0	48	10	US-09-792-818-2137	Sequence 2137, Ap
c 705	12	40.0	25	15	US-10-098-263B-125761	Sequence 125761, A	c 778	12	40.0	48	16	US-10-617-070-488	Sequence 488, Appl
c 706	12	40.0	25	15	US-10-098-263B-130501	Sequence 130501, A	c 779	12	40.0	49	15	US-10-026-925-34	Sequence 34, Appl
c 707	12	40.0	25	15	US-10-061-201-2401	Sequence 2401, Ap	c 780	12	40.0	49	15	US-10-174-992-8	Sequence 8, Appl
c 708	12	40.0	25	15	US-10-061-201-2407	Sequence 2407, Ap	c 781	12	40.0	49	18	US-10-666-806A-2	Sequence 2, Appl
c 709	12	40.0	25	17	US-10-717-597-4237	Sequence 4237, Ap	c 782	12	40.0	50	16	US-10-131-827-3392	Sequence 3392, Ap
c 710	12	40.0	27	10	US-09-833-039-17	Sequence 17, Appl	c 783	12	40.0	50	16	US-10-131-827-3393	Sequence 3393, Ap
c 711	12	40.0	27	18	US-10-177-277-17	Sequence 17, Appl	c 784	12	40.0	50	16	US-10-131-827-3452	Sequence 3452, Ap
c 712	12	40.0	27	18	US-10-851-884-25	Sequence 25, Appl	c 785	12	40.0	50	16	US-10-111-827-3452	Sequence 4732, Ap
c 713	12	40.0	28	9	US-09-795-006A-8	Sequence 8, Appl	c 786	12	40.0	50	16	US-10-131-827-4732	Sequence 4732, Ap
c 714	12	40.0	28	16	US-10-321-039-161	Sequence 161, Appl	c 787	12	40.0	50	16	US-10-131-827-4778	Sequence 4778, Ap
c 715	12	40.0	28	16	US-10-336-638-551	Sequence 551, Appl	c 788	12	40.0	50	16	US-10-131-827-7239	Sequence 7239, Ap
c 716	12	40.0	30	9	US-09-827-933A-19	Sequence 19, Appl	c 789	11.8	39.3	17	9	US-09-735-787-33	Sequence 33, Appl
c 717	12	40.0	30	9	US-09-888-938-9	Sequence 9, Appl	c 790	11.8	39.3	17	10	US-09-740-332-1113	Sequence 1113, Ap
c 718	12	40.0	30	11	US-09-852-238A-12	Sequence 12, Appl	c 791	11.8	39.3	17	10	US-09-817-879-1113	Sequence 1113, Ap
c 719	12	40.0	30	14	US-10-093-958-11	Sequence 11, Appl	c 792	11.8	39.3	17	15	US-10-138-870-33	Sequence 33, Appl
c 720	12	40.0	30	14	US-10-093-958-12	Sequence 12, Appl	c 793	11.8	39.3	17	17	US-10-669-841-3706	Sequence 3706, Ap
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c 722	12	40.0	31	17	US-10-287-949A-19449	Sequence 19449, A	c 795	11.8	39.3	19	11	US-09-864-636A-1950	Sequence 1950, Ap
c 723	12	40.0	31	18	US-10-712-633-5246	Sequence 5246, Ap	c 796	11.8	39.3	19	15	US-10-084-839-1950	Sequence 1950, Ap
c 724	12	40.0	32	15	US-10-293-239-39	Sequence 39, Appl	c 797	11.8	39.3	19	16	US-10-669-724-6	Sequence 6, Appl
c 725	12	40.0	32	15	US-10-116-298A-2	Sequence 2, Appl	c 798	11.8	39.3	19	16	US-10-252-155-184	Sequence 184, Appl
c 726	12	40.0	33	16	US-10-374-953-2	Sequence 2, Appl	c 799	11.8	39.3	20	10	US-09-382-860-266	Sequence 266, Appl
c 727	12	40.0	33	16	US-10-465-789A-64	Sequence 64, Appl	c 800	11.8	39.3	20	15	US-10-032-585-4319	Sequence 4319, Ap
c 728	12	40.0	34	14	US-10-229-747-5	Sequence 5, Appl	c 801	11.8	39.3	20	15	US-10-093-463-338	Sequence 338, Appl
c 729	12	40.0	35	9	US-09-753-126-60	Sequence 60, Appl	c 802	11.8	39.3	20	17	US-10-303-541-61	Sequence 24, Appl
c 730	12	40.0	35	16	US-10-330-697-60	Sequence 60, Appl	c 803	11.8	39.3	20	17	US-10-671-395-1643	Sequence 61, Appl
c 731	12	40.0	36	14	US-10-083-168-25	Sequence 25, Appl	c 804	11.8	39.3	20	17	US-10-671-395-1708	Sequence 1643, Ap
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c 734	12	40.0	38	15	US-10-291-480-15	Sequence 15, Appl	c 807	11.8	39.3	20	17	US-10-671-395-1737	Sequence 1727, Ap
c 735	12	40.0	38	15	US-10-291-480-15	Sequence 15, Appl	c 808	11.8	39.3	20	17	US-10-671-395-1743	Sequence 1737, Ap
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c 737	12	40.0	38	18	US-10-721-997A-14	Sequence 14, Appl	c 810	11.8	39.3	21	9	US-09-817-014-73	Sequence 73, Appl
c 738	12	40.0	39	10	US-09-826-509-295	Sequence 295, Appl	c 811	11.8	39.3	22	9	US-09-755-665-113	Sequence 113, Appl
c 739	12	40.0	39	15	US-10-219-227-16	Sequence 16, Appl	c 812	11.8	39.3	22	9	US-09-755-665-114	Sequence 114, Appl
c 740	12	40.0	39	17	US-10-327-598-845	Sequence 845, Appl	c 813	11.8	39.3	22	14	US-10-074-246-26	Sequence 26, Appl
c 741	12	40.0	41	10	US-09-826-509-294	Sequence 294, Appl	c 814	11.8	39.3	22	15	US-10-056-229-73	Sequence 73, Appl
c 742	12	40.0	41	15	US-10-319-227A-34	Sequence 34, Appl	c 815	11.8	39.3	22	15		

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817	11.8	39.3	22	17	US-10-629-248-113	Sequence 113, App	11.8	39.3	28	15	US-10-411-076-27	Sequence 27, Appl
818	11.8	39.3	22	17	US-10-629-248-114	Sequence 114, App	11.8	39.3	28	15	US-10-411-076-29	Sequence 29, Appl
819	11.8	39.3	23	14	US-10-269-557-58	Sequence 58, Appl	11.8	39.3	28	15	US-10-410-872-22	Sequence 22, Appl
820	11.8	39.3	23	14	US-10-296-995-89	Sequence 89, Appl	11.8	39.3	28	15	US-10-410-885-15	Sequence 15, Appl
821	11.8	39.3	23	16	US-10-374-077-13	Sequence 13, Appl	11.8	39.3	28	17	US-10-675-738B-8	Sequence 8, Appl
822	11.8	39.3	23	16	US-10-398-757-16	Sequence 16, Appl	11.8	39.3	28	18	US-10-622-869A-23	Sequence 23, Appl
823	11.8	39.3	24	9	US-09-904-389-6	Sequence 6, Appl	11.8	39.3	30	9	US-09-297-910-4	Sequence 4, Appl
824	11.8	39.3	24	10	US-09-468-147-63	Sequence 63, Appl	11.8	39.3	30	9	US-10-364-649-48	Sequence 48, Appl
825	11.8	39.3	24	15	US-10-319-745-63	Sequence 63, Appl	11.8	39.3	30	16	US-10-692-605-46	Sequence 46, Appl
826	11.8	39.3	24	16	US-10-072-012-926	Sequence 926, App	11.8	39.3	31	9	US-09-801-274-797	Sequence 797, App
827	11.8	39.3	24	16	US-10-072-012-928	Sequence 928, App	11.8	39.3	31	15	US-10-235-079B-81	Sequence 81, Appl
828	11.8	39.3	25	9	US-09-866-108-4870	Sequence 4970, Ap	11.8	39.3	31	16	US-10-239-656-88	Sequence 88, Appl
829	11.8	39.3	25	9	US-09-866-108-4871	Sequence 4971, Ap	11.8	39.3	32	8	US-08-911-824-88	Sequence 88, Appl
830	11.8	39.3	25	14	US-10-074-246-49	Sequence 49, Appl	11.8	39.3	33	10	US-09-864-636A-246	Sequence 246, App
831	11.8	39.3	25	14	US-10-215-112-3893	Sequence 3893, Ap	11.8	39.3	33	10	US-09-758-282-45	Sequence 45, Appl
832	11.8	39.3	25	14	US-10-215-112-4826	Sequence 4826, Ap	11.8	39.3	33	11	US-09-864-426A-246	Sequence 246, App
833	11.8	39.3	25	14	US-10-215-112-6375	Sequence 6375, Ap	11.8	39.3	33	15	US-10-084-839-246	Sequence 246, App
834	11.8	39.3	25	15	US-10-098-263B-2946	Sequence 2946, Ap	11.8	39.3	34	10	US-09-949-427-108	Sequence 108, App
835	11.8	39.3	25	15	US-10-098-263B-5698	Sequence 5698, Ap	11.8	39.3	34	16	US-10-332-155-5	Sequence 5, Appl
836	11.8	39.3	25	15	US-10-098-263B-5698	Sequence 5698, Ap	11.8	39.3	35	10	US-09-854-867-520	Sequence 520, App
837	11.8	39.3	25	15	US-10-098-263B-8967	Sequence 8967, Ap	11.8	39.3	35	15	US-10-317-832-226	Sequence 226, App
838	11.8	39.3	25	15	US-10-098-263B-10291	Sequence 10291, A	11.8	39.3	35	15	US-10-733-878-226	Sequence 226, App
839	11.8	39.3	25	15	US-10-098-263B-13913	Sequence 13913, A	11.8	39.3	36	15	US-10-084-814-31	Sequence 31, Appl
840	11.8	39.3	25	15	US-10-098-263B-21484	Sequence 21484, A	11.8	39.3	36	16	US-10-462-128-31	Sequence 31, Appl
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845	11.8	39.3	25	15	US-10-098-263B-38809	Sequence 38809, A	11.8	39.3	38	16	US-10-342-902-4236	Sequence 4236, Ap
846	11.8	39.3	25	15	US-10-098-263B-38810	Sequence 38810, A	11.8	39.3	38	16	US-10-342-902-4236	Sequence 4236, Ap
847	11.8	39.3	25	15	US-10-098-263B-39770	Sequence 39770, A	11.8	39.3	38	16	US-10-342-902-4348	Sequence 4348, Ap
848	11.8	39.3	25	15	US-10-098-263B-41897	Sequence 41897, A	11.8	39.3	38	17	US-10-669-841-9127	Sequence 9127, Ap
849	11.8	39.3	25	15	US-10-098-263B-42032	Sequence 42032, A	11.8	39.3	38	17	US-10-669-841-9239	Sequence 9239, Ap
850	11.8	39.3	25	15	US-10-098-263B-46867	Sequence 46867, A	11.8	39.3	39	10	US-09-093-972C-990	Sequence 990, App
851	11.8	39.3	25	15	US-10-098-263B-62572	Sequence 62572, A	11.8	39.3	39	15	US-10-178-673-16	Sequence 16, Appl
852	11.8	39.3	25	15	US-10-098-263B-68004	Sequence 68004, A	11.8	39.3	39	16	US-10-453-827-447	Sequence 447, App
853	11.8	39.3	25	15	US-10-098-263B-71643	Sequence 71643, A	11.8	39.3	39	16	US-10-453-827-448	Sequence 448, App
854	11.8	39.3	25	15	US-10-098-263B-72259	Sequence 72259, A	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
855	11.8	39.3	25	15	US-10-098-263B-72259	Sequence 72259, A	11.8	39.3	40	9	US-09-989-723-25	Sequence 25, Appl
856	11.8	39.3	25	15	US-10-098-263B-73526	Sequence 73526, A	11.8	39.3	40	9	US-09-989-727-25	Sequence 25, Appl
857	11.8	39.3	25	15	US-10-098-263B-74898	Sequence 74898, A	11.8	39.3	40	9	US-09-989-727-25	Sequence 25, Appl
858	11.8	39.3	25	15	US-10-098-263B-78527	Sequence 78527, A	11.8	39.3	40	9	US-09-989-731-25	Sequence 25, Appl
859	11.8	39.3	25	15	US-10-098-263B-94376	Sequence 94376, A	11.8	39.3	40	9	US-09-989-732-25	Sequence 25, Appl
860	11.8	39.3	25	15	US-10-098-263B-97982	Sequence 97982, A	11.8	39.3	40	9	US-09-989-732-25	Sequence 25, Appl
861	11.8	39.3	25	15	US-10-098-263B-101430	Sequence 101430, A	11.8	39.3	40	9	US-09-991-073-25	Sequence 25, Appl
862	11.8	39.3	25	15	US-10-098-263B-108180	Sequence 108180, A	11.8	39.3	40	9	US-09-991-073-25	Sequence 25, Appl
863	11.8	39.3	25	15	US-10-098-263B-108352	Sequence 108352, A	11.8	39.3	40	9	US-09-991-163-25	Sequence 25, Appl
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865	11.8	39.3	25	15	US-10-098-263B-119984	Sequence 119984, A	11.8	39.3	40	9	US-09-990-456-25	Sequence 25, Appl
866	11.8	39.3	25	15	US-10-098-263B-120547	Sequence 120547, A	11.8	39.3	40	9	US-09-989-721-25	Sequence 25, Appl
867	11.8	39.3	25	15	US-10-098-263B-120548	Sequence 120548, A	11.8	39.3	40	9	US-09-992-598-25	Sequence 25, Appl
868	11.8	39.3	25	15	US-10-098-263B-121342	Sequence 121342, A	11.8	39.3	40	9	US-09-989-293A-25	Sequence 25, Appl
869	11.8	39.3	25	15	US-10-098-263B-121342	Sequence 121342, A	11.8	39.3	40	9	US-09-989-735-25	Sequence 25, Appl
870	11.8	39.3	25	15	US-10-098-263B-124191	Sequence 124191, A	11.8	39.3	40	9	US-09-990-444-25	Sequence 25, Appl
871	11.8	39.3	25	15	US-10-098-263B-128190	Sequence 128190, A	11.8	39.3	40	9	US-09-991-181-25	Sequence 25, Appl
872	11.8	39.3	25	15	US-10-098-263B-130350	Sequence 130350, A	11.8	39.3	40	9	US-09-989-730-25	Sequence 25, Appl
873	11.8	39.3	25	17	US-10-061-201-4105	Sequence 4105, Ap	11.8	39.3	40	9	US-09-990-436-25	Sequence 25, Appl
874	11.8	39.3	25	17	US-10-717-597-3165	Sequence 3165, Ap	11.8	39.3	40	10	US-09-989-734-25	Sequence 25, Appl
875	11.8	39.3	25	17	US-10-723-361-4970	Sequence 4970, Ap	11.8	39.3	40	10	US-09-997-653-25	Sequence 25, Appl
876	11.8	39.3	25	17	US-10-723-361-4971	Sequence 4971, Ap	11.8	39.3	40	10	US-09-989-724-25	Sequence 25, Appl
877	11.8	39.3	25	17	US-10-723-361-4972	Sequence 4972, Ap	11.8	39.3	40	10	US-09-989-728-25	Sequence 25, Appl
878	11.8	39.3	25	17	US-10-775-169-4880	Sequence 4880, Ap	11.8	39.3	40	10	US-09-990-441-25	Sequence 25, Appl
879	11.8	39.3	26	9	US-09-802-669-89	Sequence 89, Appl	11.8	39.3	40	10	US-09-993-667-25	Sequence 25, Appl
880	11.8	39.3	26	16	US-10-619-220-89	Sequence 89, Appl	11.8	39.3	40	10	US-09-997-428-25	Sequence 25, Appl
881	11.8	39.3	27	10	US-09-961-077-908	Sequence 908, App	11.8	39.3	40	10	US-09-997-666-25	Sequence 25, Appl
882	11.8	39.3	28	9	US-09-975-553-22	Sequence 22, Appl	11.8	39.3	40	10	US-09-990-438-25	Sequence 25, Appl
883	11.8	39.3	28	14	US-10-125-792-13	Sequence 13, Appl	11.8	39.3	40	10	US-09-990-562-25	Sequence 25, Appl
884	11.8	39.3	28	14	US-10-125-778-13	Sequence 13, Appl	11.8	39.3	40	10	US-09-990-711-25	Sequence 25, Appl
885	11.8	39.3	28	14	US-10-270-795-22	Sequence 22, Appl	11.8	39.3	40	10	US-09-989-726-25	Sequence 25, Appl
886	11.8	39.3	28	15	US-10-270-876-22	Sequence 22, Appl	11.8	39.3	40	10	US-09-998-156-25	Sequence 25, Appl
887	11.8	39.3	28	15	US-10-268-051-12	Sequence 11, Appl	11.8	39.3	40	10	US-09-990-437-25	Sequence 25, Appl
888	11.8	39.3	28	15	US-10-125-772-13	Sequence 13, Appl	11.8	39.3	40	10	US-09-991-157-25	Sequence 25, Appl

RESOL 4
US-10-147-679A-22

Matches	19;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
QY	3	GACTCAGTCCTTGGTCATCTCAC	25						
Db	3	GACTCAGTCCTTGGTCGTCCTC	25						
RESULT 6									
US-08-944-410-52/c									
; Sequence 52, Application US/08944410									
; Publication No. US20030050453A1									
; GENERAL INFORMATION:									
; APPLICANT: Sorge, Joseph A.									
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES									
; FILE REFERENCE: 04121.0018-00000									
; CURRENT APPLICATION NUMBER: US/08/944,410									
; CURRENT FILING DATE: 1997-10-06									
; NUMBER OF SEQ ID NOS: 113									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 52									
; LENGTH: 46									
; TYPE: DNA									
; ORGANISM: Artificial									
; FEATURE:									
; OTHER INFORMATION: Synthetic primer									
US-08-944-410-52									
Query Match 54.7%; Score 16.4; DB 8; Length 46;									
Best Local Similarity 76.9%; Pred. No. 1.6e+03;									
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	3	GACTCAGTCCTTGGTCATCTCAC	28						
Db	41	GACTCAGACCTTGTGTCATCTGACGTT	16						
RESULT 7									
US-10-098-263B-123322									
; Sequence 123322, Application US/10098263B									
; Publication No. US20030104410A1									
; GENERAL INFORMATION:									
; APPLICANT: Mittman, Michael									
; TITLE OF INVENTION: Human Microarray									
; FILE REFERENCE: 3118.1									
; CURRENT APPLICATION NUMBER: US/10/098,263B									
; CURRENT FILING DATE: 2003-01-08									
; PRIOR APPLICATION NUMBER: 60/276,759									
; PRIOR FILING DATE: 2001-03-16									
; NUMBER OF SEQ ID NOS: 131066									
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1									
; SEQ ID NO 123322									
; LENGTH: 25									
; TYPE: DNA									
; ORGANISM: Homo sapien									
US-10-098-263B-123322									
Query Match 54.0%; Score 16.2; DB 15; Length 25;									
Best Local Similarity 85.7%; Pred. No. 1.9e+03;									
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	7	CAGTCCTTGGTCATCTCACCT	27						
Db	5	CAGTCCGTCGTCACACTCACTT	25						
RESULT 8									
US-10-098-263B-101913/c									
; Sequence 101913, Application US/10098263B									
; Publication No. US20030104410A1									
; GENERAL INFORMATION:									
; APPLICANT: Mittman, Michael									
; TITLE OF INVENTION: Human Microarray									
; FILE REFERENCE: 3118.1									

```

; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 101913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-101913

Query Match      53.3%; Score 16; DB 15; Length 25;
Best Local Similarity 79.2%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCA 24
Db 25 TGGGCTCAGTCATGGTTCTCTCA 2

RESULT 9
US-10-038-835-56/c
; Sequence 56, Application US/10038835
; Publication No. US20030130497A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Yue-Luen
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: DETECTION OF RESPIRATORY VIRUSES
; FILE REFERENCE: 12674-006001
; CURRENT APPLICATION NUMBER: US/10/038,835
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Human adenovirus
US-10-038-835-56

Query Match      52.7%; Score 15.8; DB 15; Length 26;
Best Local Similarity 81.0%; Pred. No. 2.8e+03;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCT 22
Db 22 GGACCAGTCYTTGGTCATCT 2

RESULT 10
US-10-131-827-405
; Sequence 405, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 405
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

US-10-131-827-405

Query Match      52.0%; Score 15.6; DB 16; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 13 TGCACCCAGTCTCTCTTATCTCACTTAT 42

RESULT 11
US-10-131-827-4918
; Sequence 4918, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4918
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4918

Query Match      52.0%; Score 15.6; DB 16; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.7e+03;
Matches 21; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db 13 TGCACCCAGTCTCTCTTATCTCACTTAT 42

RESULT 12
US-10-098-263B-112496
; Sequence 112496, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 112496
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-112496

Query Match      51.3%; Score 15.4; DB 15; Length 25;
Best Local Similarity 76.0%; Pred. No. 4.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGACTCAGTCCTTGGTCATCTCACC 26
Db 1 GGACTTCGACATTTGGTAATCCACC 25

```

RESULT 13

US-09-912-976-93/c
; Sequence 93, Application US/09912976
; Publication No. US20030212255A1

; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara

; APPLICANT: Mezes, Peter
; APPLICANT: Burgess, Catherine

; APPLICANT: Casman, Stacie
; APPLICANT: Grosse, William M

; APPLICANT: Alsbrook II, John P
; APPLICANT: Lepley, Denise M

; APPLICANT: Gerlach, Valerie L
; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda
; APPLICANT: Mishra, Vishnu

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-070
; CURRENT APPLICATION NUMBER: US/09/912,976

; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/221,336

; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/238,333

; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/260,675

; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/271,025

; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/278,164

; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/280,876

; PRIOR FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93

; LENGTH: 22
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Ag1279/Ag2590
; OTHER INFORMATION: PCR Primer Sequence

US-09-912-976-93

Query Match 50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 TCCTTGGTCATCTCACCTTC 29
DB 21 TCCTTTCTCATCTCTCCTTC 2

RESULT 14

US-09-965-422-76/c

; Sequence 76, Application US/09965422
; Publication No. US20030216545A1

; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A

; APPLICANT: Casman, Stacie
; APPLICANT: Padigar, Muralidhara

; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine

; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G

; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen

; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda
; APPLICANT: Li, Li

; APPLICANT: Malyankar, Urial M
; APPLICANT: Taylor, Sarah

; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik

; APPLICANT: Tchernev, Velizar T
; FILE REFERENCE: 21401-132

; CURRENT APPLICATION NUMBER: US/09/965,422
; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06

; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16

; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18

; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19

; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24

; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26

; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 76
; LENGTH: 22

; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer

; OTHER INFORMATION: Sequence
US-09-965-422-76

Query Match 50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 10 TCCTTGGTCATCTCACCTTC 29
DB 21 TCCTTTCTCATCTCTCCTTC 2

RESULT 15

US-09-965-422-82/c

; Sequence 82, Application US/09965422
; Publication No. US20030216545A1

; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A

; APPLICANT: Casman, Stacie
; APPLICANT: Padigar, Muralidhara

; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine

; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G

; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen

; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R

; APPLICANT: Smithson, Glennda
; APPLICANT: Li, Li

; APPLICANT: Malyankar, Urial M
; APPLICANT: Taylor, Sarah

```

; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: No. US20030216545A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT FILING DATE: 2001-09-27
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; OTHER INFORMATION: Sequence
US-09-965-422-82

Query Match      50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 TCCTTGGTCATCTCACCTTC 29
Db      21 TCCTTTCATCTCTCCTTC 2

RESULT 16
US-10-005-041A-202/c
; Sequence 202, Application US/10005041A
; Publication No. US200302331A1
; GENERAL INFORMATION:
; APPLICANT: Casman, Stacie J
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gilbert, Jennifer A
; APPLICANT: Mayotte, Jane E
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine AM
; APPLICANT: Dickinson, Kevin S
; APPLICANT: Ballinger, Robert A
; APPLICANT: Wolenc, Adam R
; APPLICANT: Edinger, Shlomit R
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glennda

Query Match      50.7%; Score 15.2; DB 10; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 TCCTTGGTCATCTCACCTTC 29
Db      21 TCCTTTCATCTCTCCTTC 2

RESULT 17
US-10-023-831A-7/c
; Sequence 7, Application US/10023831A
; Publication No. US20030064436A1
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; APPLICANT: WERKMEISTER, Jerome A.
; TITLE OF INVENTION: METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE HELICAL PRO
; TITLE OF INVENTION: AND YEAST HOST CELLS USEFUL IN SAID METHOD
; FILE REFERENCE: Q67867
; CURRENT APPLICATION NUMBER: US/10/023,831A
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/297,269
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: P03310
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: P04306
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/AU97/00721
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-023-831A-7

Query Match      50.7%; Score 15.2; DB 14; Length 24;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 TCCTTGGTCATCTCACCTTC 29
Db      20 TCCTTGGTGACCTCCCTTC 1
```

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; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Gerlach, Valerie
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-215
; CURRENT APPLICATION NUMBER: US/10/005,041A
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/251,459
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/259,007
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 202
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; OTHER INFORMATION: Sequence
US-10-005-041A-202

Query Match      50.7%; Score 15.2; DB 15; Length 22;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 TCCTTGGTCATCTCACCTTC 29
Db      21 TCCTTTCATCTCTCCTTC 2

RESULT 17
US-10-023-831A-7/c
; Sequence 7, Application US/10023831A
; Publication No. US20030064436A1
; GENERAL INFORMATION:
; APPLICANT: VAUGHAN, Paul R.
; APPLICANT: GALANIS, Maria
; APPLICANT: RAMSHAW, John A.M.
; APPLICANT: WERKMEISTER, Jerome A.
; TITLE OF INVENTION: METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE HELICAL PRO
; TITLE OF INVENTION: AND YEAST HOST CELLS USEFUL IN SAID METHOD
; FILE REFERENCE: Q67867
; CURRENT APPLICATION NUMBER: US/10/023,831A
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/297,269
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: P03310
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: P04306
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/AU97/00721
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-023-831A-7

Query Match      50.7%; Score 15.2; DB 14; Length 24;
Best Local Similarity 85.0%; Pred. No. 5.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      10 TCCTTGGTCATCTCACCTTC 29
Db      20 TCCTTGGTGACCTCCCTTC 1
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```

; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-263B-106308

Query Match
Best Local Similarity 50.0%; Score 15; DB 15; Length 25;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTC 23
Db 3 TGGACCTCTACTTGGTCTCTC 25

RESULT 23
US-09-801-274-1484/c
; Sequence 1484, Application US/09801274
; Patent No. US2002032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2025-209-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1484
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-1484

Query Match
Best Local Similarity 50.0%; Score 15; DB 9; Length 31;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGGTCATCTCAC 25
Db 31 TGGACTAGCCTTTGKCCATGCC 7

RESULT 24
US-10-131-827-4195
; Sequence 4195, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4195
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4195
```

```

Query Match
Best Local Similarity 50.0%; Score 15; DB 16; Length 50;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CTCAGTCCTTGGTCATCTCACCT 27
Db 4 CTCAGTCCTTGGTCATCTCACCT 26

RESULT 25
US-10-038-835-27
; Sequence 27, Application US/10038835
; Publication No. US20030130497A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Yue-Luen
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: DETECTION OF RESPIRATORY VIRUSES
; FILE REFERENCE: 12674-006001
; CURRENT APPLICATION NUMBER: US/10/038,835
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human adenovirus type 1
US-10-038-835-27

Query Match
Best Local Similarity 49.3%; Score 14.8; DB 15; Length 20;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTTGGTCATCT 22
Db 1 GAACCACTCTTGGTCATGT 20

RESULT 26
US-10-427-696-311/c
; Sequence 311, Application US/10427696
; Publication No. US20040220750A1
; GENERAL INFORMATION:
; APPLICANT: Hinds, David
; APPLICANT: Stokowski, Renee
; TITLE OF INVENTION: Method for identifying matched groups
; FILE REFERENCE: PERLP024
; CURRENT APPLICATION NUMBER: US/10/427,696
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 311
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Human
US-10-427-696-311

Query Match
Best Local Similarity 49.3%; Score 14.8; DB 18; Length 25;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCAGTCCTTGGTCATCTCA 24
Db 21 CTCATCTCTTGGTCATCTGA 2

RESULT 27
US-10-035-833A-347
; Sequence 347, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuhio
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
```

; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 347
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-347

Query Match 49.3%; Score 14.8; DB 16; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTCA 24
| | | | | : | | | | | | | | | |
Db 13 CTCGAATTCYGGTCATCTGA 32

RESULT 28
US-10-035-833A-6498
; Sequence 6498, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihiro
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6498
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-6498

Query Match 49.3%; Score 14.8; DB 16; Length 41;
Best Local Similarity 80.0%; Pred. No. 8.2e+03;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTCA 24
| | | | | : | | | | | | | | | |
Db 13 CTCGAATTCYGGTCATCTGA 32

RESULT 29
US-08-944-410-53/c
; Sequence 53, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-53

Query Match 49.3%; Score 14.8; DB 8; Length 46;

Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | | | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGACTGACGTT 16

RESULT 30
US-08-944-410-54/c
; Sequence 54, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-54

Query Match 49.3%; Score 14.8; DB 8; Length 46;
Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | | | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGACTGACGTT 16

RESULT 31
US-08-944-410-55/c
; Sequence 55, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-00000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-55

Query Match 49.3%; Score 14.8; DB 8; Length 46;
Best Local Similarity 73.1%; Pred. No. 8.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 GACTCAGTCCTTGGTCATCTCACCTT 28
| | | | | | | | | | | | | | | |
Db 41 GACTCAGACCTTGTGCGAACTGACGTT 16

RESULT 32
US-10-349-143-1893
; Sequence 1893, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta

```
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020Cp1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1893
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-7144-261 : polymorphic base C or T
US-10-349-143-1893

Query Match          49.3%; Score 14.8; DB 16; Length 47;
Best Local Similarity 67.9%; Pred. No. 8.3e+03;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 GACTCAGTCCTGGTCAATCTCACCTTCT 30
   ||||| : | | | | |
Db 14 GTCTCAGTTCYGTGGAACCCACCTTCT 41

RESULT 33
US-10-098-263B-102519
; Sequence 102519, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 102519
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-102519

Query Match          48.7%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCAGTCCTTGGTCAATCTCACCTCACC 26
   ||| ||||| ||||| |||||
Db 5 TCTGTCCTTGGTCCCTGACC 25

RESULT 34
US-10-098-263B-123321
; Sequence 123321, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
```

```
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 123321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-123321

Query Match          48.7%; Score 14.6; DB 15; Length 25;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CAGTCCTTGGTCAATCTCACCT 27
   ||||| ||||| ||||| |||||
Db 5 CAGTCCTGTCGTCACCTCACTT 25

RESULT 35
US-10-210-130-295
; Sequence 295, Application US/10210130
; Publication No. US20040014053A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Patturajan, Meera
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles E.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shmukets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Berghs, Constance
; APPLICANT: Zhong, Mei
; APPLICANT: Casman, Stacie J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Smithson, Glennda
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Leite, Mario W.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Anderson, David W.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Khrantsov, Nikolai V.
; APPLICANT: Ort, Tatiana
; APPLICANT: Ellerman, Karen
; APPLICANT: Rastelli, Luca
; APPLICANT: Agee, Michele L.
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Chant, John S.
; APPLICANT: DiPippo, Vincent A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Giot, Loic
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Rothenberg, Mark E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Hjal, Tord
; APPLICANT: Liu, Xiaohong
; APPLICANT: Taupier, Raymond J., Jr.
; APPLICANT: Catterton, Elina
; APPLICANT: Shenoy, Suresh G.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-416C (Cura-716 SMT)
; CURRENT APPLICATION NUMBER: US/10/210,130
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
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; PRIOR APPLICATION NUMBER: 60/316,508
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/354,655
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/383,887
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/323,936
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/381,039
; PRIOR FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 295
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-210-130-295

Query Match      48.7%; Score 14.6; DB 16; Length 26;
Best Local Similarity 81.0%; Pred. No. 9.7e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 10 TCCTTGGTCATCTCACCTTCT 30
    ||||| ||||| ||||| |||||
Db 3 TCCTGGCTGACCTCACCTTCT 23

RESULT 36
US-09-916-510A-20
; Sequence 20, Application US/09916510A
; Patent No. US20020168349A1
; GENERAL INFORMATION:
; APPLICANT: IGGO, RICHARD D.
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: 604-596
; CURRENT APPLICATION NUMBER: US/09/916,510A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-916-510A-20

Query Match      48.7%; Score 14.6; DB 9; Length 36;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| |||||
Db 2 TGGCGCCGCTATTGGTCATCTGACCTTC 30

RESULT 37
US-10-376-630-20
; Sequence 20, Application US/10376630
```

```
; Publication No. US20040047836A1
; GENERAL INFORMATION:
; APPLICANT: BTG INTERNATIONAL LTD
; APPLICANT: IGGO DR, RICHARD D
; APPLICANT: BRUNORI DR, MICHELE A
; TITLE OF INVENTION: ANTI-NEOPLASTIC VIRAL AGENTS
; FILE REFERENCE: ADENOVIRUS
; CURRENT APPLICATION NUMBER: US/10/376,630
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: GB 9906815.7
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-376-630-20

Query Match      48.7%; Score 14.6; DB 16; Length 36;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| |||||
Db 2 TGGCGCCGCTATTGGTCATCTGACCTTC 30

RESULT 38
US-10-453-827-1043/c
; Sequence 1043, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1043
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-453-827-1043

Query Match      48.7%; Score 14.6; DB 16; Length 38;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
    ||||| ||||| ||||| |||||
Db 32 TTGCGCCGCTGCTTGGTCATAGCTGTTTC 4

RESULT 39
US-10-453-827-1190/c
; Sequence 1190, Application US/10453827
; Publication No. US20040033582A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0211 NP
; CURRENT APPLICATION NUMBER: US/10/453,827
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: U.S. 60/384,980
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 1219
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 1190
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-453-827-1190

Query Match      48.7%; Score 14.6; DB 16; Length 38;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGGACTCAGTCCTTGGTCATCTCACCTTC 29
Db      32 TTGCCCTCTCCTTGGTCATAGCTGTTTC 4

RESULT 40
US-09-530-139-28/c
; Sequence 28, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-09-530-139-28

Query Match      48.7%; Score 14.6; DB 10; Length 42;
Best Local Similarity 69.0%; Pred. No. 1e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGACTCAGTCCTTGGTCATCTCACCTTCT 30
Db      41 GGACCCAGGTCACCGTCTCCTCACCGTCT 13

Search completed: November 24, 2004, 03:42:25
Job time : 151.774 secs
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:59:28 ; Search time 1438.31 Seconds
(without alignments)
760.051 Million cell updates/sec

Title: US-10-087-631B-4

Perfect score: 30

Sequence: 1 tggactcagtccttggtcattcaccattctt 30

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 158194

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	53.3	35	9	CL436787 PST3831-N
2	15.6	52.0	42	8	BH864588 SALK_0963
3	14.8	49.3	50	1	AU106879 AU106879
4	14.2	47.3	41	9	CL212954 G028G03 G
5	14.2	47.3	49	2	B9770036 601680150
6	14.2	47.3	49	9	BA531144 Arabidops
7	14.2	47.3	50	1	AU105600 AU105600
8	13.8	46.0	42	9	AJ622668 Drosophil
9	13.8	46.0	46	1	AA954628 oes3e04.s
10	13.8	46.0	50	1	AU106264 AU106264
11	13.6	45.3	34	1	AA259780 va87b10.r
12	13.6	45.3	41	8	A2604835 AU10425E19
13	13.6	45.3	48	9	AJ950922 Arabidops
14	13.4	44.7	44	1	AU264313 AU264313
15	13.4	44.7	50	1	AU107621 AU107621
16	13.4	44.7	50	1	AU107622 AU107622
17	13.4	44.7	50	1	AU107623 AU107623
18	13.2	44.0	37	4	BG260157 60371257
19	13.2	44.0	50	1	AU102328 AU102328
20	13	43.3	28	9	H26079 Y156d10.r1
21	13	43.3	28	9	CC795628 SALK_0876
22	13	43.3	47	8	AZ309567 IM0016F07
23	13	43.3	49	1	A1746816 u107907.Y
24	12.8	42.7	24	8	AZ607692 IM0430113

C	25	12.8	42.7	24	8	AZ662752	IM0542G06
C	26	12.8	42.7	31	1	AI582089	ar9ec09.x
C	27	12.8	42.7	34	9	AJ545069	Drosophil
C	28	12.8	42.7	37	7	H13124	Y106d12.r1
C	29	12.8	42.7	37	8	BH759504	KG04665-5
C	30	12.8	42.7	43	7	CN762433	ID0AAA4AE
C	31	12.8	42.7	44	8	AZ479665	IM0300D01
C	32	12.8	42.7	44	9	CL675662	PR10115C
C	33	12.8	42.7	45	8	AZ328994	IM0053105
C	34	12.8	42.7	48	8	BH791670	SALK_0608
C	35	12.8	42.7	49	1	AV833344	AV833344
C	36	12.6	42.0	24	9	AG198679	Pan trogl
C	37	12.6	42.0	28	8	AZ309679	IM0016B17
C	38	12.6	42.0	29	9	CC798624	SALK_1466
C	39	12.6	42.0	32	9	AG198685	Pan trogl
C	40	12.6	42.0	36	8	BH011404	BG01613-5
C	41	12.6	42.0	41	8	BZ381303	SALK_1165
C	42	12.6	42.0	45	8	BH848020	SALK_0673
C	43	12.6	42.0	45	9	EX292770	Arabidops
C	44	12.6	42.0	46	4	BI488502	603021011
C	45	12.6	42.0	48	8	AZ408184	IM0179F15
C	46	12.6	42.0	48	8	AZ504262	IM0344F19
C	47	12.6	42.0	49	1	AI019053	ub18c12.r
C	48	12.4	41.3	26	8	AZ662138	IM0541L05
C	49	12.4	41.3	34	1	AV844944	AV844944
C	50	12.4	41.3	34	8	AZ600325	IM0418C13
C	51	12.4	41.3	35	8	AZ664145	IM0544J07
C	52	12.4	41.3	36	8	AZ482058	IM0306J21
C	53	12.4	41.3	39	4	BI766377	603052614
C	54	12.4	41.3	43	1	AA947665	OQ32d02.s
C	55	12.4	41.3	43	1	AI282013	QQ88C02.x
C	56	12.4	41.3	45	9	AJ597160	Arabidops
C	57	12.4	41.3	46	1	AI036878	ub66g11.r
C	58	12.4	41.3	47	6	C20881	HUMGS000495
C	59	12.4	41.3	49	6	CD530579	O6012 Ara
C	60	12.4	41.3	49	9	EX659968	Arabidops
C	61	12.4	41.3	50	1	AU107220	AU107220
C	62	12.4	41.3	50	1	AU107979	AU107979
C	63	12.4	41.3	50	1	AU107979	AU107979
C	64	12.2	40.7	27	8	AZ623080	IM0460G21
C	65	12.2	40.7	28	8	AZ456389	IM0259B23
C	66	12.2	40.7	30	8	AZ645878	IM0511D08
C	67	12.2	40.7	32	8	AZ775049	2M0007B01
C	68	12.2	40.7	32	8	BH911753	SALK_0719
C	69	12.2	40.7	35	8	AZ801831	2M0060N19
C	70	12.2	40.7	37	1	AA704663	zf86e12.s
C	71	12.2	40.7	37	4	BI834423	603084478
C	72	12.2	40.7	37	9	AG201843	Pan trogl
C	73	12.2	40.7	38	9	CC795484	SALK_0809
C	74	12.2	40.7	40	9	AL764467	Arabidops
C	75	12.2	40.7	41	8	AZ813179	2M0080016
C	76	12.2	40.7	41	9	CG399825	O1S0423-0
C	77	12.2	40.7	45	4	BI916371	603178318
C	78	12.2	40.7	45	8	AZ662522	IM0541K09
C	79	12.2	40.7	46	1	AA641248	nr74c03.s
C	80	12.2	40.7	46	4	BI837191	603089967
C	81	12.2	40.7	46	8	BH628167	1007080F1
C	82	12.2	40.7	46	9	TA5A02P	AL452272 T. brucei
C	83	12.2	40.7	48	1	AV847374	AV847374
C	84	12.2	40.7	48	4	EG403326	602419487
C	85	12.2	40.7	48	8	AZ775146	2M0007A15
C	86	12.2	40.7	48	8	BH850842	SALK_0719
C	87	12.2	40.7	50	1	AU103005	AU103005
C	88	12.2	40.7	50	1	AU103636	AU103636
C	89	12.2	40.7	50	1	AU103999	AU103999
C	90	12.2	40.7	50	1	AU104000	AU104000
C	91	12.2	40.7	50	1	AU104001	AU104001
C	92	12.2	40.7	50	1	AU104002	AU104002
C	93	12.2	40.7	50	1	AU104003	AU104003
C	94	12.2	40.7	50	1	AU104004	AU104004
C	95	12.2	40.7	50	1	AU104005	AU104005
C	96	12.2	40.7	50	1	AU104007	AU104007
C	97	12.2	40.7	50	1	AU104008	AU104008

c 98	12.2	40.7	50	1	AU104009	AU104009	AU104009	171	11.6	38.7	42	8	BH740786	BH740786
c 99	12.2	40.7	50	1	AU106265	AU106265	AU106265	c 172	11.6	38.7	42	8	BH850477	BH850477
c 100	12.2	40.7	50	6	CF329688	NACL--05-	CF329688	c 173	11.6	38.7	42	8	BH911378	BH911378
c 101	12.2	40.7	50	8	AZ480460	1M0302E05	AZ480460	c 174	11.6	38.7	42	9	CL459539	CL459539
c 102	12.2	40.7	50	8	BZ766933	SALK_1380	BZ766933	c 175	11.6	38.7	42	9	CL528326	CL528326
c 103	12.2	40.7	24	9	CL670084	PR10161a	CL670084	c 176	11.6	38.7	43	7	N57043	N57043
c 104	12.2	40.7	31	8	AZ368771	1M019E01	AZ368771	c 177	11.6	38.7	43	7	AZ960728	AZ960728
c 105	12.2	40.7	33	9	CR358676	Arabidops	CR358676	c 178	11.6	38.7	44	1	A1118713	A1118713
c 106	12.2	40.7	33	9	CR986586	SALK_1487	CR986586	c 179	11.6	38.7	44	1	BH911599	BH911599
c 107	12.2	40.7	34	9	CG723116	111974G1	CG723116	c 180	11.6	38.7	44	1	BZ664959	BZ664959
c 108	12.2	40.7	36	3	CNS0916S	Single re	BM400180	c 181	11.6	38.7	45	8	BZ664961	BZ664961
c 109	12.2	40.7	37	4	AA889301	ak13f03.s	AA889301	c 182	11.6	38.7	46	1	A1035942	A1035942
c 110	12.2	40.7	37	4	BM400180	5009-0-68	BM400180	c 183	11.6	38.7	46	6	CA908621	CA908621
c 111	12.2	40.7	39	1	AV955711	AV955711	AV955711	c 184	11.6	38.7	46	8	AZ489801	AZ489801
c 112	12.2	40.7	39	3	CNS09H9S	Single re	BM400180	c 185	11.6	38.7	46	8	AZ659931	AZ659931
c 113	12.2	40.7	39	8	BZ594107	SALK_0828	BZ594107	c 186	11.6	38.7	47	8	AZ805275	AZ805275
c 114	12.2	40.7	42	1	AU009032	AU009032	AU009032	c 187	11.6	38.7	47	8	BH791124	BH791124
c 115	12.2	40.7	43	1	AA829397	od06d01.s	AA829397	c 188	11.6	38.7	47	8	BH791157	BH791157
c 116	12.2	40.7	43	1	A1363387	qy55h06.x	A1363387	c 189	11.6	38.7	47	9	AG204311	AG204311
c 117	12.2	40.7	43	1	AU009031	AU009031	AU009031	c 190	11.6	38.7	47	9	AG216926	AG216926
c 118	12.2	40.7	44	9	BX129899	Danio rer	BX129899	c 191	11.6	38.7	48	4	EM041668	EM041668
c 119	12.2	40.7	45	9	AL763705	Arabidops	AL763705	c 192	11.6	38.7	48	4	EM041668	EM041668
c 120	12.2	40.7	46	1	AL539046	tp76911.x	AL539046	c 193	11.6	38.7	49	1	AA922891	AA922891
c 121	12.2	40.7	46	8	AZ429958	1M0214N07	AZ429958	c 194	11.6	38.7	49	4	BM280302	BM280302
c 122	12.2	40.7	48	9	BX286631	Arabidops	BX286631	c 195	11.6	38.7	49	4	BM280302	BM280302
c 123	12.2	40.7	49	8	AZ814214	2M081N13	AZ814214	c 196	11.6	38.7	49	4	N40856	N40856
c 124	12.2	40.7	49	9	CG718294	1119052D0	CG718294	c 197	11.6	38.7	49	8	BH608677	BH608677
c 125	12.2	40.7	49	9	CG722873	1119073G1	CG722873	c 198	11.6	38.7	49	8	BH901307	BH901307
c 126	12.2	40.7	50	1	AU105857	AU105857	AU105857	c 199	11.6	38.7	49	8	BH901307	BH901307
c 127	12.2	40.7	50	1	AU107935	AU107935	AU107935	c 200	11.6	38.7	50	1	AU102326	AU102326
c 128	12.2	40.7	50	2	BF571906	602078216	BF571906	c 201	11.6	38.7	50	1	AU103621	AU103621
c 129	11.8	39.3	28	8	AZ309062	1M0012B14	AZ309062	c 202	11.6	38.7	50	1	AU108036	AU108036
c 130	11.8	39.3	32	8	AZ303920	1M0003F19	AZ303920	c 203	11.6	38.7	50	2	AW459434	AW459434
c 131	11.8	39.3	32	8	BZ594797	SALK_0852	BZ594797	c 204	11.6	38.7	50	2	AW459434	AW459434
c 132	11.8	39.3	34	1	AL662334	uj63c01.y	AL662334	c 205	11.6	38.7	50	6	CB219956	CB219956
c 133	11.8	39.3	36	9	CG466758	01S0638-0	CG466758	c 206	11.6	38.7	50	6	CB219956	CB219956
c 134	11.8	39.3	41	8	AZ441689	1M0233K24	AZ441689	c 207	11.6	38.7	50	8	BH856729	BH856729
c 135	11.8	39.3	42	5	BQ585504	E012306-0	BQ585504	c 208	11.4	38.0	29	9	AG188890	AG188890
c 136	11.8	39.3	42	5	BQ585504	E012306-0	BQ585504	c 209	11.4	38.0	29	9	AG188890	AG188890
c 137	11.8	39.3	44	6	CF298055	7LEAP--01	CF298055	c 210	11.4	38.0	30	8	BH740820	BH740820
c 138	11.8	39.3	44	8	AZ778971	2M0014M09	AZ778971	c 211	11.4	38.0	30	8	BH740820	BH740820
c 139	11.8	39.3	45	9	DR6119S	Danio rer	DR6119S	c 212	11.4	38.0	30	8	BH789905	BH789905
c 140	11.8	39.3	46	1	AL146894	ty23g04.s	AL146894	c 213	11.4	38.0	32	6	CD531546	CD531546
c 141	11.8	39.3	46	1	AL146894	ty23g04.s	AL146894	c 214	11.4	38.0	36	9	TA124B04P	TA124B04P
c 142	11.8	39.3	46	6	CA967893	CxLX05a15	CA967893	c 215	11.4	38.0	37	1	AA882396	AA882396
c 143	11.8	39.3	46	9	TA57A07P	T. brucei	TA57A07P	c 216	11.4	38.0	39	9	AL756928	AL756928
c 144	11.8	39.3	47	8	BH631605	1007085G0	BH631605	c 217	11.4	38.0	40	8	CC040316	CC040316
c 145	11.8	39.3	48	1	AA930873	vz71e07.s	AA930873	c 218	11.4	38.0	40	9	CL436831	CL436831
c 146	11.8	39.3	48	1	AL172854	uc10c07.r	AL172854	c 219	11.4	38.0	43	9	CL528741	CL528741
c 147	11.8	39.3	48	1	AA386692	vb55c05.r	AA386692	c 220	11.4	38.0	44	8	B07611	B07611
c 148	11.8	39.3	48	8	AZ805363	2M0066B13	AZ805363	c 221	11.4	38.0	45	8	AZ487209	AZ487209
c 149	11.8	39.3	48	8	AZ805363	2M0066B13	AZ805363	c 222	11.4	38.0	46	1	AA940161	AA940161
c 150	11.8	39.3	48	8	AZ805363	2M0066B13	AZ805363	c 223	11.4	38.0	46	1	AA956485	AA956485
c 151	11.8	39.3	49	1	AL282035	qq8e06.x	AL282035	c 224	11.4	38.0	46	8	BZ763623	BZ763623
c 152	11.8	39.3	49	1	AA515410	nf69a09.s	AA515410	c 225	11.4	38.0	47	8	AZ321341	AZ321341
c 153	11.8	39.3	50	1	AU103379	AU103379	AU103379	c 226	11.4	38.0	47	8	AZ778132	AZ778132
c 154	11.8	39.3	50	1	AU106735	AU106735	AU106735	c 227	11.4	38.0	47	8	BH801184	BH801184
c 155	11.6	38.7	24	8	AZ626098	1M0466109	AZ626098	c 228	11.4	38.0	47	8	BH847193	BH847193
c 156	11.6	38.7	27	4	BG927411	HNC1-1-G9	BG927411	c 229	11.4	38.0	47	8	CC039002	CC039002
c 157	11.6	38.7	29	8	BZ592652	SALK_0283	BZ592652	c 230	11.4	38.0	48	8	AZ621115	AZ621115
c 158	11.6	38.7	31	1	A1382798	tc08f05.x	A1382798	c 231	11.4	38.0	48	8	BH901106	BH901106
c 159	11.6	38.7	32	9	AL764287	Arabidops	AL764287	c 232	11.4	38.0	48	8	BH902185	BH902185
c 160	11.6	38.7	34	4	BM397004	5009-0-28	BM397004	c 233	11.4	38.0	49	1	A1036013	A1036013
c 161	11.6	38.7	35	9	CL234779	03S3051-0	CL234779	c 234	11.4	38.0	49	1	AA146697	AA146697
c 162	11.6	38.7	36	8	AZ759424	1M0551H17	AZ759424	c 235	11.4	38.0	49	1	AA146697	AA146697
c 163	11.6	38.7	36	8	AZ809373	2M0073A20	AZ809373	c 236	11.4	38.0	49	1	AA146697	AA146697
c 164	11.6	38.7	37	1	AI002874	an23d08.s	AI002874	c 237	11.4	38.0	49	7	T68434	T68434
c 165	11.6	38.7	38	8	BH853522	SALK_0770	BH853522	c 238	11.4	38.0	50	1	AU102629	AU102629
c 166	11.6	38.7	38	8	BZ355823	SALK_1375	BZ355823	c 239	11.4	38.0	50	1	AU103222	AU103222
c 167	11.6	38.7	39	8	BZ355823	SALK_1375	BZ355823	c 240	11.4	38.0	50	1	AU103491	AU103491
c 168	11.6	38.7	39	8	BZ355823	SALK_1375	BZ355823	c 241	11.4	38.0	50	1	AU104542	AU104542
c 169	11.6	38.7	40	1	AI882509	ub97a09.r	AI882509	c 242	11.4	38.0	50	1	AU104786	AU104786
c 170	11.6	38.7	42	2	BF683654	602139883	BF683654	c 243	11.4	38.0	50	1	AU104787	AU104787

C 244	11.4	38.0	50	1	AUI04788	AUI04788	AUI04788	C 317	11.2	37.3	50	1	AUI06721	AUI06721
C 245	11.4	38.0	50	1	AUI04789	AUI04789	AUI04789	C 318	11.2	37.3	50	1	AUI07040	AUI07040
C 246	11.4	38.0	50	1	AUI04790	AUI04790	AUI04790	C 319	11.2	37.3	50	1	AA411320	zV2B09.s
C 247	11.4	38.0	50	1	AUI04791	AUI04791	AUI04791	C 320	11.2	37.3	50	6	BF222716	nah37e07.f
C 248	11.4	38.0	50	1	AUI04792	AUI04792	AUI04792	C 321	11.2	37.3	50	6	CG222649	HDN--01-K
C 249	11.4	38.0	50	1	AUI04793	AUI04793	AUI04793	C 322	11.2	37.3	50	9	CR357976	Arabidops
C 250	11.4	38.0	50	1	AUI04794	AUI04794	AUI04794	C 323	11	36.7	24	9	TA100C01Q	T. brucei
C 251	11.4	38.0	50	1	AUI04795	AUI04795	AUI04795	C 324	11	36.7	25	9	AJ589502	Arabidops
C 252	11.4	38.0	50	1	AUI04796	AUI04796	AUI04796	C 325	11	36.7	27	9	CL680326	PR101284
C 253	11.4	38.0	50	1	AUI04797	AUI04797	AUI04797	C 326	11	36.7	29	9	TA635E07P	AL495741 T. brucei
C 254	11.4	38.0	50	1	AUI04798	AUI04798	AUI04798	C 327	11	36.7	31	1	AI248130	qh75b02.x
C 255	11.4	38.0	50	1	AUI04799	AUI04799	AUI04799	C 328	11	36.7	31	8	AZ308453	1M0011L20
C 256	11.4	38.0	50	1	AUI04800	AUI04800	AUI04800	C 329	11	36.7	31	8	AZ769140	1M0569B04
C 257	11.4	38.0	50	1	AUI04801	AUI04801	AUI04801	C 330	11	36.7	34	8	EG536263	602565486
C 258	11.4	38.0	50	1	AUI04802	AUI04802	AUI04802	C 331	11	36.7	34	8	AZ467072	1M0278A13
C 259	11.4	38.0	50	1	AUI04803	AUI04803	AUI04803	C 332	11	36.7	34	9	CL265773	03F3660-0
C 260	11.4	38.0	50	1	AUI05007	AUI05007	AUI05007	C 333	11	36.7	35	7	R37139	YF54911.s1
C 261	11.4	38.0	50	1	AUI05008	AUI05008	AUI05008	C 334	11	36.7	35	8	AZ760810	1M0554K16
C 262	11.4	38.0	50	1	AUI05010	AUI05010	AUI05010	C 335	11	36.7	36	9	AL752498	Arabidops
C 263	11.4	38.0	50	1	AUI06303	AUI06303	AUI06303	C 336	11	36.7	37	1	AA570314	nm22f06.s
C 264	11.4	38.0	50	9	CG801160	CG801160	118018C0	C 337	11	36.7	37	9	TA223F03P	AL480274 T. brucei
C 265	11.2	37.3	21	8	AZ336281	AZ336281	1M0066B02	C 338	11	36.7	38	8	BZ291479	BZ291479 SALK 1208
C 266	11.2	37.3	23	8	AZ501330	AZ501330	1M0340F11	C 339	11	36.7	39	1	AJ794161	AJ794161
C 267	11.2	37.3	27	8	AZ345930	AZ345930	1M0080K21	C 340	11	36.7	39	1	AV956618	AV956618
C 268	11.2	37.3	27	8	AZ347008	AZ347008	1M0082J02	C 341	11	36.7	39	8	AZ795977	2M0051C03
C 269	11.2	37.3	27	8	AZ580733	AZ580733	1M0369B14	C 342	11	36.7	39	8	BH907942	SALK 0449
C 270	11.2	37.3	29	8	AZ771858	AZ771858	1M0574P16	C 343	11	36.7	39	9	AG193663	AG193663 Pan trogl
C 271	11.2	37.3	31	1	TA84F02Q	TA84F02Q	AL461164 T. brucei	C 344	11	36.7	40	9	CL438956	CL438956 PST8429-N
C 272	11.2	37.3	31	1	AI313645	AI313645	EST100 Mo	C 345	11	36.7	41	9	TA381G12Q	AL497639 T. brucei
C 273	11.2	37.3	32	9	AG193703	AG193703	Pan trogl	C 346	11	36.7	42	8	BH889726	BH889726 3526.1.11
C 274	11.2	37.3	35	8	BH908490	BH908490	SALK_0486	C 347	11	36.7	42	8	BH908449	SALK_0485
C 275	11.2	37.3	35	8	TA352802Q	TA352802Q	AL496490 T. brucei	C 348	11	36.7	42	9	AG215405	AG215405 Drosophila
C 276	11.2	37.3	39	1	AJ673474	AJ673474	AJ673474	C 349	11	36.7	42	9	AG217432	AG217432 Drosophila
C 277	11.2	37.3	39	1	AZ308522	AZ308522	1M0011001	C 350	11	36.7	43	7	W09084	W09084 ma06c08.r1
C 278	11.2	37.3	39	9	TA306D11P	TA306D11P	AL491253 T. brucei	C 351	11	36.7	43	8	AZ346681	1M0082G01
C 279	11.2	37.3	40	1	AA767606	AA767606	Ob47e05.s	C 352	11	36.7	43	8	AZ439166	1M0229J07
C 280	11.2	37.3	40	1	AA860078	AA860078	ak45C03.s	C 353	11	36.7	43	9	CR404094	CR404094 Arabidops
C 281	11.2	37.3	40	1	AA417630	AA417630	zu99g11.s	C 354	11	36.7	43	9	DMES45184	DMES45184
C 282	11.2	37.3	40	7	N91653	N91653	za20h02.r1	C 355	11	36.7	43	9	AG214307	AG214307 Oryza sat
C 283	11.2	37.3	40	8	AZ859943	AZ859943	2M0165B18	C 356	11	36.7	44	6	CA969875	CA969875 CcLX06a24
C 284	11.2	37.3	40	9	BX659989	BX659989	Arabidops	C 357	11	36.7	44	6	CA969875	CA969875 CcLX06a24
C 285	11.2	37.3	41	8	AZ361377	AZ361377	1M0106J05	C 358	11	36.7	44	8	AZ309938	1M0017120
C 286	11.2	37.3	41	9	AO7601244	AO7601244	Arabidops	C 359	11	36.7	44	8	AZ646714	1M0512D21
C 287	11.2	37.3	43	7	COJ782826	COJ782826	BL016B.D0	C 360	11	36.7	44	8	AZ801644	2M0060L09
C 288	11.2	37.3	43	8	BH851172	BH851172	SALK_0726	C 361	11	36.7	44	8	BH890625	3526.1.14
C 289	11.2	37.3	44	1	AI185812	AI185812	qe49G07.x	C 362	11	36.7	44	9	AJ587765	Arabidops
C 290	11.2	37.3	44	1	AU255583	AU255583	SALK_1356	C 363	11	36.7	44	9	AG202126	Pan trogl
C 291	11.2	37.3	44	8	BZ384529	BZ384529	SALK_1356	C 364	11	36.7	45	1	AJ666198	AJ666198
C 292	11.2	37.3	45	8	BH171689	BH171689	SALK_0046	C 365	11	36.7	45	7	TI0835	hbc1343 Hum
C 293	11.2	37.3	45	8	BZ352401	BZ352401	SALK_0790	C 366	11	36.7	45	8	AZ423992	1M0203A16
C 294	11.2	37.3	46	1	AI001117	AI001117	0896C12.s	C 367	11	36.7	45	8	BH895159	3526.1.33
C 295	11.2	37.3	46	1	AA447381	AA447381	zw87d05.s	C 368	11	36.7	45	9	CG782500	1123050F1
C 296	11.2	37.3	46	1	AA485011	AA485011	aa39e10.r	C 369	11	36.7	46	1	AI096001	SWOVU3CAN
C 297	11.2	37.3	46	9	AL765362	AL765362	Arabidops	C 370	11	36.7	46	8	BH814201	SALK_0659
C 298	11.2	37.3	47	8	AQ074021	AQ074021	EP(3)3460	C 371	11	36.7	46	9	AJ587419	Arabidops
C 299	11.2	37.3	47	8	AZ783950	AZ783950	2M0026D08	C 372	11	36.7	46	9	AL770028	Arabidops
C 300	11.2	37.3	47	8	BH855918	BH855918	SALK_0843	C 373	11	36.7	46	9	BX290413	Arabidops
C 301	11.2	37.3	47	9	CG799680	CG799680	111800A40	C 374	11	36.7	47	1	AA972457	op41C04.s
C 302	11.2	37.3	48	9	AL751670	AL751670	Arabidops	C 375	11	36.7	47	4	BJ084362	BJ084362
C 303	11.2	37.3	49	1	AA659355	AA659355	nc92h06.s	C 376	11	36.7	47	6	C30881	HUMGS000495
C 304	11.2	37.3	49	1	AI032978	AI032978	ox22b01.s	C 377	11	36.7	47	7	H97244	YV98e05.s1
C 305	11.2	37.3	49	1	AJ649730	AJ649730	AJ649730	C 378	11	36.7	47	8	AZ606685	1M0428A17
C 306	11.2	37.3	49	7	COJ780197	COJ780197	BL009A.A0	C 379	11	36.7	47	8	CC049920	01S0518-0
C 307	11.2	37.3	49	8	AZ359000	AZ359000	1M0101I08	C 380	11	36.7	47	9	DR46K108	AL982012 Danio rer
C 308	11.2	37.3	49	8	AZ768953	AZ768953	1M0569M11	C 381	11	36.7	48	7	H13556	VJ15910.s1
C 309	11.2	37.3	49	8	BH902551	BH902551	SALK_0977	C 382	11	36.7	49	1	AA814244	AA814244 nz06a12.s
C 310	11.2	37.3	49	9	CG775874	CG775874	1123007C0	C 383	11	36.7	49	1	AI116299	AI116299 uc18h06.f
C 311	11.2	37.3	50	1	AUI03196	AUI03196	AUI03196	C 384	11	36.7	49	1	AI457977	AI457977 tJ54007.x
C 312	11.2	37.3	50	1	AUI03197	AUI03197	AUI03197	C 385	11	36.7	49	1	AV960495	AV960495
C 313	11.2	37.3	50	1	AUI03199	AUI03199	AUI03199	C 386	11	36.7	49	7	W61695	md16C12.r1
C 314	11.2	37.3	50	1	AUI03202	AUI03202	AUI03202	C 387	11	36.7	49	8	AZ307436	1M0090M05
C 315	11.2	37.3	50	1	AUI04744	AUI04744	AUI04744	C 388	11	36.7	49	8	AZ604391	AZ604391 1M0436A11
C 316	11.2	37.3	50	1	AUI04745	AUI04745	AUI04745	C 389	11	36.7	50	1	AUI03219	AUI03219

C 390	11	36.7	50	1	AU103220	AU103220	AU103220	463	10.8	36.0	42	6	C00705	C00705 HUMGS000826
C 391	11	36.7	50	1	AU103221	AU103221	AU103221	464	10.8	36.0	42	7	CK577724	CK577724 IST WT5 1
C 392	11	36.7	50	1	AU103223	AU103223	AU103223	C 465	10.8	36.0	42	8	BH641345	BH641345 1008046H0
C 393	11	36.7	50	1	AU103635	AU103635	AU103635	C 466	10.8	36.0	42	9	CR395913	CR395913 Arabidops
C 394	11	36.7	50	1	AU103637	AU103637	AU103637	C 467	10.8	36.0	42	9	AG215405	AG215405 Arabidops
C 395	11	36.7	50	1	AU103638	AU103638	AU103638	C 468	10.8	36.0	42	1	AA838558	AA838558 oe3909.s
C 396	11	36.7	50	1	AU103640	AU103640	AU103640	C 469	10.8	36.0	43	1	AI1356829	AI1356829 qv23c11.x
C 397	11	36.7	50	1	AU104382	AU104382	AU104382	C 470	10.8	36.0	43	1	AA103211	AA103211 mo22807.r
C 398	11	36.7	50	1	AU104383	AU104383	AU104383	C 471	10.8	36.0	43	1	AI583773	AI583773 tt71304.x
C 399	11	36.7	50	1	AU104385	AU104385	AU104385	C 472	10.8	36.0	43	1	AA594823	AA594823 no20c10.s
C 400	11	36.7	50	1	AU106326	AU106326	AU106326	C 473	10.8	36.0	43	2	AW698575	AW698575 g377 glan
C 401	11	36.7	50	1	AU106715	AU106715	AU106715	C 474	10.8	36.0	43	2	CA969808	CA969808 CGLX06a24
C 402	11	36.7	50	1	AU106716	AU106716	AU106716	C 475	10.8	36.0	43	7	H57259	H57259 yr10906.r1
C 403	11	36.7	50	1	AU106725	AU106725	AU106725	C 476	10.8	36.0	43	8	AZ443922	AZ443922 IM0238N08
C 404	11	36.7	50	1	AU106728	AU106728	AU106728	C 477	10.8	36.0	43	9	CG869477	CG869477 XP0160 Sa
C 405	11	36.7	50	1	AU106732	AU106732	AU106732	C 478	10.8	36.0	43	9	CL656268	CL656268 PRI0126a
C 406	11	36.7	50	1	AU107381	AU107381	AU107381	C 479	10.8	36.0	43	9	AG215223	AG215223 Drosophill
C 407	11	36.7	50	2	AW248365	AW248365	AW248365	C 480	10.8	36.0	44	8	AQ025982	AQ025982 EP(2)0358
C 408	11	36.7	50	4	BM733456	BM733456	BM733456	C 481	10.8	36.0	44	8	BZ290554	BZ290554 SALK_0901
C 409	11	36.7	50	4	BM733804	BM733804	BM733804	C 482	10.8	36.0	44	8	BZ767073	BZ767073 SALK_1383
C 410	11	36.7	50	7	R98157	R98157	R98157	C 483	10.8	36.0	45	6	CD028928	CD028928 mgmV001xL
C 411	11	36.7	50	8	BH641149	BH641149	BH641149	C 484	10.8	36.0	45	9	EX948434	EX948434 Arabidops
C 412	11	36.7	50	9	AL947641	AL947641	AL947641	C 485	10.8	36.0	45	9	CR395481	CR395481 Arabidops
C 413	10.8	36.0	21	6	CF279674	CF279674	CF279674	C 486	10.8	36.0	46	8	AZ476040	AZ476040 IM0294G04
C 414	10.8	36.0	27	9	CL655506	CL655506	CL655506	C 487	10.8	36.0	46	8	BH901021	BH901021 KG0833-3
C 415	10.8	36.0	28	1	AI131886	AI131886	AI131886	C 488	10.8	36.0	46	9	EX143450	EX143450 Danio rer
C 416	10.8	36.0	28	9	AJ598776	AJ598776	AJ598776	C 489	10.8	36.0	46	9	CG721749	CG721749 1119068G1
C 417	10.8	36.0	29	8	AZ633359	AZ633359	IM0488K02	C 490	10.8	36.0	46	9	CL655496	CL655496 PRI0123C
C 418	10.8	36.0	29	8	AZ775535	AZ775535	2M0008UJ12	C 491	10.8	36.0	47	2	AW059631	AW059631 RUTH.bssc
C 419	10.8	36.0	31	1	AA885849	AA885849	OJ36C01.s	C 492	10.8	36.0	47	2	CO787749	CO787749 NT002B.D0
C 420	10.8	36.0	31	1	AI001917	AI001917	OT42D10.s	C 493	10.8	36.0	47	8	AZ403608	AZ403608 IM0003I17
C 421	10.8	36.0	31	4	EG537808	EG537808	602566163	C 494	10.8	36.0	47	8	AZ403867	AZ403867 IM0171A16
C 422	10.8	36.0	31	4	BM392644	BM392644	50071-2-1	C 495	10.8	36.0	47	8	AZ974877	AZ974877 2M0249N10
C 423	10.8	36.0	31	4	BM393821	BM393821	50072-2-1	C 496	10.8	36.0	47	8	BZ380035	BZ380035 SALK_1144
C 424	10.8	36.0	31	8	AZ815323	AZ815323	2M0083B05	C 497	10.8	36.0	47	9	EX532135	EX532135 Arabidops
C 425	10.8	36.0	32	9	TA222D01P	TA222D01P	TA222D01P	C 498	10.8	36.0	47	9	CG869479	CG869479 XP0166 Sa
C 426	10.8	36.0	33	9	AL600534	AL600534	Arabidops	C 499	10.8	36.0	47	9	AG189046	AG189046 Pan trogl
C 427	10.8	36.0	34	1	AA148571	AA148571	Z104B02.r	C 500	10.8	36.0	48	8	AZ412179	AZ412179 IM0185H06
C 428	10.8	36.0	34	9	TA368C01Q	TA368C01Q	TA368C01Q	C 501	10.8	36.0	48	8	BH913087	BH913087 3526.1.38
C 429	10.8	36.0	34	9	CG711407	CG711407	1119021C0	C 502	10.8	36.0	48	9	CC799604	CC799604 01S0579-0
C 430	10.8	36.0	35	9	AL949791	AL949791	Arabidops	C 503	10.8	36.0	49	1	AI198147	AI198147 q151b10.x
C 431	10.8	36.0	35	9	DR421248	DR421248	Danio rer	C 504	10.8	36.0	49	1	AI340390	AI340390 tb40C01.x
C 432	10.8	36.0	35	9	TA275C03P	TA275C03P	TA275C03P	C 505	10.8	36.0	49	1	AI800933	AI800933 wg14g11.x
C 433	10.8	36.0	35	9	CL438234	CL438234	PST7051-N	C 506	10.8	36.0	49	1	AI941380	AI941380 sc12e11.y
C 434	10.8	36.0	36	8	BH849834	BH849834	SALK_0703	C 507	10.8	36.0	49	1	AA413837	AA413837 vc67405.s
C 435	10.8	36.0	36	8	AL941436	AL941436	Arabidops	C 508	10.8	36.0	49	2	BF970220	BF970220 602273453
C 436	10.8	36.0	37	1	AI900168	AI900168	sc01910.y	C 509	10.8	36.0	49	7	CF350566	CF350566 r160409.y
C 437	10.8	36.0	37	8	AQ073641	AQ073641	EP(2)2504	C 510	10.8	36.0	49	8	AZ807976	AZ807976 2M0071N10
C 438	10.8	36.0	37	8	BH417967	BH417967	W22-05 Mu	C 511	10.8	36.0	49	9	CR395482	CR395482 Arabidops
C 439	10.8	36.0	38	2	BF302851	BF302851	602032746	C 512	10.8	36.0	49	9	CG869475	CG869475 XP0159 Sa
C 440	10.8	36.0	38	8	AZ332275	AZ332275	IM0060M11	C 513	10.8	36.0	49	9	CG869476	CG869476 XP0159 Sa
C 441	10.8	36.0	38	9	EX662465	EX662465	Arabidops	C 514	10.8	36.0	50	1	AIU103201	AIU103201 AU103201
C 442	10.8	36.0	38	9	BM662465	BM662465	Arabidops	C 515	10.8	36.0	50	1	AIU104145	AIU104145 AU104145
C 443	10.8	36.0	38	9	DMES47594	DMES47594	Drosophill	C 516	10.8	36.0	50	1	AIU104558	AIU104558 AU104558
C 444	10.8	36.0	39	9	CG677721	CG677721	O2F2009-0	C 517	10.8	36.0	50	1	AIU104567	AIU104567 AU104567
C 445	10.8	36.0	39	9	CL528554	CL528554	ASV20E06.	C 518	10.8	36.0	50	1	AIU105214	AIU105214 AU105214
C 446	10.8	36.0	40	1	AV833543	AV833543	AV833543	C 519	10.8	36.0	50	1	AIU105216	AIU105216 AU105216
C 447	10.8	36.0	40	1	AA566138	AA566138	ESTK3037	C 520	10.8	36.0	50	1	AIU105219	AIU105219 AU105219
C 448	10.8	36.0	40	4	BJ082487	BJ082487	BJ082487	C 521	10.8	36.0	50	1	AIU105221	AIU105221 AU105221
C 449	10.8	36.0	40	8	AZ938886	AZ938886	2M0197F07	C 522	10.8	36.0	50	1	AIU105222	AIU105222 AU105222
C 450	10.8	36.0	40	8	CC199659	CC199659	XH683 Bay	C 523	10.8	36.0	50	1	AIU105223	AIU105223 AU105223
C 451	10.8	36.0	40	9	CR358612	CR358612	Arabidops	C 524	10.8	36.0	50	1	AIU105224	AIU105224 AU105224
C 452	10.8	36.0	40	9	TA187A02Q	TA187A02Q	T. brucei	C 525	10.8	36.0	50	1	AIU105225	AIU105225 AU105225
C 453	10.8	36.0	40	9	CG892121	CG892121	01S0592-0	C 526	10.8	36.0	50	1	AIU105226	AIU105226 AU105226
C 454	10.8	36.0	40	9	CL639115	CL639115	G080F09 G	C 527	10.8	36.0	50	1	AIU105228	AIU105228 AU105228
C 455	10.8	36.0	41	1	AV967151	AV967151	AV967151	C 528	10.8	36.0	50	1	AIU105230	AIU105230 AU105230
C 456	10.8	36.0	41	5	BQ589105	BQ589105	E012580-0	C 529	10.8	36.0	50	1	AIU105604	AIU105604 AU105604
C 457	10.8	36.0	41	6	CD530780	CD530780	07007 Ara	C 530	10.8	36.0	50	1	AIU107078	AIU107078 AU107078
C 458	10.8	36.0	41	8	BH909688	BH909688	SALK_0554	C 531	10.8	36.0	50	1	AIU107144	AIU107144 AU107144
C 459	10.8	36.0	41	8	BH909688	BH909688	SALK_0554	C 532	10.8	36.0	50	1	AIU107148	AIU107148 AU107148
C 460	10.8	36.0	41	9	BZ358843	BZ358843	SALK_1333	C 533	10.8	36.0	50	1	AIU107149	AIU107149 AU107149
C 461	10.8	36.0	41	9	CL256600	CL256600	XP0167 Sa	C 534	10.8	36.0	50	1	AIU107150	AIU107150 AU107150
C 462	10.8	36.0	42	2	AW059799	AW059799	LE6602.y5	C 535	10.8	36.0	50	1	AIU107150	AIU107150 AU107150

C 536	10.8	36.0	50	1	AU107151	AU107151	609	10.6	35.3	42	9	AL756014	Arabidops
C 537	10.8	36.0	50	2	AM459434	sh24c05.y	610	10.6	35.3	42	9	AL756480	Arabidops
C 538	10.8	36.0	50	6	CB275220	ku71c05.y	611	10.6	35.3	42	9	DM5547352	Drosophila
C 539	10.8	36.0	50	6	CB858048	NISC na12	612	10.6	35.3	43	1	AA902242	Q107f02.s
C 540	10.8	36.0	50	8	AZ666374	1M0548C19	613	10.6	35.3	43	1	BG756501	602715642
C 541	10.8	36.0	50	8	BZ596617	SALK_0928	614	10.6	35.3	43	6	CD533224	30K5 Arab
C 542	10.8	36.0	50	9	CC885693	SALK_1477	615	10.6	35.3	43	6	CD533224	30K5 Arab
C 543	10.8	36.0	50	9	CG869478	XP0161 Sa	616	10.6	35.3	43	8	AZ345872	1M0080L14
C 544	10.8	36.0	50	9	CG869480	XP0168 Sa	617	10.6	35.3	43	8	AZ809933	2M0074K07
C 545	10.6	35.3	21	4	BM398975	5009-0-51	618	10.6	35.3	44	2	BE294167	601172934
C 546	10.6	35.3	21	8	AZ820318	2M0092L19	619	10.6	35.3	44	7	H94616	vW56e06.s1
C 547	10.6	35.3	21	9	TA37H07P	T. brucei	620	10.6	35.3	45	4	BM392671	50071-2-1
C 548	10.6	35.3	24	6	CD530829	08C09 Ara	621	10.6	35.3	45	4	BM392671	50071-2-1
C 549	10.6	35.3	25	1	AJ657062	AJ657062	622	10.6	35.3	45	6	CA794943	Cac BL 19
C 550	10.6	35.3	25	8	BZ766895	SALK_1380	623	10.6	35.3	45	7	TI7578	mps v8 The
C 551	10.6	35.3	26	8	AZ792942	2M0045N21	624	10.6	35.3	45	8	BH633389	SALK_0462
C 552	10.6	35.3	26	8	CC455971	SALK_0912	625	10.6	35.3	45	8	BH748760	SALK_0466
C 553	10.6	35.3	27	8	BZ358060	SALK_1318	626	10.6	35.3	46	1	AJ7973945	sd1a09.y
C 554	10.6	35.3	27	8	BZ358896	SALK_1324	627	10.6	35.3	46	8	AZ434072	1M0220K13
C 555	10.6	35.3	28	7	W11835	mb20h01.r1	628	10.6	35.3	46	8	CC031287	3591_1_12
C 556	10.6	35.3	30	8	AZ969026	2M0241E12	629	10.6	35.3	46	9	CC887026	SALK_1493
C 557	10.6	35.3	30	8	CC455639	CC455639	630	10.6	35.3	46	9	CG778195	1123026G0
C 558	10.6	35.3	30	9	AG192903	Pan trogl	631	10.6	35.3	47	1	AJ669335	AJ669335
C 559	10.6	35.3	31	1	AI097891	AI097891	632	10.6	35.3	47	2	B534847	601231985
C 560	10.6	35.3	31	1	AI174157	v982d09.r	633	10.6	35.3	47	2	B534847	601231985
C 561	10.6	35.3	31	9	TA131A06P	AL464159 T. brucei	634	10.6	35.3	47	8	AZ760561	1M0554G23
C 562	10.6	35.3	32	2	BF568357	BF568357	635	10.6	35.3	47	8	AZ822668	2M0096B09
C 563	10.6	35.3	32	6	CO1097	CO1097 HJMS000775	636	10.6	35.3	47	8	AZ822668	2M0096B09
C 564	10.6	35.3	33	8	AZ479535	1M0300B16	637	10.6	35.3	47	8	AZ835122	2M0159M08
C 565	10.6	35.3	33	8	AZ513143	1M0359E08	638	10.6	35.3	47	8	AZ835122	2M0159M08
C 566	10.6	35.3	33	8	AZ513143	1M0359E08	639	10.6	35.3	47	9	AG189368	Pan trogl
C 567	10.6	35.3	33	9	TA154808Q	AL473267 T. brucei	640	10.6	35.3	48	1	AV969497	AV969497
C 568	10.6	35.3	33	9	TA339810P	AL497413 T. brucei	641	10.6	35.3	48	8	AZ320508	1M0040A07
C 569	10.6	35.3	33	9	CT979625	CT979625 SALK_1451	642	10.6	35.3	48	8	AZ576656	AST-T14C0
C 570	10.6	35.3	34	1	AI721161	AI721161 as73h12.x	643	10.6	35.3	48	8	AZ801292	2M0059M10
C 571	10.6	35.3	34	2	BE271165	601178504	644	10.6	35.3	48	8	BZ290571	SALK_0901
C 572	10.6	35.3	34	7	R84653	yo38c05.r1	645	10.6	35.3	48	9	EX150228	Danio rer
C 573	10.6	35.3	34	8	BZ356400	SALK_1289	646	10.6	35.3	49	1	AI147249	qb36g08.x
C 574	10.6	35.3	35	2	BE867678	BE867678	647	10.6	35.3	49	1	AI160561	qc87d06.x
C 575	10.6	35.3	35	8	AZ579575	1M0367M07	648	10.6	35.3	49	1	AI709135	as6201.x
C 576	10.6	35.3	35	9	CC888512	CC888512 SALK_1519	649	10.6	35.3	49	1	AI814770	wk65e08.x
C 577	10.6	35.3	36	1	AJ746775	AJ746775	650	10.6	35.3	49	8	AZ605742	1M0437E13
C 578	10.6	35.3	36	2	AW063331	AW063331 TN0242 KR	651	10.6	35.3	49	8	AZ872239	2M0185C03
C 579	10.6	35.3	36	8	BZ381466	BZ381466 SALK_1167	652	10.6	35.3	49	9	CG869945	X50950 Sa
C 580	10.6	35.3	36	9	TA126A03P	AL463811 T. brucei	653	10.6	35.3	50	1	AI103158	1M03158
C 581	10.6	35.3	37	6	CF297401	CF297401 3ODGS--08	654	10.6	35.3	50	1	AI103158	1M03158
C 582	10.6	35.3	37	8	AZ308362	AZ308362 1M0011F16	655	10.6	35.3	50	1	AI103614	1M03614
C 583	10.6	35.3	37	8	AZ832421	AZ832421 2M0112N13	656	10.6	35.3	50	1	AI104307	1M04307
C 584	10.6	35.3	38	1	AL637555	AL637555	657	10.6	35.3	50	1	AI104308	1M04308
C 585	10.6	35.3	38	7	D19136	MUSGS01352	658	10.6	35.3	50	1	AI104310	1M04310
C 586	10.6	35.3	38	8	AZ312598	AZ312598 1M0028H06	659	10.6	35.3	50	1	AI104311	1M04311
C 587	10.6	35.3	38	8	AZ439902	AZ439902 1M0230C13	660	10.6	35.3	50	1	AI104311	1M04311
C 588	10.6	35.3	38	8	AZ806846	AZ806846 2M0069K10	661	10.6	35.3	50	1	AI105459	1M05459
C 589	10.6	35.3	38	8	BH751791	BH751791 SALK_0506	662	10.6	35.3	50	1	AI105856	1M05856
C 590	10.6	35.3	39	4	BJ051176	BJ051176	663	10.6	35.3	50	1	AI106551	1M06551
C 591	10.6	35.3	39	8	AZ309582	AZ309582 1M0016K11	664	10.6	35.3	50	1	AI106554	1M06554
C 592	10.6	35.3	39	8	AZ856438	AZ856438 2M0160B23	665	10.6	35.3	50	1	AI106723	1M06723
C 593	10.6	35.3	39	8	BH847395	BH847395 SALK_0531	666	10.6	35.3	50	1	AI107199	1M07199
C 594	10.6	35.3	39	8	BZ665246	BZ665246 SALK_1109	667	10.6	35.3	50	4	EG409021	gb85f04.y
C 595	10.6	35.3	39	9	CL800300	CL800300 02S0088-0	668	10.6	35.3	50	5	EX629197	EX629197
C 596	10.6	35.3	39	9	CL685477	CL685477	669	10.6	35.3	50	7	CO578886	ta159f10.
C 597	10.6	35.3	40	1	AI692266	AI692266 w83f04.r	670	10.6	35.3	50	8	AZ386495	1M045E01
C 598	10.6	35.3	40	1	AA589938	AA589938 1M0262N11	671	10.6	35.3	50	8	AZ756885	ew02h09.x
C 599	10.6	35.3	40	8	AZ458268	AZ458268 1M0262N11	672	10.6	35.3	50	8	AZ852818	2M0155K12
C 600	10.6	35.3	40	8	BH251215	BH251215 SALK_0112	673	10.6	35.3	50	8	BH748752	SALK_0466
C 601	10.6	35.3	40	8	BZ768127	BZ768127 SALK_1398	674	10.6	35.3	50	9	CR207109	Forward s
C 602	10.6	35.3	41	6	CA851520	CA851520 D14F06_L0	675	10.6	35.3	50	9	CR230363	Reverse s
C 603	10.6	35.3	41	8	AZ630326	AZ630326 1M0483L11	676	10.6	35.3	50	9	AG211154	Oryza sat
C 604	10.6	35.3	41	8	BH802422	BH802422 1008026B0	677	10.6	34.7	19	8	AZ991531	2M0275K15
C 605	10.6	35.3	42	1	AV839107	AV839107	678	10.4	34.7	22	1	AJ806746	AJ806746
C 606	10.6	35.3	42	8	AZ628072	AZ628072 1M0480A05	679	10.4	34.7	24	4	BM397115	5009-0-29
C 607	10.6	35.3	42	8	AZ645652	AZ645652 1M0511P07	680	10.4	34.7	24	4	BM399801	5009-0-61
C 608	10.6	35.3	42	8	BH752131	SALK_0518	681	10.4	34.7	24	9	CL694812	PR10165a_

682	10.4	34.7	25	4	BM400178	5009-0-68	BM400178	5009-0-68	10.4	34.7	43	1	AA134736
683	10.4	34.7	25	8	AZ817392	2M0086E08	AZ817392	2M0086E08	10.4	34.7	43	1	AV955378
684	10.4	34.7	26	4	BM397261	5009-0-30	BM397261	5009-0-30	10.4	34.7	43	1	BM397324
685	10.4	34.7	27	5	BM565326	EX565326	BM565326	EX565326	10.4	34.7	43	6	CA969020
686	10.4	34.7	27	8	AZ433910	1M0220H06	AZ433910	1M0220H06	10.4	34.7	43	7	R73866
687	10.4	34.7	27	8	AZ599857	1M0416K19	AZ599857	1M0416K19	10.4	34.7	43	7	W60657
688	10.4	34.7	27	8	AZ623078	1M0460G19	AZ623078	1M0460G19	10.4	34.7	43	8	AZ320464
689	10.4	34.7	27	9	CL680176	PR10128A	CL680176	PR10128A	10.4	34.7	43	8	AZ759952
690	10.4	34.7	28	1	AA994218	cu49405.S	AA994218	cu49405.S	10.4	34.7	43	9	CC799108
691	10.4	34.7	28	2	AW250231	2822603.3	AW250231	2822603.3	10.4	34.7	43	9	CC894144
692	10.4	34.7	28	8	BZ592883	SALK_0476	BZ592883	SALK_0476	10.4	34.7	43	9	AG264217
693	10.4	34.7	31	6	CD028820	mgmy006xA	CD028820	mgmy006xA	10.4	34.7	44	6	CA794547
694	10.4	34.7	31	7	H04593	YJ49C03.S1	H04593	YJ49C03.S1	10.4	34.7	44	6	CA794547
695	10.4	34.7	32	8	AZ317543	1M0036F11	AZ317543	1M0036F11	10.4	34.7	44	8	CA794547
696	10.4	34.7	32	9	AJ598209	ArabiDops	AJ598209	ArabiDops	10.4	34.7	44	8	CA794547
697	10.4	34.7	33	4	BM392440	50071-2-1	BM392440	50071-2-1	10.4	34.7	44	8	CA794547
698	10.4	34.7	33	4	BM393652	50072-2-1	BM393652	50072-2-1	10.4	34.7	44	8	CA794547
699	10.4	34.7	33	8	AZ834737	2M0117O06	AZ834737	2M0117O06	10.4	34.7	44	8	CA794547
700	10.4	34.7	33	9	AL769444	ArabiDops	AL769444	ArabiDops	10.4	34.7	44	8	CA794547
701	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
702	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
703	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
704	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
705	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
706	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
707	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
708	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
709	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
710	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
711	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
712	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
713	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
714	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
715	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
716	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
717	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
718	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
719	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
720	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
721	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
722	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
723	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
724	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
725	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
726	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
727	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
728	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
729	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
730	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
731	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
732	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
733	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
734	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
735	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
736	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
737	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
738	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
739	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
740	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
741	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
742	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
743	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
744	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
745	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
746	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
747	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
748	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
749	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
750	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
751	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
752	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
753	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547
754	10.4	34.7	34	1	AJ667018	AJ667018	AJ667018	AJ667018	10.4	34.7	44	8	CA794547

C 828	10.4	34.7	50	1	AV833335	AV833335	AV833335	901	10.2	34.0	36	9	CL002068
C 829	10.4	34.7	50	6	CB275263	ku56e09.y	C 902	10.2	34.0	36	9	AG203157	Pan trogl
C 830	10.4	34.7	50	7	CK584111	IST WIS 1	C 903	10.2	34.0	36	9	BF792074	602325002
C 831	10.4	34.7	50	8	AQ025065	EP(3) 0339	C 904	10.2	34.0	37	4	BG035903	602326007
C 832	10.4	34.7	50	8	AZ862310	2M0169022	C 905	10.2	34.0	37	4	BG390448	602416006
C 833	10.4	34.7	50	8	AZ918144	1006003D0	C 906	10.2	34.0	37	7	T70898	yc49c08.s1
C 834	10.4	34.7	50	8	AZ289491	SALK_0228	C 907	10.2	34.0	37	8	AZ460041	1M0265A13
C 835	10.4	34.7	50	9	BX286949	Arabidops	C 908	10.2	34.0	37	8	AZ817852	2M0087K03
C 836	10.4	34.7	50	9	BX997240	Forward s	C 909	10.2	34.0	37	9	AG195359	Pan trogl
C 837	10.4	34.7	50	9	CR105282	Forward s	C 910	10.2	34.0	38	8	AZ785597	2M0029C08
C 838	10.2	34.0	16	1	AI154875	ud80f04.r	C 911	10.2	34.0	38	8	AZ812945	2M0080C03
C 839	10.2	34.0	16	1	AI168794	ox67a03.s	C 912	10.2	34.0	38	8	DR2415T	Arabidops
C 840	10.2	34.0	21	1	AJ798892	AJ798892	C 913	10.2	34.0	38	9	TA206806Q	T. brucei
C 841	10.2	34.0	24	8	AZ767824	1M0567K22	C 914	10.2	34.0	39	4	BJ063882	BJ063882
C 842	10.2	34.0	24	8	BZ378740	SALK_1118	C 915	10.2	34.0	39	4	AQ025356	EP(X) 0773
C 843	10.2	34.0	24	8	BZ592769	SALK_0291	C 916	10.2	34.0	39	8	AZ438608	1M0228116
C 844	10.2	34.0	24	8	BZ596305	SALK_0923	C 917	10.2	34.0	39	8	AZ810683	2M0076G19
C 845	10.2	34.0	25	8	AZ0309210	1M0013F16	C 918	10.2	34.0	39	9	BX291484	Arabidops
C 846	10.2	34.0	25	8	AZ654827	1M0529L16	C 919	10.2	34.0	39	9	BX946649	Arabidops
C 847	10.2	34.0	25	9	AG190823	AG190823	C 920	10.2	34.0	39	9	CG719218	1119056F0
C 848	10.2	34.0	26	8	AZ345919	1M0080I22	C 921	10.2	34.0	40	1	AA887375	oj53908.s
C 849	10.2	34.0	27	8	AZ987358	2M0269H21	C 922	10.2	34.0	40	1	AI268767	Qo48C06.x
C 850	10.2	34.0	27	8	BZ378777	SALK_1119	C 923	10.2	34.0	40	8	AZ835260	2M0129H20
C 851	10.2	34.0	27	8	BZ381552	SALK_1169	C 924	10.2	34.0	40	8	CC060483	EXY02755-5
C 852	10.2	34.0	27	8	BZ762293	SALK_1109	C 925	10.2	34.0	41	7	CK575900	IST_WIS_9
C 853	10.2	34.0	27	9	TA81H06P	AL461740 T. brucei	C 926	10.2	34.0	41	8	AZ399407	1M0165D15
C 854	10.2	34.0	27	9	TA81H06P	AL461740 T. brucei	C 927	10.2	34.0	41	8	AZ435350	1M0222M13
C 855	10.2	34.0	28	8	BZ595209	SALK_0863	C 928	10.2	34.0	41	8	AZ466544	1M0277Q13
C 856	10.2	34.0	28	8	BZ595211	SALK_0863	C 929	10.2	34.0	41	9	BX657645	Arabidops
C 857	10.2	34.0	28	8	BZ596382	SALK_0924	C 930	10.2	34.0	41	9	CR399886	Arabidops
C 858	10.2	34.0	28	8	BZ596387	SALK_0924	C 931	10.2	34.0	41	9	CG726268	1119089B0
C 859	10.2	34.0	28	8	BZ596389	SALK_0924	C 932	10.2	34.0	42	1	AV832615	AV832615
C 860	10.2	34.0	28	8	BZ596390	SALK_0924	C 933	10.2	34.0	42	6	CA966788	CLX06a23
C 861	10.2	34.0	28	8	BZ596397	SALK_0925	C 934	10.2	34.0	42	7	H14364	ym18e07.s1
C 862	10.2	34.0	28	8	BZ596404	SALK_0925	C 935	10.2	34.0	42	8	AZ343437	1M0076E22
C 863	10.2	34.0	28	8	BZ767739	SALK_1392	C 936	10.2	34.0	42	8	BH614189	SALK_0356
C 864	10.2	34.0	29	8	AZ307834	1M0010M12	C 937	10.2	34.0	42	8	BH910379	SALK_0592
C 865	10.2	34.0	29	8	AZ827011	2M0103112	C 938	10.2	34.0	42	8	BZ287430	SALK_0208
C 866	10.2	34.0	29	8	BZ766871	SALK_1410	C 939	10.2	34.0	42	8	CC457007	SALK_1049
C 867	10.2	34.0	31	1	AI037963	ox53D09.x	C 940	10.2	34.0	42	9	BX127928	Danio rer
C 868	10.2	34.0	31	1	AI159285	vz85b12.r	C 941	10.2	34.0	42	9	BX946870	Arabidops
C 869	10.2	34.0	31	1	AI366379	ox82h02.x	C 942	10.2	34.0	42	9	TA50F09P	Arabidops
C 870	10.2	34.0	31	4	B1335185	602998054	C 943	10.2	34.0	43	1	AV962413	AV962413
C 871	10.2	34.0	31	8	AZ462523	1M0271105	C 944	10.2	34.0	43	1	AA510314	vg32a11.r
C 872	10.2	34.0	31	8	AZ780613	2M0018H07	C 945	10.2	34.0	43	1	AA569427	nf22d07.s
C 873	10.2	34.0	31	8	BZ595213	SALK_0863	C 946	10.2	34.0	43	8	AZ469586	1M0283112
C 874	10.2	34.0	31	8	BZ596044	SALK_0919	C 947	10.2	34.0	43	8	BZ380206	SALK_1147
C 875	10.2	34.0	31	8	BZ596385	SALK_0924	C 948	10.2	34.0	43	9	AJ591996	Arabidops
C 876	10.2	34.0	31	8	BZ596395	SALK_0925	C 949	10.2	34.0	43	9	CL256591	AF0229 Sa
C 877	10.2	34.0	31	9	CC887820	SALK_1508	C 950	10.2	34.0	43	9	AG220919	Lotus cor
C 878	10.2	34.0	32	7	H63110	yr48b03.s1	C 951	10.2	34.0	44	9	AL753874	Arabidops
C 879	10.2	34.0	32	7	R38536	yc87d04.s1	C 952	10.2	34.0	44	9	AL757341	Arabidops
C 880	10.2	34.0	32	8	AZ490918	1M0324M09	C 953	10.2	34.0	44	9	BX142777	Danio rer
C 881	10.2	34.0	32	8	AZ599521	1M0414K22	C 954	10.2	34.0	44	9	EX197881	Danio rer
C 882	10.2	34.0	32	8	BZ378081	SALK_1070	C 955	10.2	34.0	45	6	CF304966	ABF1--06-
C 883	10.2	34.0	32	8	BZ381611	SALK_1170	C 956	10.2	34.0	45	7	D44866	HUMSUPY325
C 884	10.2	34.0	32	8	BZ384943	SALK_1362	C 957	10.2	34.0	45	8	AZ803772	2M0064P15
C 885	10.2	34.0	32	8	BZ596391	SALK_0924	C 958	10.2	34.0	45	8	BH252295	SALK_0130
C 886	10.2	34.0	32	9	BX532188	Arabidops	C 959	10.2	34.0	45	8	BH613192	SALK_0338
C 887	10.2	34.0	32	9	CC887822	SALK_1508	C 960	10.2	34.0	45	8	BH613496	SALK_0343
C 888	10.2	34.0	33	1	AU240358	AU240358	C 961	10.2	34.0	45	9	AJ597990	Arabidops
C 889	10.2	34.0	33	8	AZ617294	1M0448E04	C 962	10.2	34.0	45	9	BX120374	Danio rer
C 890	10.2	34.0	33	8	AZ785738	2M0029J22	C 963	10.2	34.0	45	9	CR402674	Arabidops
C 891	10.2	34.0	33	9	AL770136	Arabidops	C 964	10.2	34.0	45	9	CC886318	SALK_1484
C 892	10.2	34.0	34	1	AA114877	z103b12.r	C 965	10.2	34.0	46	1	AI735184	as88g10.x
C 893	10.2	34.0	34	4	BM400034	5009-0-65	C 966	10.2	34.0	46	1	AA209176	zq65a05.s
C 894	10.2	34.0	34	7	H43178	yo02906.r1	C 967	10.2	34.0	46	1	AA255908	AU255908
C 895	10.2	34.0	34	8	AZ425761	1M0206F03	C 968	10.2	34.0	46	1	AV832895	AV832895
C 896	10.2	34.0	35	8	AZ822670	2M0096B11	C 969	10.2	34.0	46	6	CA587290	LBE10P60
C 897	10.2	34.0	35	8	BH853545	SALK_0771	C 970	10.2	34.0	46	6	CF317892	HD--07-M0
C 898	10.2	34.0	36	2	BF969721	602272124	C 971	10.2	34.0	46	7	CO577181	TVEST067G
C 899	10.2	34.0	36	8	AZ766765	1M0564K02	C 972	10.2	34.0	46	8	AZ496495	1M0332N24
C 900	10.2	34.0	36	9	AL757413	Arabidops	C 973	10.2	34.0	46	8	AZ662880	1M0542A16

CL002068	01S0614-0
AG203157	Pan trogl
BF792074	602252502
BG035903	602326007
BG390448	602416086
T70898	yc49c08.s1
AZ460041	1M0285AL3
AZ817852	2M0087K03
AG195359	Pan trogl
AZ785597	2M0029C08
AZ812945	2M0080C03
AZ737219	Danio rer
AL476128	T. brucei
BJ063882	Bu063882
AQ025356	EP(X) 0773
AZ438608	1M0228G16
AZ810683	2M0076G19
BX291484	Arabidops
BX946649	Arabidops
CG719218	1119056F0
AZ835260	2M0129H20
AA887375	0J53Q08.s
AI268767	QO48C06.x
CC060483	EY02755.s
CK575900	IST_WIS_9
AZ399407	1M0165D15
AZ435350	1M0222M13
AZ466544	1M0277O13
BX657645	Arabidops
CR399886	Arabidops
CG726268	1119089B0
AV832615	AV832615
CA966788	CLX06a23
H14364	Ym18e07.s1
AZ343437	1M0076E22
BH614189	SALK_0356
BH910379	SALK_0592
BZ287430	SALK_0208
CC457007	SALK_1049
BX127928	Danio rer
BX946870	Arabidops
AL455865	T. brucei
AV962413	AV962413
AA510314	vg32a11.r
AA569427	nE22407.s
AZ469586	1M0283I12
BZ380206	SALK_1147
AJ591996	Arabidops
CL256591	AF0229 Sa
AG220919	Lotus cor
AL753874	Arabidops
AL757341	Arabidops
BX142777	Danio rer
EX197881	Danio rer
CF304966	ABF1--06-
D44866	HUMSUPX325
AZ803772	2M0064P15
BH252295	SALK_0130
BH613192	SALK_0338
BH613496	SALK_0343
AJ597990	Arabidops
BX120374	Danio rer
CR402674	Arabidops
CC886318	SALK_1484
AI735184	ae88G10.x
AA209176	zg65805.s
AU255908	AU255908
AV832895	AV832895
CA587290	LBE10p60
CF317892	HD- -07-MO
CO577181	TVEST067G
AZ496495	1M0322N24
AZ662880	1M0542A16

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974 10.2 34.0 46 8 BH644452 1008049B0
C 975 10.2 34.0 46 8 CC183633 RST407 Ba
C 976 10.2 34.0 46 8 CC249191 XF289 Bay
C 977 10.2 34.0 46 8 AJ592098 Arabidops
C 978 10.2 34.0 46 9 TA296G08Q
C 979 10.2 34.0 47 1 AL038110 DKFp566M
C 980 10.2 34.0 47 8 AZ611937 1M0438N06
C 981 10.2 34.0 47 8 AZ820416 2M0922F16
C 982 10.2 34.0 47 8 BZ291481 SALK 1208
C 983 10.2 34.0 47 8 BZ661110 SALK 0245
C 984 10.2 34.0 47 9 AJ592846 Arabidops
C 985 10.2 34.0 48 4 BI906001 603062308
C 986 10.2 34.0 48 7 CO739707 SLLB06a24
C 987 10.2 34.0 48 8 AZ300919 EP(2)0882
C 988 10.2 34.0 48 8 AZ361863 1M0106RH17
C 989 10.2 34.0 48 9 AG218322 Drosophila
C 990 10.2 34.0 49 1 AA935229 0666C12.s
C 991 10.2 34.0 49 1 AI018702 0V63901.s
C 992 10.2 34.0 49 1 AI624828 t871f09.x
C 993 10.2 34.0 49 1 AI662938 uJ69c07.Y
C 994 10.2 34.0 49 1 AJ394062 AJ394062
C 995 10.2 34.0 49 1 AA288062 va25f06.r
C 996 10.2 34.0 49 1 AA437396 aa84a08.r
C 997 10.2 34.0 49 4 BG526632 61-17 Ste
C 998 10.2 34.0 49 5 BQ101179 BQ101179
C 999 10.2 34.0 49 5 AZ355782 1M0095B09
C1000 10.2 34.0 49 8 AZ450961 1M0250B05
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ALIGNMENTS

RESULT 1
CL436787 35 bp DNA linear GSS 18-MAR-2004
LOCUS PST3831-NL.Seq MICB1 Mus musculus genomic clone PST3831-NL.Seq,
DEFINITION genomic survey sequence.
ACCESSION CL436787.1 GI:45571935
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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FEATURES
source
1..35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST3831-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
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Class: Gene Trap.
Location/Qualifiers
1..35
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST3831-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
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Query Match 53.3%; Score 16; DB 9; Length 35;
Best Local Similarity 79.2%; Pred. No. 4.4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 7 CAGTCCTGGTCATCTCACCTTCT 30
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Db 1 CATGCTTGGTCATCTCATGCTCT 24
|||
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```
RESULT 2
BH864588/c 42 bp DNA linear GSS 05-AUG-2002
LOCUS SALK_096301 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_096301, genomic survey sequence.
ACCESSION BH864588
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM
REFERENCE
AUTHORS
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FEATURES
source
1..42
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_096301"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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```
Query Match 52.0%; Score 15.6; DB 8; Length 42;
Best Local Similarity 81.8%; Pred. No. 6.6e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 9 GTCCTTGGTCATCTCACCTTCT 30
|||
Db 42 GTCGCTCGTCATCTCGCTTCT 21
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```
RESULT 3
AU106879 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU106879 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNG00759, mRNA sequence.
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ORIGIN
/note="Vector: U3NeosV1"
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Query Match 53.3%; Score 16; DB 9; Length 35;
Best Local Similarity 79.2%; Pred. No. 4.4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 7 CAGTCCTGGTCATCTCACCTTCT 30
|||
Db 1 CATGCTTGGTCATCTCATGCTCT 24
|||
```

```
RESULT 2
BH864588/c 42 bp DNA linear GSS 05-AUG-2002
LOCUS SALK_096301 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION thaliana genomic clone SALK_096301, genomic survey sequence.
ACCESSION BH864588
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM
REFERENCE
AUTHORS
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FEATURES
source
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
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/clone="SALK_096301"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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Query Match 52.0%; Score 15.6; DB 8; Length 42;
Best Local Similarity 81.8%; Pred. No. 6.6e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 9 GTCCTTGGTCATCTCACCTTCT 30
|||
Db 42 GTCGCTCGTCATCTCGCTTCT 21
|||
```

```
RESULT 3
AU106879 50 bp mRNA linear EST 28-JAN-2004
LOCUS AU106879 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION LNG00759, mRNA sequence.
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ACCESSION   AU106879
VERSION     AU106879.1  GI:13556400
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
            Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
            Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
            Sugano,S. Construction and characterization of a full
            length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
            149-156 (1997).

FEATURES             Location/Qualifiers
     source           1..50
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      49.3%; Score 14.8; DB 1; Length 50;
Best Local Similarity 73.1%; Pred. No. 1.4e+05;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy  5 CTCAGCTCTTGTCATCTCACCTTCT 30
    ||||| ||| |||||
Db   19 CTCAGCTCAGCGCAACCTCACCTTCT 44

RESULT 4
CL212954
LOCUS      CL212954
DEFINITION G028G03 GGTC Gene Trap Library GV07C05 Mus musculus cDNA clone
ACCESSION  CL212954
VERSION     G028G03, mRNA sequence.
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 41)
AUTHORS     Hansen,J., Floss,T., van Sloun,P., Fuchtbauer,E.M., Vauti,F.,
            Arnold,H.H., Schmutgen,F., Wurst,W., Von Melchner,H. and Ruiz,P.
TITLE       A large-scale, gene-driven mutagenesis approach for the functional
            analysis of the mouse genome
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 100 (17), 9918-9922 (2003)
MEDLINE     22810117
PUBMED      12904583
COMMENT     On Jun 30, 2004 this sequence version replaced gi:40729855.
            Contact: GGTC
            German Genetrap Consortium (GGTC)
            Email: info@genetrap.de
            U3C80 gene trap. Sequence tag generated by 5'RACE. Additional
            sequence information can be found at:
            'http://genetrap.gsf.de/project/web_new/database/result_clone.html?
            clone_id=G028G03'. ES cell line harboring insertion mutation of
            target gene is available at:
            'http://genetrap.gsf.de/project/web_new/order_clones/howtoorder.htm

1' Inhouse Sequence Identifier: 15667
Class: Gene trap.
Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="129 Sv"
                     /db_xref="taxon:10090"
                     /clone="G028G03"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_lines="ES cells [C57BL/6J x 129Sv/SvEvTac] F1"
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                     /note="Vector: U3CEO"

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Best Local Similarity 70.4%; Pred. No. 2.5e+05;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy  4 ACTCAGTCTTGTCATCTCACCTTCT 30
    ||||| ||| |||||
Db   8 ACTTAGTCGTTGCTCGTCTAGTCTTGT 34

RESULT 5
BE970036/c
LOCUS      BE970036
DEFINITION 601680150F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3950172 5',
            mRNA sequence.
ACCESSION  BE970036
VERSION     BE970036.1  GI:10582969
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 49)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM816 row: d column: 13
            High quality sequence stop: 49.

FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_78"
                     /note="Organ: pancreas; Vector: pDNR-LIB (Clontech);
            Site 1: Sfil (ggcgctcgcc); Site 2: Sfil
            (ggccatggcc); 5' and 3' adaptors were used in cloning
            as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
            and 3' adaptor sequence:
            5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.2
            kb (range 0.5-4.0 kb). 14/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones
            and was constructed by Clontech Laboratories (Palo Alto,
            CA)."

ORIGIN

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τ -DNA derived sequences were removed."

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REFERENCE
AUTHORS      1  Ryder,E.J., Ashburner,M., Bagunya,J., Blows,F., Bucheton,A.,
              Coulson,D., Dickson,B., Drummond,J., Glover,D., Guntton,N.,
              Hafien,E., Hall,S., Heisenberg,M., Lepesant,J.A., Maroy,P.,
              Mechler,B., O'Kane,C., Pflugfelder,G., Rasmuson-Lestander,A.,
              Reuter,G., Roote,J., Szydony,J., Wang,S., Webster,J. and
              Russell,S.
TITLE        Mapping of RS P element insertions in Drosophila melanogaster for
              the DrosDel second generation deficiency kit
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 42)
AUTHORS      Ryder,E.J.
TITLE        Direct Submission
JOURNAL      Submitted (19-JAN-2004) Ryder E.J., Department of Genetics,
              University Of Cambridge, Downing Street, CB23EH, UNITED KINGDOM
COMMENT      The insertion point of the P element is before base 1 of the
              sequence. Further information about this P element insertion line
              can be found at http://www.flyseq.org.uk and
              http://www.drosdel.org.uk.
FEATURES
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Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 6 TCAGTCCTTGGTCATCTCACCCTTCT 30
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Db 9 TCTGTCAATTTCTCAATGCCCATCT 33

RESULT 9
AA954628
LOCUS      o083e04.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1572798 3'
DEFINITION similar to SW:SM22.HUMAN P43330 SMALL NUCLEAR RIBONUCLEOPROTEIN SM
D2 ; mRNA sequence.
ACCESSION  AA954628
VERSION     AA954628.1 GI:3118323
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46)
AUTHORS     Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES
source       1. .50
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              /mol_type="mRNA"
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              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 3.8e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

High quality sequence stop: 1.
Location/Qualifiers
1. .46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1572798"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kids"
/note="Organ: kidney; Vector: pTT3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AATCGAAGAATTCGGCGCCCAATATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
FEATURES
source       1. .46
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 46;
Best Local Similarity 72.0%; Pred. No. 3.7e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCCTTGGTCATCTCAC 25
    ||||| ||||| ||||| |||||
Db 12 TGCAGCCCTCCGGGTCATCTCAC 36

RESULT 10
AA106264/c
LOCUS      AU106264 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HSI07556, mRNA sequence.
ACCESSION  AU106264
VERSION     AU106264.1 GI:13555785
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
              Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
              Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE       Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
JOURNAL     EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE     21270072
PUBMED      11375929
COMMENT     Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: ysuzuki@ims.u-tokyo.ac.jp
              Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
              Sugano,S. Construction and characterization of a full
              length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
              149-156 (1997).
FEATURES
source       1. .50
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
Query Match      46.0%; Score 13.8; DB 1; Length 50;
Best Local Similarity 72.0%; Pred. No. 3.8e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

[illegible]

[illegible]

Db 1 GGACTGAAGCCATTGACCTCTTATCTTC 28

RESULT 14
LOCUS AU264313/c
DEFINITION AU264313 VS Dictyostelium discoideum cDNA clone VSD616 3', mRNA
44 bp mRNA linear EST 26-APR-2004

ACCESSION AU264313
VERSION AU264313
KEYWORDS AU264313.1 GI:20523111
EST.

SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyostelid; Dictyostelium.
REFERENCE 1 (bases 1 to 44)
AUTHORS Urushihara,H., Morio,T., Saito,T., Kohara,Y., Koriki,E., Ochiai,H.,
Maeda,M., Williams,J.G., Takeuchi,I. and Tanaka,Y.
TITLE Analyses of cDNAs from growth and slug stages of Dictyostelium
discoideum
JOURNAL Nucleic Acids Res. 32 (5), 1647-1653 (2004)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source 1..44
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSD616"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

ORIGIN
Query Match 44.7%; Score 13.4; DB 1; Length 44;
Best Local Similarity 70.8%; Pred. No. 5.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 7 CAGTCCTTGTCATCTCACCTTCT 30
||| ||||| ||||| |||||
32 CANTAATTGGTAATCTATCTCTAT 9

Db

RESULT 15
LOCUS AU107621
DEFINITION AU107621 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF4230, mRNA sequence.
ACCESSION AU107621
VERSION AU107621
KEYWORDS AU107621.1 GI:13557142
EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Oka,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL ENBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
PubMed 11375929
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan


```

Email: yszuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
FEATURES             source
    Location/Qualifiers
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="COLF4230"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      44.7%; Score 13.4; DB 1; Length 50;
Best Local Similarity 73.9%; Pred.No.5.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GACTCAGTCCTTGGTCATCTCAC 25
DB      14  GCGTGACTGCTTGTTCGTCTCAC 36

RESULT 16
LOCUS   AU107622 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC12232, mRNA sequence.
ACCESSION AU107622
VERSION   AU107622.1 GI:13557143
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
          Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
          Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
          Diverse transcriptional initiation revealed by fine, large-scale
          mapping of mRNA start sites
          EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL 21270072
MEDLINE 11375929
PubMed
COMMENT Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yszuki@ims.u-tokyo.ac.jp
          Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
          Sugano,S. Construction and characterization of a full
          length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
          149-156 (1997).
FEATURES             source
    Location/Qualifiers
        1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="HRC12232"
        /clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match      44.7%; Score 13.4; DB 1; Length 50;
Best Local Similarity 73.9%; Pred.No.5.5e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      3  GACTCAGTCCTTGGTCATCTCAC 25
DB      17  GCGTGACTGCTTGTTCGTCTCAC 39

RESULT 17

```



```

FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4479254"
        /tissue_type="transitional cell papilloma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC_93"
        /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      44.0%; Score 13.2; DB 4; Length 37;
  Best Local Similarity 83.3%; Pred. No. 6.5e+05;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCTTGCTC 18
    ||| ||| ||| ||| |||
Db 30 TGGTCACAGTCTTGCTC 13

RESULT 19
AUI02328
LOCUS
DEFINITION
  50 bp mRNA linear EST 28-JAN-2004
  Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
  KAT06002, mRNA sequence.
ACCESSION
AUI02328
VERSION
AUI02328.1 GI:13551848
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 50)
  Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
  Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
  Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
  Diverse transcriptional initiation revealed by fine, large-scale
  mapping of mRNA start sites
  EMBO Rep. 2 (5), 388-393 (2001)
  21270072
  11375929
  Contact: Yutaka Suzuki
  Department of Virology
  Institute of Medical Science, University of Tokyo
  4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
  Email: yusuzuki@ims.u-tokyo.ac.jp
  Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
  Sugano, S. Construction and characterization of a full
  length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
  149-156 (1997).
FEATURES
  source
    Location/Qualifiers
      1..50
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="KAT06002"
        /clone_lib="Sugano Homo sapiens cDNA library"
ORIGIN
  Query Match      44.0%; Score 13.2; DB 1; Length 50;
  Best Local Similarity 69.2%; Pred. No. 6.7e+05;
  Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 CTCAGTCTTGCTCATCTCCTTCT 30
    ||| ||| ||| ||| |||
Db 5 CTGGTTCCCGGCCCATCTCAGCGGCT 30

FEATURES
  source
    Location/Qualifiers
      1..37
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:4479254"
        /tissue_type="transitional cell papilloma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC_93"
        /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: Not I; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN
  Query Match      44.0%; Score 13.2; DB 4; Length 37;
  Best Local Similarity 83.3%; Pred. No. 6.5e+05;
  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TGGACTCAGTCTTGCTC 18
    ||| ||| ||| ||| |||
Db 30 TGGTCACAGTCTTGCTC 13

RESULT 20
H26079/c
LOCUS
DEFINITION
  28 bp mRNA linear EST 10-JUL-1995
  Y156d10.r1 Soares breast 3NbHst Homo sapiens cDNA clone
  IMAGE:162259 5' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION
  (HUMAN);, mRNA sequence.
ACCESSION
H26079
VERSION
H26079.1 GI:895202
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 28)
  Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
  Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
  Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
  Wilson, R.
  The WashU-Merck EST Project
  Unpublished (1995)
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  Insert Size: 663
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Insert Length: 663 Std Error: 0.00
  Seq primer: M13Rev
  High quality sequence stop: 1.
  Location/Qualifiers
    1..28
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:576499"
      /db_xref="taxon:9606"
      /clone="IMAGE:162259"
      /sex="Female"
      /dev_stage="adult"
      /lab_hosts="DH10B (ampicillin resistant)"
      /clone_lib="Soares breast 3NbHst"
      /note="Organ: breast; Vector: p7T3D (Pharmacia) with a
      modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
      strand cDNA was primed with a Not I - oligo(dT) primer [5',
      TGTTCACCAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
      double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not I
      and Eco RI sites of a modified p7T3 vector (Pharmacia).
      Library went through one round of normalization to a Cot =
      20. Library constructed by Bento Soares and M.Fatima
      Bonaldo."
ORIGIN
  Query Match      43.3%; Score 13; DB 7; Length 28;
  Best Local Similarity 76.2%; Pred. No. 7.6e+05;
  Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GACTCAGTCTTGCTCATCTC 23
    ||| ||| ||| ||| |||
Db 21 GACCTGGTCTTGCTCATCTC 1

RESULT 21
CC795628
LOCUS
DEFINITION
  28 bp DNA linear GSS 01-JUL-2003
  SALK_087613.35.10.x Arabidopsis thaliana TDNA insertion lines

```

Arabidopsis thaliana genomic clone SALK_087613.35.10.x, genomic survey sequence.
 CC795628
 CC795628.1 GI:32390851
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 28)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_087613.35.10.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 43.3%; Score 13; DB 9; Length 28;
 Best Local Similarity 76.2%; Pred. No. 7.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 TCCTTGGTCATCTCACCCTTCT 30
 |||||
 Db 2 TACTTGGTCATCTTAGATTCT 22

RESULT 22
 A2309567/c
 LOCUS
 DEFINITION
 1M0016F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016F07 F, genomic survey sequence.
 A2309567
 A2309567.1 GI:10350865
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 47)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss

Arabidopsis thaliana genomic clone SALK_087613.35.10.x, genomic survey sequence.
 CC795628
 CC795628.1 GI:32390851
 GSS.
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 28)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1. .28
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone="SALK_087613.35.10.x"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
 Query Match 43.3%; Score 13; DB 9; Length 28;
 Best Local Similarity 76.2%; Pred. No. 7.6e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 10 TCCTTGGTCATCTCACCCTTCT 30
 |||||
 Db 2 TACTTGGTCATCTTAGATTCT 22

RESULT 22
 A2309567/c
 LOCUS
 DEFINITION
 1M0016F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0016F07 F, genomic survey sequence.
 A2309567
 A2309567.1 GI:10350865
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 47)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mamoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: F column: 07
 Seq primer: CGTTGTAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 47.
 Location/Qualifiers
 1. .47
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0016F07"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource.
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Query Match 43.3%; Score 13; DB 8; Length 47;
 Best Local Similarity 76.2%; Pred. No. 8.1e+05;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 6 TCAGTCCTTGGTCATCTCACC 26
 |||||
 Db 21 TCAGTCCTTGGTCATCTCACC 1

RESULT 23
 A1746816
 LOCUS
 DEFINITION
 u107g07.y1 Sugano mouse kidney mRna Mus musculus cDNA clone IMAGE:2065404 5' similar to WP:ZK721.1 CE05105 ; mRNA sequence.
 A1746816
 A1746816.1 GI:5125080
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 49)
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,B., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999

Insert Length: 10000 Std Error: 0.00
 Plate: 0542 row: G column: 06
 Seq primer: CTTTGAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 24.

FEATURES

source

1. .24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0542G06"
 /sex="Male"

/lab_host="F. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb Plasmid UUGC1M library"
 /note="Vector: pW42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G1/4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.7%; Score 12.8; DB 8; Length 24;
 Best Local Similarity 70.8%; Pred. No. 9e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 CAGTCCTGTGTCATCTCACCTTCT 30
 ||||| ||||| ||||| ||||| |||||
 Db 24 CAGTCAGTGGCCATCATGTATT 1

RESULT 26

AI582089/c
 LOCUS AI582089 31 bp mRNA linear EST 06-APR-1999
 DEFINITION a:96c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173456 3' similar to TR:021792 O21792 CYTOCHROME B ;contains element MSRL repetitive element ;, mRNA sequence.

ACCESSION AI582089
 VERSION AI582089.1 GI:4567986
 EST.

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens

ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 31)
 Hillier, L., Allen, M., Bowles, J., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project
 Unpublished (1997)

TITLE Contact: Wilson RK
 JOURNAL Washington University School of Medicine
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
 1. .31
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2173456"
 /sex="male"
 /dev_stage="adult, age 25"
 /lab_host="DH10B (phage resistant)"
 /clone_lib="Barstead colon HPLRB7"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCATAGTAAT 3' and 5' ATTACTAGT 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 42.7%; Score 12.8; DB 1; Length 31;
 Best Local Similarity 87.5%; Pred. No. 9.3e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGACTCAGTCCTTGG 16
 ||||| ||||| ||||| |||||
 Db 27 TGGGCTCACTCCTTGG 12

RESULT 27

DME545069
 LOCUS DME545069 34 bp DNA linear GSS 24-FEB-2003
 DEFINITION Drosophila melanogaster flanking sequence of RS p element insertion P[RS5]5-HA-1190, clone library P[RS5], genomic survey sequence.

ACCESSION AJ545069
 VERSION AJ545069.1 GI:28552745

KEYWORDS GSS; genome survey sequence.
 SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1
 Ryder, E.J., Ashburner, M., Bagunya, J., Blows, F., Bucheton, A., Coulson, D., Dickson, B., Drummond, J., Glover, D., Gunton, N., Hafen, E., Hall, S., Heisenberg, M., Lepesant, J.A., Maroy, P., Mechler, B., O'Kane, C., Pflugfelder, G., Rasnussen-Lestander, A., Reuter, G., Roote, J., Szidonya, J., Wang, S., Webster, J. and Russell, S.
 Mapping of RS p element insertions in Drosophila melanogaster for the DrosDel second generation deficiency kit

Unpublished
 2 (bases 1 to 34)

JOURNAL Ryder, E.J.
 REFERENCE Direct Submission
 AUTHORS Title

JOURNAL Submitted (17-FEB-2003) Ryder E.J., Department of Genetics,
 University of Cambridge, Downing Street, CB2 3EH, UNITED KINGDOM

COMMENT The insertion point of the P element is before base 1 of the sequence. Further information about this P element insertion line can be found at <http://www.flyseq.org.uk> and <http://www.drosdel.org.uk>.

Location/Qualifiers

1. .34
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /chromosome="2R"
 /clone="P[RS5]5-HA-1190"

```

misc_feature
1..34
/clone_lib="P{RSS}"
/note="read-5' end"
/note="P element insertion in the 5' to 3' orientation"

ORIGIN
Query Match 42.7%; Score 12.8; DB 9; Length 34;
Best Local Similarity 70.8%; Pred. No. 9.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 CAGTCCTTGGTCATCTCACCTTCT 30
Db 8 CATTTCATCAGTCATCTGACTCTCT 31

RESULT 28
H13124/c
LOCUS
DEFINITION
H13124 37 bp mRNA linear EST 27-JUN-1995
IMAGE:147959.5 similar to gb:U03496_cds1 GAP JUNCTION ALPHA-5
PROTEIN (HUMAN);, mRNA sequence.
H13124
ACCESSION H13124.1 GI:877944
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1178
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1178 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
FEATURES
source
1..37
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:559671"
/db_xref="taxon:9606"
/clone="IMAGE:147959"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="PH108 (ampicillin resistant)"
/clone_lib="Soares placenta Mb2HP"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGGAGAAATTCGGCGCAGGAATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

```

```

Query Match 42.7%; Score 12.8; DB 7; Length 37;
Best Local Similarity 87.5%; Pred. No. 9.5e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TTGGTCATCTCACCTT 28
Db 28 TAGGTCATCTGACCTT 13

RESULT 29
BH759504/c
LOCUS
DEFINITION
BH759504 37 bp DNA linear GSS 12-MAR-2002
KG04665-Sprime Drosophila melanogaster P{SUPor-P} P element
insertion lines Drosophila melanogaster genomic sequence recovered
from 5' end of P element, genomic survey sequence.
BH759504
ACCESSION BH759504.1 GI:19352743
VERSION GSS.
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster
REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 37)
Levis, R., Hoskins, R., Liao, G., Mozdén, N., Teang, G., He, Y.,
Karpen, G., Bellen, H., Rubin, G. and Spradling, A.
The Berkeley Drosophila Genome Project Gene Disruption Project
Unpublished (2001)
CONTACT: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element
The P element insertion position is base 30 in the 37 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
FEATURES
source
1..37
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster P{SUPor-P} P element
insertion lines"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P{SUPor-P} P-element transposon insertion. The resultant
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruitfly.org/about/methods/inverse.pcr.html."

ORIGIN
Query Match 42.7%; Score 12.8; DB 8; Length 37;
Best Local Similarity 70.8%; Pred. No. 9.5e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 7 CAGTCCTTGGTCATCTCACCTTCT 30
Db 30 CATTTCATCAGTCATCTGACTCTCT 7

RESULT 30
CN762433/c
LOCUS
DEFINITION
CN762433 43 bp mRNA linear EST 20-MAY-2004
ID04AAA4E04RM1 ApMS Acyrthosiphon pisum cDNA clone ID04AAA4E04 5',
mRNA sequence.
CN762433
ACCESSION CN762433

```

VERSION
KEYWORDS
SOURCE
ORGANISM

CN762433.1 GI:47536356
EST.
Acyrtosiphon pisum (pea aphid)
Acyrtosiphon pisum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae; Macrosiphini; Acyrthosiphon.
REFERENCE
AUTHORS
1 (bases 1 to 43)
Hunter W., Martinez-Torres D., Rabhe Y., Sabater-Munoz B.,
Stern D., Tagu D. and Wincker P.
TITLE
An expressed sequence tags database for the pea aphid Acyrthosiphon
pisum
JOURNAL
COMMENT
Unpublished (2004)
Contact: D. Tagu
INRA Rennes
UMR BIO3P, BP 35327, F-35653 Le Rheu Cedex France
Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
PCR Primers
FORWARD: CAGGAACAGCTATGACC
Plate: 4 row: E column: 4.
Location/Qualifiers
1. 43
/organism="Acyrtosiphon pisum"
/mol_type="mRNA"
/cultivar="development stage"
/db_xref="taxon:7029"
/clone="ID08AA4AE04"
/tissue_type="whole insect"
/dev_stage="nymphs and adults (parthenogenetic females)"
/lab_host="Xli-Blue"
/clone_lib="ApMS"
/note="Vector: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI;
Sample name: ID08AA; Plant growth place: Department of
Ecology & Evolutionary Biology, Princeton University;
Soil conditions: Soil; Sowing date: 01/06/1999;
Harvesting date: 01/06/1999; Stress date: no stress;
Description: Aphids inoculated on one-week old Vicia faba
under non-sterile conditions. All parthenogenetic stages
and both winged and wingless adults were collected for
library construction. experimental condition: long
photoperiod (16-hr light/8-hr dark at 18 c)"

FEATURES
source
1. 44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match 42.7%; Score 12.8; DB 8; Length 44;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGACTCAGTCCTGGTGGT 17
Db 5 GGACCCAGGCGCTGGT 20

RESULT 32
CL675662/c
LOCUS
DEFINITION
CL675662
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CL675662 44 bp DNA linear GSS 09-JUL-2004
PRI0115C B08_2 - PRI0115C-BR (44) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL675662 GI:50180358
CL675662.1 GI:50180358
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 44)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppABD: an AcedB database for the nematode satellite organism

Query Match 42.7%; Score 12.8; DB 7; Length 43;
Best Local Similarity 70.8%; Pred. No. 9.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TGGACTCAGTCCTGGTCACTCA 24
Db 28 TTGACATAATCATTAGTCACTCA 5

RESULT 31
AZ479665
LOCUS
DEFINITION
AZ479665
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AZ479665 44 bp DNA linear GSS 04-OCT-2000
1M0300D01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0300D01 R, genomic survey sequence.
AZ479665 GI:10639494
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0300 row: D column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers
1. 44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0300D01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498

Email: raif.sommer@uebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.

Seq primer: 17

Class: fosmid ends.

Location/Qualifiers

1. .44
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match 42.7%; Score 12.8; DB 9; Length 44;
Best Local Similarity 87.5%; Pred. No. 9.7e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGTCATCA 19

DB 18 ACTCAGTCTCGATCA 3

RESULT 33
A2328994
LOCUS 45 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0053105F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0053105 F, genomic survey sequence.

ACCESSION A2328994.1 GI:10389268

VERSION GSS.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 45)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0053 row: I column: 05

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 45.

Location/Qualifiers

1. .45

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0053105"

FEATURES

source

/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 42.7%; Score 12.8; DB 8; Length 45;
Best Local Similarity 70.8%; Pred. No. 9.7e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TCAGTCTTGTCATCTCACCTTC 29

DB 1 TCATTACTGCTCTCTCTTTTC 24

RESULT 34

BH791670/c

LOCUS 48 bp DNA linear GSS 02-APR-2002

DEFINITION SALK_060817.42.80.x Arabidopsis thaliana TDNA insertion lines

Arabidopsis thaliana genomic clone SALK_060817.42.80.x, genomic

survey sequence.

ACCESSION BH791670.1 GI:19885779

VERSION GSS.

KEYWORDS Arabidopsis thaliana (chale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 48)

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,

Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

Shinn, P., Zimmermann, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)

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This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At4g33590.

Class: TDNA tagged.

Location/Qualifiers

1. .48

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_060817.42.80.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines"

FEATURES

source

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
Query Match 42.7%; Score 12.8; DB 8; Length 48;
Best Local Similarity 70.8%; Pred. No. 9.8e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TCACTGCTTGGTCATCTCACCTTC 29
DB 36 TCTCTCCCTTGACATTCACCTTC 13

RESULT 35
AV833344
LOCUS
DEFINITION AV833344 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare cDNA
clone bags6112, mRNA sequence.
ACCESSION AV833344
VERSION AV833344.1 GI:14525433
KEYWORDS
SOURCE
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 49)
Sato, K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)
COMMENT Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp/barley/
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>.

FEATURES
source
1..49
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Niho"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="bags6112"
/tissue_type="shoots"
/dev_stage="germination"
/clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination"

ORIGIN
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Best Local Similarity 68.0%; Pred. No. 9.8e+05;
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 ACTCAGTCTTGGTCATCTCACCTTC 28
DB 23 ACTTCGCCGCTGGCATTACACCAT 47

RESULT 36
AG198679/c
LOCUS
DEFINITION Pan troglodytes DNA, clone: RP43-079K02.T7, genomic survey sequence.
ACCESSION AG198679
VERSION AG198679.1 GI:45230855

GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
BAC end sequences of Library RP-43
Unpublished
2 (bases 1 to 24)
Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC); 52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
(E-mail: redstone@mail.kribb.re.kr, URL: <http://phs.grc.kribb.re.kr/>, Tel: 82-42-866-7181, Fax: 82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI.
R.Site 2 : EcoRI.
1..24
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-079K02.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"

ORIGIN
Query Match 42.0%; Score 12.6; DB 9; Length 24;
Best Local Similarity 78.9%; Pred. No. 1.1e+06;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 CTGTGTCATCTCACCTTCT 30
DB 24 CATGTCATGTCCTCTCT 6

RESULT 37
AZ309679
LOCUS
DEFINITION 28 bp DNA linear GSS 29-SEP-2000
clone UUGC1M0016B17 F, genomic survey sequence.
ACCESSION AZ309679
VERSION AZ309679.1 GI:10350733
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: B column: 17
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.

FEATURES

source
 1. .28

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0016B17"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 42.0%; Score 12.6; DB 8; Length 28;
 Best Local Similarity 78.9%; Pred. No. 1.1e+06;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 11 CCTTGTCATCTCACCCTTC 29

Db 8 CCTTGTCATCTCACCCTTC 26

RESULT 38
 CC798624

LOCUS
 DEFINITION
 SALK_146625.31.65.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_146625.31.65.x, genomic survey sequence.

ACCESSION
 CC798624

VERSION
 CC798624.1 GI:32393847

KEYWORDS
 GSS.

SOURCE
 Arabidopsis thaliana (thale cress)

ORGANISM
 Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
 1 (bases 1 to 29)

AUTHORS
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shinn,P., Zimmerman,J. and Ecker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

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Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_146625.31.65.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 42.0%; Score 12.6; DB 9; Length 29;

Best Local Similarity 78.9%; Pred. No. 1.1e+06;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 CTCAGTCCTTGGTCATCTC 23

Db 10 CTCAGTCCTTGGTCATCTC 28

LOCUS

AG189685

Pan troglodytes DNA, clone: RP43-064G18.T7, genomic survey

sequence.

ACCESSION

AG189685

VERSION

AG189685.1 GI:45221861

KEYWORDS

GSS.

SOURCE

Pan troglodytes (chimpanzee)

ORGANISM

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE

1

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

BAC end sequences of Library RP-43

Unpublished

2 (bases 1 to 32)

Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,

Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.

Direct Submission

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of

Bioscience and Biotechnology (KRIIB), Genome Research Center (GRC);

52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea

(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,

Tel:82-42-866-7181, Fax:82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC

end was generated during the R&D process and may have higher chance

of clone tracking errors.

PRIMERS

Sequencing: T7

LIBRARY

Vector : pBACE3.6

R.Site 1 : ECORI

R.Site 2 : ECORI.

Location/Qualifiers

1. .32

/organism="Pan troglodytes"

/mol_type="genomic DNA"

/db_xref="taxon:9598"

/clone="RP43-064G18.T7"

/sex="male"

FEATURES

source

Search completed: November 23, 2004, 22:23:03
Job time : 1472.31 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:50:22 ; Search time 594.247 Seconds
(without alignments)
2626.113 Million cell updates/sec

Title: US-10-087-631B-5
Perfect score: 33
Sequence: I gccacatgagtggaaggcgtctggtgataccg 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1785872

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : GenEmbl.*

1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pi:*
9: gb_pr:*
10: gb_ro:*
11: gb_ats:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	66.7	34	6	BD181366 A method
2	22	66.7	34	6	AX523946 Sequence
3	22	66.7	34	6	AX523946 Sequence
4	16.4	49.7	43	6	AX524844 Sequence
5	15.6	47.3	40	6	AX403706 Sequence
6	15.6	47.3	42	6	CQ753200 Sequence
7	15.4	46.7	30	6	AX930614 Sequence
8	15.4	46.7	30	6	BD263504 Humanized
9	15.4	46.7	33	6	AR124548 Sequence
10	15.4	46.7	33	6	AR163199 Sequence
11	15.4	46.7	33	6	AR493800 Sequence
12	15.4	46.7	33	6	AX491667 Sequence
13	15.4	46.7	33	6	AX498638 Sequence
14	15.4	46.7	33	6	BD131354 Recombina
15	15.4	46.7	34	6	AR048018 Sequence
16	15.4	46.7	34	6	AR048020 Sequence
17	15.4	46.7	34	6	AR059770 Sequence
18	15.4	46.7	34	6	AR059772 Sequence
19	15.4	46.7	34	6	AR068646 Sequence

20	15.4	46.7	34	6	AR068648	Sequence
21	15.4	46.7	34	6	AR094254	Sequence
22	15.4	46.7	34	6	AR094256	Sequence
23	15.4	46.7	38	6	AR048019	Sequence
24	15.4	46.7	38	6	AR048021	Sequence
25	15.4	46.7	38	6	AR059773	Sequence
26	15.4	46.7	38	6	AR068647	Sequence
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29	15.4	46.7	38	6	AR094257	Sequence
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32	15	45.5	38	6	AX961520	Sequence
33	15	45.5	46	6	AX665040	Sequence
34	15	45.5	46	6	AX961519	Sequence
35	15	45.5	50	6	CQ006075	Sequence
36	14.8	44.8	21	6	AX539350	Sequence
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38	14.6	44.2	30	6	BD091354	Methods a
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40	14.6	44.2	40	6	AR195317	Sequence
41	14.6	44.2	48	6	AR119460	Sequence
42	14.6	44.2	48	6	AR231748	Sequence
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46	14.4	43.6	21	6	AX706574	Sequence
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53	14.2	43.0	50	6	CQ009166	Sequence
54	14	42.4	37	6	I33378	Sequence 1
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56	14	42.4	40	6	E15204	PCR primer
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58	14	42.4	45	6	AX662209	Sequence
59	13.8	41.8	23	6	AR083022	Sequence
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61	13.8	41.8	23	6	AR157559	Sequence
62	13.8	41.8	23	6	BD232812	Diagnosti
63	13.8	41.8	23	6	AX224933	Sequence
64	13.8	41.8	23	6	AX039711	Sequence
65	13.8	41.8	23	6	BD006031	An optima
66	13.8	41.8	23	6	BD070491	Methods f
67	13.8	41.8	36	6	A30931	oligonucleo
68	13.8	41.8	36	6	AR362484	Sequence
69	13.8	41.8	38	6	AX219893	Sequence
70	13.8	41.8	39	6	BD190225	Humanized
71	13.8	41.8	39	6	BD190226	Humanized
72	13.8	41.8	41	6	AR036473	Sequence
73	13.8	41.8	41	6	AR069432	Sequence
74	13.8	41.8	41	6	I73454	Sequence 6
75	13.8	41.8	45	6	AR164104	Sequence
76	13.8	41.8	46	9	HSAGCT10	Human aggre
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78	13.8	41.8	50	6	AX093078	Sequence
79	13.6	41.2	20	6	AR170760	Sequence
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81	13.6	41.2	22	6	AX003312	Sequence
82	13.6	41.2	33	6	AR143453	Sequence
83	13.6	41.2	33	6	AX598104	Sequence
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86	13.6	41.2	42	6	AR042987	Sequence
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88	13.6	41.2	42	6	AR164106	Sequence
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90	13.6	41.2	42	6	I62978	Sequence 10
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93	13.6	41.2	42	6	BD096551	BD096551 Transgeni	166	13.2	40.0	39	6	AX763682	AX763682 Sequence
c 94	13.6	41.2	44	6	AR076166	AR076166 Sequence	c 167	13.2	40.0	40	6	AX703378	AX703378 Sequence
c 95	13.6	41.2	44	6	AR076857	AR076857 Sequence	c 168	13.2	40.0	41	6	AX515036	AX515036 Sequence
c 96	13.6	41.2	44	6	AR149824	AR149824 Sequence	c 169	13.2	40.0	41	6	AX516762	AX516762 Sequence
c 97	13.6	41.2	45	6	AR164108	AR164108 Sequence	c 170	13.2	40.0	41	6	AX518925	AX518925 Sequence
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c 99	13.6	41.2	50	6	CQ003466	CQ003466 Sequence	c 172	13.2	40.0	42	6	AR079470	AR079470 Sequence
c 100	13.6	41.2	50	6	CQ004857	CQ004857 Sequence	c 173	13.2	40.0	42	6	AX394937	AX394937 Sequence
c 101	13.6	41.2	50	6	AX107690	AX107690 Sequence	c 174	13.2	40.0	44	6	AX80437	AX80437 Sequence 32
c 102	13.6	41.2	20	6	AX128604	AX128604 Sequence	c 175	13.2	40.0	44	6	I04544	I04544 Sequence 6
c 103	13.4	40.6	21	6	BD268689	BD268689 Isolation	c 176	13.2	40.0	44	6	AR217968	AR217968 Sequence
c 104	13.4	40.6	21	6	IB7914	IB7914 Sequence 3	c 177	13.2	40.0	44	6	BD134913	BD134913 High-affi
c 105	13.4	40.6	24	6	AX289974	AX289974 Sequence	c 178	13.2	40.0	44	6	BD134919	BD134919 High-affi
c 106	13.4	40.6	27	6	AR012082	AR012082 Sequence	c 179	13.2	40.0	45	6	AR088048	AR088048 Sequence
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c 108	13.4	40.6	30	6	CQ0802941	CQ0802941 Sequence	c 181	13.2	40.0	45	6	AX025282	AX025282 Sequence
c 109	13.4	40.6	35	6	BD170140	BD170140 Method of	c 182	13.2	40.0	47	6	AR284920	AR284920 Sequence
c 110	13.4	40.6	38	6	I41102	I41102 Sequence 5	c 183	13.2	40.0	47	6	AR289723	AR289723 Sequence
c 111	13.4	40.6	41	6	AX514019	AX514019 Sequence	c 184	13.2	40.0	48	6	CQ0809436	CQ0809436 Sequence
c 112	13.4	40.6	41	6	AX516285	AX516285 Sequence	c 185	13.2	40.0	49	9	AB010655	AB010655 Homo sapi
c 113	13.4	40.6	41	6	AX518485	AX518485 Sequence	c 186	13.2	40.0	16	6	AR211597	AR211597 Sequence
c 114	13.4	40.6	41	6	AX518619	AX518619 Sequence	c 187	13.2	39.4	17	6	AR211617	AR211617 Sequence
c 115	13.4	40.6	41	6	AX520844	AX520844 Sequence	c 188	13.2	39.4	17	6	AX802008	AX802008 Sequence
c 116	13.4	40.6	42	6	I32723	I32723 Sequence 50	c 189	13.2	39.4	18	6	BD244768	BD244768 Isolation
c 117	13.4	40.6	50	6	AR075351	AR075351 Sequence	c 190	13.2	39.4	18	6	AR255274	AR255274 Sequence
c 118	13.4	40.6	50	6	AX159930	AX159930 Sequence	c 191	13.2	39.4	25	6	BD245830	BD245830 Developme
c 119	13.2	40.0	20	6	BD012252	BD012252 A novel g	c 192	13.2	39.4	25	6	I81294	I81294 Sequence 45
c 120	13.2	40.0	21	6	AX539354	AX539354 Sequence	c 193	13.2	39.4	25	6	AX784857	AX784857 Sequence
c 121	13.2	40.0	21	6	AX539355	AX539355 Sequence	c 194	13.2	39.4	25	6	AX784858	AX784858 Sequence
c 122	13.2	40.0	21	6	AX706572	AX706572 Sequence	c 195	13.2	39.4	25	6	AX784859	AX784859 Sequence
c 123	13.2	40.0	21	6	AX706573	AX706573 Sequence	c 196	13.2	39.4	25	6	AX784860	AX784860 Sequence
c 124	13.2	40.0	21	6	AX707502	AX707502 Sequence	c 197	13.2	39.4	25	6	AX784861	AX784861 Sequence
c 125	13.2	40.0	21	6	AX707503	AX707503 Sequence	c 198	13.2	39.4	27	6	BD206663	BD206663 Enzymatic
c 126	13.2	40.0	25	6	AX782528	AX782528 Sequence	c 199	13.2	39.4	27	6	BD206912	BD206912 Enzymatic
c 127	13.2	40.0	25	6	AX782529	AX782529 Sequence	c 200	13.2	39.4	27	6	BD211734	BD211734 Drug as c
c 128	13.2	40.0	25	6	AX782530	AX782530 Sequence	c 201	13.2	39.4	29	6	AR153594	AR153594 Sequence
c 129	13.2	40.0	25	6	AX782531	AX782531 Sequence	c 202	13.2	39.4	30	6	CQ816714	CQ816714 Sequence
c 130	13.2	40.0	25	6	AX782532	AX782532 Sequence	c 203	13.2	39.4	30	6	CQ816715	CQ816715 Sequence
c 131	13.2	40.0	25	6	AX782533	AX782533 Sequence	c 204	13.2	39.4	30	6	CQ816717	CQ816717 Sequence
c 132	13.2	40.0	25	6	AX782534	AX782534 Sequence	c 205	13.2	39.4	33	6	BD246982	BD246982 Improved
c 133	13.2	40.0	25	6	AX782535	AX782535 Sequence	c 206	13.2	39.4	34	6	BD010736	BD010736 Helicobac
c 134	13.2	40.0	30	6	A38307	A38307 Sequence 41	c 207	13.2	39.4	37	9	AF505544	AF505544 Homo sapi
c 135	13.2	40.0	30	6	BD244422	BD244422 Mutants o	c 208	13.2	39.4	38	6	AR091388	AR091388 Sequence
c 136	13.2	40.0	30	6	BD244423	BD244423 Mutants o	c 209	13.2	39.4	38	6	AR392579	AR392579 Sequence
c 137	13.2	40.0	30	6	AX027139	AX027139 Sequence	c 210	13.2	39.4	38	6	BD165911	BD165911 Human sta
c 138	13.2	40.0	30	6	AX027140	AX027140 Sequence	c 211	13.2	39.4	39	1	AFU430249	AFU430249 Archaeogl
c 139	13.2	40.0	30	6	AX244134	AX244134 Sequence	c 212	13.2	39.4	39	6	AB3184	AB3184 Sequence 4
c 140	13.2	40.0	30	6	AX244135	AX244135 Sequence	c 213	13.2	39.4	39	6	AR182916	AR182916 Sequence
c 141	13.2	40.0	33	6	AR012128	AR012128 Sequence	c 214	13.2	39.4	39	6	BD096889	BD096889 Chemical
c 142	13.2	40.0	33	6	AR012130	AR012130 Sequence	c 215	13.2	39.4	40	6	CQ816732	CQ816732 Sequence
c 143	13.2	40.0	33	6	AR012132	AR012132 Sequence	c 216	13.2	39.4	41	6	CQ816733	CQ816733 Sequence
c 144	13.2	40.0	33	6	AR108210	AR108210 Sequence	c 217	13.2	39.4	41	6	I81295	I81295 Sequence 46
c 145	13.2	40.0	33	6	AR108212	AR108212 Sequence	c 218	13.2	39.4	41	6	I81299	I81299 Sequence 50
c 146	13.2	40.0	33	6	AR108214	AR108214 Sequence	c 219	13.2	39.4	41	6	AX515201	AX515201 Sequence
c 147	13.2	40.0	33	6	AR374477	AR374477 Sequence	c 220	13.2	39.4	41	6	AX517669	AX517669 Sequence
c 148	13.2	40.0	33	6	AR374479	AR374479 Sequence	c 221	13.2	39.4	41	6	AX694485	AX694485 Sequence
c 149	13.2	40.0	33	6	AR374481	AR374481 Sequence	c 222	13.2	39.4	42	6	AR055004	AR055004 Sequence
c 150	13.2	40.0	36	6	BD079949	BD079949 Genetic m	c 223	13.2	39.4	42	6	AR156253	AR156253 Sequence
c 151	13.2	40.0	38	6	CQ816290	CQ816290 Sequence	c 224	13.2	39.4	42	6	E33305	E33305 DsbaA/Dabb/D
c 152	13.2	40.0	38	6	CQ816322	CQ816322 Sequence	c 225	13.2	39.4	42	6	AR448527	AR448527 Sequence
c 153	13.2	40.0	38	6	CQ818885	CQ818885 Sequence	c 226	13.2	39.4	42	6	AX343177	AX343177 Sequence
c 154	13.2	40.0	38	6	CQ818917	CQ818917 Sequence	c 227	13.2	39.4	45	6	E11413	E11413 Primer. 9/1
c 155	13.2	40.0	38	6	AR333190	AR333190 Sequence	c 228	13.2	39.4	46	6	AR101846	AR101846 Sequence
c 156	13.2	40.0	38	6	AX022994	AX022994 Sequence	c 229	13.2	39.4	46	6	BD135890	BD135890 Methods f
c 157	13.2	40.0	38	6	AX220494	AX220494 Sequence	c 230	13.2	39.4	50	6	CQ003415	CQ003415 Sequence
c 158	13.2	40.0	38	6	AX228254	AX228254 Sequence	c 231	13.2	39.4	50	6	CQ005618	CQ005618 Sequence
c 159	13.2	40.0	38	6	AX273923	AX273923 Sequence	c 232	13.2	39.4	50	6	CQ005619	CQ005619 Sequence
c 160	13.2	40.0	38	6	AX424577	AX424577 Sequence	c 233	13.2	39.4	50	6	AX923393	AX923393 Sequence
c 161	13.2	40.0	38	6	AX424610	AX424610 Sequence	c 234	12.8	38.8	20	6	AX295467	AX295467 Sequence
c 162	13.2	40.0	38	6	AX701035	AX701035 Sequence	c 235	12.8	38.8	21	6	AX095832	AX095832 Sequence
c 163	13.2	40.0	39	6	A59579	A59579 Sequence 7	c 236	12.8	38.8	22	6	AX117850	AX117850 Sequence
c 164	13.2	40.0	39	6	AR223819	AR223819 Sequence	c 237	12.8	38.8	24	6	AX059420	AX059420 Sequence
c 165	13.2	40.0	39	6	AX763674	AX763674 Sequence	c 238	12.8	38.8	24	6	AX290834	AX290834 Sequence

239	12.8	38.8	25	6	AR217972 Sequence	312	12.6	38.2	36	6	AX637082	AX637082 Sequence
240	12.8	38.8	25	6	BD134917	313	12.6	38.2	36	6	AX637592	AX637592 Sequence
c 241	12.8	38.8	27	6	BD207842 Enzymatic	314	12.6	38.2	36	6	AX638187	AX638187 Sequence
242	12.8	38.8	28	6	AG9149	c 315	12.6	38.2	38	6	AX1274	AX1274 Sequence 3
243	12.8	38.8	29	6	BD253320 Regulation	316	12.6	38.2	38	6	I37811	I37811 Sequence 82
244	12.8	38.8	29	6	I73291 Sequence 22	317	12.6	38.2	38	6	I94661	I94661 Sequence 82
245	12.8	38.8	29	6	AX546608 Sequence	318	12.6	38.2	38	6	AR330446	AR330446 Sequence
c 246	12.8	38.8	30	6	AR074455 Sequence	319	12.6	38.2	38	6	AX219515	AX219515 Sequence
c 247	12.8	38.8	30	6	AR081135 Sequence	320	12.6	38.2	38	6	AX228694	AX228694 Sequence
c 248	12.8	38.8	30	6	AR085332 Sequence	321	12.6	38.2	38	6	AX423892	AX423892 Sequence
c 249	12.8	38.8	30	6	AR088080 Sequence	322	12.6	38.2	38	6	AX424817	AX424817 Sequence
c 250	12.8	38.8	30	6	AR104239 Sequence	323	12.6	38.2	39	6	AR059295	AR059295 Sequence
c 251	12.8	38.8	30	6	AR143503 Sequence	324	12.6	38.2	39	6	BD248568	BD248568 Identific
c 252	12.8	38.8	30	6	AR171407 Sequence	c 325	12.6	38.2	39	6	AR305263	AR305263 Sequence
c 253	12.8	38.8	30	6	AR171578 Sequence	c 326	12.6	38.2	39	6	AR309367	AR309367 Sequence
c 254	12.8	38.8	30	6	BD243168 MN gene a	c 327	12.6	38.2	39	6	AX025656	AX025656 Sequence
255	12.8	38.8	31	6	AX192433	c 328	12.6	38.2	39	6	BD106174	BD106174 Novel LDL
256	12.8	38.8	33	10	S76560 Rattus norv	329	12.6	38.2	40	6	I62864	I62864 Sequence 10
257	12.8	38.8	34	6	AR148507 Sequence	330	12.6	38.2	41	6	AX514279	AX514279 Sequence
258	12.8	38.8	34	6	AR179180 Sequence	c 331	12.6	38.2	41	6	AX514522	AX514522 Sequence
c 259	12.8	38.8	36	6	AR056642 Sequence	c 332	12.6	38.2	41	6	AX514885	AX514885 Sequence
c 260	12.8	38.8	36	6	AR114400 Sequence	c 333	12.6	38.2	41	6	AX517236	AX517236 Sequence
c 261	12.8	38.8	36	6	AX633701	c 334	12.6	38.2	41	6	AX520060	AX520060 Sequence
262	12.8	38.8	38	6	I05821	335	12.6	38.2	41	6	AX520461	AX520461 Sequence
263	12.8	38.8	38	6	I06863	336	12.6	38.2	42	6	AR231384	AR231384 Sequence
264	12.8	38.8	38	6	I07314	337	12.6	38.2	42	6	AR231385	AR231385 Sequence
c 265	12.8	38.8	38	6	AR332005 Sequence	338	12.6	38.2	42	6	BD003035	BD003035 Design, c
c 266	12.8	38.8	38	6	AR334176 Sequence	c 339	12.6	38.2	42	6	BD003036	BD003036 Design, c
c 267	12.8	38.8	38	6	AR335227 Sequence	c 340	12.6	38.2	45	6	AR168070	AR168070 Sequence
c 268	12.8	38.8	38	6	AX228271	c 341	12.6	38.2	45	6	AR204841	AR204841 Sequence
c 269	12.8	38.8	38	6	AX424923	342	12.6	38.2	45	6	YSCMTCBL2	YJ1473 Saccharomyc
c 270	12.8	38.8	39	6	BD249050 Centrifug	c 343	12.6	38.2	47	6	AR289765	AR289765 Sequence
c 271	12.8	38.8	41	6	AX280210 Sequence	344	12.6	38.2	47	6	AR290078	AR290078 Sequence
c 272	12.8	38.8	42	6	E31999 Process for	345	12.6	38.2	48	6	AR021432	AR021432 Sequence
c 273	12.8	38.8	48	6	AX277271	346	12.6	38.2	48	6	AR042994	AR042994 Sequence
c 274	12.8	38.8	48	9	SG2614 COL1A2=alph	347	12.6	38.2	48	6	AR161328	AR161328 Sequence
c 275	12.8	38.8	50	6	CQ004080	348	12.6	38.2	48	6	I43973	I43973 Sequence 64
c 276	12.8	38.8	50	6	CQ008430	349	12.6	38.2	48	6	I62985	I62985 Sequence 11
c 277	12.8	38.8	50	6	AR356249	350	12.6	38.2	48	6	I88738	I88738 Sequence 11
c 278	12.6	38.2	24	6	A46857	351	12.6	38.2	48	6	AR369921	AR369921 Sequence
c 279	12.6	38.2	24	6	AX289976	352	12.6	38.2	48	6	BD096558	BD096558 Transgeni
c 280	12.6	38.2	24	6	AX444343	353	12.6	38.2	50	6	AR032882	AR032882 Sequence
c 281	12.6	38.2	25	6	AX448308	354	12.6	38.2	50	6	CQ003473	CQ003473 Sequence
c 282	12.6	38.2	25	6	AX689218	355	12.6	38.2	50	6	CQ005412	CQ005412 Sequence
283	12.6	38.2	25	6	AX689219	356	12.6	38.2	50	6	I29622	I29622 Sequence 49
284	12.6	38.2	25	6	AX689220	357	12.6	38.2	50	6	I91296	I91296 Sequence 49
285	12.6	38.2	25	6	AX689221	358	12.6	38.2	50	6	AR209546	AR209546 Sequence
286	12.6	38.2	25	6	AX689222	c 359	12.6	38.2	50	6	AX752746	AX752746 Sequence
287	12.6	38.2	25	6	AX689223	c 360	12.6	38.2	50	6	AX752751	AX752751 Sequence
288	12.6	38.2	25	6	AX689224	c 361	12.6	38.2	50	9	HSTCRDV06	HSTCRDV06
c 289	12.6	38.2	25	6	AX689225	362	12.4	37.6	18	6	AR116124	AR116124 Sequence
c 290	12.6	38.2	27	6	AX838488	363	12.4	37.6	18	6	AR322341	AR322341 Sequence
291	12.6	38.2	27	6	BD207547	364	12.4	37.6	18	6	BD062479	BD062479 Phosphodi
292	12.6	38.2	29	6	AX117396	365	12.4	37.6	21	6	AR381404	AR381404 Sequence
c 293	12.6	38.2	29	6	BD253456	c 366	12.4	37.6	22	6	AR489251	AR489251 Sequence
c 294	12.6	38.2	29	6	E27930	c 367	12.4	37.6	22	6	AX233444	AX233444 Sequence
c 295	12.6	38.2	30	6	AR125673	c 368	12.4	37.6	23	6	I11908	I11908 Sequence 18
c 296	12.6	38.2	30	6	I47085	369	12.4	37.6	23	6	AX298783	AX298783 Sequence
c 297	12.6	38.2	31	6	A41283	370	12.4	37.6	24	6	AX106712	AX106712 Sequence
c 298	12.6	38.2	31	6	AR95065	371	12.4	37.6	25	6	C0772384	C0772384 Sequence
c 299	12.6	38.2	31	6	AR222437	c 372	12.4	37.6	25	6	AR258986	AR258986 Sequence
c 300	12.6	38.2	31	6	BD102785	c 373	12.4	37.6	25	6	AX382470	AX382470 Sequence
301	12.6	38.2	33	6	AX961199	c 374	12.4	37.6	25	6	AX769448	AX769448 Sequence
c 302	12.6	38.2	35	6	AR161365	375	12.4	37.6	26	6	AR026887	AR026887 Sequence
c 303	12.6	38.2	35	6	AR369958	376	12.4	37.6	26	6	AR049313	AR049313 Sequence
c 304	12.6	38.2	35	6	BD096592	377	12.4	37.6	26	6	AR065571	AR065571 Sequence
c 305	12.6	38.2	36	6	AR018069	378	12.4	37.6	26	6	AR089945	AR089945 Sequence
c 306	12.6	38.2	36	6	AR041624	379	12.4	37.6	26	6	AR196980	AR196980 Sequence
307	12.6	38.2	36	6	AR042134	380	12.4	37.6	26	6	AR259134	AR259134 Sequence
c 308	12.6	38.2	36	6	I39223	381	12.4	37.6	29	6	AR018053	AR018053 Sequence
309	12.6	38.2	36	6	I77468	382	12.4	37.6	29	6	AR071943	AR071943 Sequence
310	12.6	38.2	36	6	AX407217	c 383	12.4	37.6	29	6	AR157879	AR157879 Sequence
311	12.6	38.2	36	6	AX635500	384	12.4	37.6	29	6	BD197241	BD197241 Method an

385	12.4	37.6	29	6	BD198157	BD198157 Method an	458	12.2	37.0	22	6	BD103840	BD103840 A method
386	12.4	37.6	29	6	BD253413	BD253413 Regulatio	459	12.2	37.0	23	6	CQ816286	CQ816286 Sequence
387	12.4	37.6	29	6	AX657915	AX657915 Sequence	460	12.2	37.0	23	6	CQ818881	CQ818881 Sequence
388	12.4	37.6	30	6	AR118750	AR118750 Sequence	461	12.2	37.0	23	6	E06292	E06292 Primer, 9/1
389	12.4	37.6	30	6	BD175011	BD175011 Cis-regul	462	12.2	37.0	23	6	E06488	E06488 Primer, 9/1
390	12.4	37.6	30	6	CQ818732	CQ818732 Sequence	463	12.2	37.0	24	6	AX446309	AX446309 Sequence
391	12.4	37.6	30	6	I06383	I06383 Sequence 3	464	12.2	37.0	24	6	AX548409	AX548409 Sequence
392	12.4	37.6	30	6	AX589670	AX589670 Sequence	465	12.2	37.0	25	6	CQ620106	CQ620106 Sequence
393	12.4	37.6	32	6	AR213645	AR213645 Sequence	466	12.2	37.0	25	6	CQ630374	CQ630374 Sequence
394	12.4	37.6	32	6	AX695300	AX695300 Sequence	467	12.2	37.0	25	6	CQ818223	CQ818223 Sequence
395	12.4	37.6	32	6	AX740019	AX740019 Sequence	468	12.2	37.0	25	6	AR342872	AR342872 Sequence
396	12.4	37.6	32	6	BD057703	BD057703 Fusion pr	469	12.2	37.0	25	6	AR461169	AR461169 Sequence
397	12.4	37.6	32	6	BD081533	BD081533 Soluble s	470	12.2	37.0	25	6	AR471437	AR471437 Sequence
398	12.4	37.6	33	6	AR194221	AR194221 Sequence	471	12.2	37.0	25	6	AX692124	AX692124 Sequence
399	12.4	37.6	33	6	AR194233	AR194233 Sequence	472	12.2	37.0	25	6	AX692125	AX692125 Sequence
400	12.4	37.6	33	6	AR207101	AR207101 Sequence	473	12.2	37.0	25	6	AX782527	AX782527 Sequence
401	12.4	37.6	33	6	AR221356	AR221356 Sequence	474	12.2	37.0	25	6	AX782536	AX782536 Sequence
402	12.4	37.6	33	6	AR232490	AR232490 Sequence	475	12.2	37.0	25	6	BD087313	BD087313 Mammalian
403	12.4	37.6	33	6	AR281838	AR281838 Sequence	476	12.2	37.0	26	6	A31982	A31982 Synthetic H
404	12.4	37.6	33	6	AX391296	AX391296 Sequence	477	12.2	37.0	26	6	A31983	A31983 Synthetic H
405	12.4	37.6	33	6	BD075807	BD075807 TIE recep	478	12.2	37.0	26	6	AR090410	AR090410 Sequence
406	12.4	37.6	34	6	A50694	A50694 Sequence 33	479	12.2	37.0	26	6	AR131401	AR131401 Sequence
407	12.4	37.6	34	6	AR083325	AR083325 Sequence	480	12.2	37.0	26	6	AR131402	AR131402 Sequence
408	12.4	37.6	36	6	CQ832126	CQ832126 Sequence	481	12.2	37.0	26	6	AR197445	AR197445 Sequence
409	12.4	37.6	36	6	BD170141	BD170141 Method of	482	12.2	37.0	26	6	AR259599	AR259599 Sequence
410	12.4	37.6	37	6	E37999	E37999 Process for	483	12.2	37.0	26	6	BD001806	BD001806 Immunogen
411	12.4	37.6	37	6	AX183802	AX183802 Sequence	484	12.2	37.0	26	6	BD001808	BD001808 Immunogen
412	12.4	37.6	38	6	AX361213	AX361213 Sequence	485	12.2	37.0	27	6	AR019387	AR019387 Sequence
413	12.4	37.6	38	6	AX801864	AX801864 Sequence	486	12.2	37.0	27	6	AR028940	AR028940 Sequence
414	12.4	37.6	39	6	I09581	I09581 Sequence 16	487	12.2	37.0	27	6	AR049630	AR049630 Sequence
415	12.4	37.6	39	6	AX373317	AX373317 Sequence	488	12.2	37.0	27	6	AR145287	AR145287 Sequence
416	12.4	37.6	39	6	AX059020	AX059020 Sequence	489	12.2	37.0	27	6	AR183482	AR183482 Sequence
417	12.4	37.6	39	6	AX098366	AX098366 Sequence	490	12.2	37.0	27	6	AR264737	AR264737 Sequence
418	12.4	37.6	39	12	S76973	S76973 Mus sp. tra	491	12.2	37.0	27	6	BD080955	BD080955 Agonist a
419	12.4	37.6	41	6	E37997	E37997 Process for	492	12.2	37.0	28	6	BD260569	BD260569 Novel pla
420	12.4	37.6	41	6	AX516515	AX516515 Sequence	493	12.2	37.0	28	6	AR287212	AR287212 Sequence
421	12.4	37.6	41	6	AX519942	AX519942 Sequence	494	12.2	37.0	29	6	BD198030	BD198030 Method an
422	12.4	37.6	42	6	AR123483	AR123483 Sequence	495	12.2	37.0	29	6	BD198406	BD198406 Method an
423	12.4	37.6	42	6	E37995	E37995 Process for	496	12.2	37.0	29	6	BD253205	BD253205 Regulatio
424	12.4	37.6	43	6	CQ775450	CQ775450 Sequence	497	12.2	37.0	29	6	BD253275	BD253275 Regulatio
425	12.4	37.6	43	6	AR489265	AR489265 Sequence	498	12.2	37.0	29	6	BD255630	BD255630 Regulatio
426	12.4	37.6	43	6	AX484569	AX484569 Sequence	499	12.2	37.0	29	6	BD256078	BD256078 Regulatio
427	12.4	37.6	44	6	AX523102	AX523102 Sequence	500	12.2	37.0	29	6	BD257186	BD257186 Regulatio
428	12.4	37.6	45	6	AR083218	AR083218 Sequence	501	12.2	37.0	29	6	AR342616	AR342616 Sequence
429	12.4	37.6	45	6	AR164103	AR164103 Sequence	502	12.2	37.0	29	6	AX174858	AX174858 Sequence
430	12.4	37.6	45	6	BD251077	BD251077 Protectiv	503	12.2	37.0	29	6	AX298215	AX298215 Sequence
431	12.4	37.6	45	11	BX664039	BX664039 Arabidops	504	12.2	37.0	30	6	AS1855	AS1855 Sequence 19
432	12.4	37.6	46	6	AX683441	AX683441 Sequence	505	12.2	37.0	30	6	AS1859	AS1859 Sequence 23
433	12.4	37.6	49	6	CQ775464	CQ775464 Sequence	506	12.2	37.0	30	6	AR085828	AR085828 Sequence
434	12.4	37.6	49	10	NMV4PRJRN	NMV4PRJRN	507	12.2	37.0	30	6	ES4041	ES4041 Gene diagno
435	12.4	37.6	50	6	CQ008140	CQ008140 Sequence	508	12.2	37.0	30	6	AR214162	AR214162 Sequence
436	12.4	37.6	50	6	CQ008824	CQ008824 Sequence	509	12.2	37.0	31	6	AX192433	AX192433 Sequence
437	12.4	37.6	50	6	AX128400	AX128400 Sequence	510	12.2	37.0	31	6	AX249689	AX249689 Sequence
438	12.4	37.6	50	6	AX165814	AX165814 Sequence	511	12.2	37.0	32	6	AR123472	AR123472 Sequence
439	12.4	37.6	50	6	BD013721	BD013721 Method of	512	12.2	37.0	32	6	AR219996	AR219996 Sequence
440	12.4	37.6	50	10	NMTFAM07	NMTFAM07	513	12.2	37.0	32	6	AR220713	AR220713 Sequence
441	12.2	37.0	17	6	AX781784	AX781784 Sequence	514	12.2	37.0	32	6	AR287475	AR287475 Sequence
442	12.2	37.0	17	6	AX781785	AX781785 Sequence	515	12.2	37.0	32	6	AX805712	AX805712 Sequence
443	12.2	37.0	18	6	AR106973	AR106973 Sequence	516	12.2	37.0	32	6	BD063041	BD063041 Protease-
444	12.2	37.0	18	6	AR116331	AR116331 Sequence	517	12.2	37.0	33	6	AR032309	AR032309 Sequence
445	12.2	37.0	18	6	AR322348	AR322348 Sequence	518	12.2	37.0	33	6	AR084265	AR084265 Sequence
446	12.2	37.0	18	6	BD062486	BD062486 Phosphodi	519	12.2	37.0	33	6	BD243521	BD243521 Nucleotid
447	12.2	37.0	19	6	E37137	E37137 Method for	520	12.2	37.0	33	6	AX034944	AX034944 Sequence
448	12.2	37.0	20	6	AR165355	AR165355 Sequence	521	12.2	37.0	33	6	BD170411	BD170411 Method of
449	12.2	37.0	20	6	E31749	E31749 Blast resis	522	12.2	37.0	34	6	AX659015	AX659015 Sequence
450	12.2	37.0	20	6	E37107	E37107 Method for	523	12.2	37.0	35	6	I28730	I28730 Sequence 34
451	12.2	37.0	20	6	I81470	I81470 Sequence 7	524	12.2	37.0	35	6	I89384	I89384 Sequence 34
452	12.2	37.0	20	6	AX676286	AX676286 Sequence	525	12.2	37.0	36	6	AR041619	AR041619 Sequence
453	12.2	37.0	20	6	BD160833	BD160833 Method fo	526	12.2	37.0	36	6	AR133028	AR133028 Sequence
454	12.2	37.0	20	6	BD169536	BD169536 Method of	527	12.2	37.0	36	6	AR133467	AR133467 Sequence
455	12.2	37.0	21	6	AX154181	AX154181 Sequence	528	12.2	37.0	36	6	AR133468	AR133468 Sequence
456	12.2	37.0	21	6	AR112932	AR112932 Sequence	529	12.2	37.0	36	6	I62099	I62099 Sequence 65
457	12.2	37.0	22	6	AR112932	AR112932 Sequence	530	12.2	37.0	36	6	I62099	I62099 Sequence 65

C 531	12.2	37.0	36	6	I89302	I89302 Sequence 16	604	12	36.4	15	6	I38943	I38943 Sequence 53
C 532	12.2	37.0	36	6	AX636505	AX636505 Sequence	605	12	36.4	15	6	I87974	I87974 Sequence 53
C 533	12.2	37.0	36	6	AX637077	AX637077 Sequence	606	12	36.4	17	6	AX687721	AX687721 Sequence
C 534	12.2	37.0	37	6	AR411038	AR411038 Sequence	607	12	36.4	17	6	AX687722	AX687722 Sequence
C 535	12.2	37.0	38	6	AR046649	AR046649 Sequence	608	12	36.4	17	6	AX687723	AX687723 Sequence
C 536	12.2	37.0	38	6	I37753	I37753 Sequence 76	609	12	36.4	17	6	AX687724	AX687724 Sequence
C 537	12.2	37.0	38	6	I35501	I35501 Sequence 12	610	12	36.4	17	6	AX687725	AX687725 Sequence
C 538	12.2	37.0	38	6	I94603	I94603 Sequence 76	611	12	36.4	17	6	AX687726	AX687726 Sequence
C 539	12.2	37.0	38	6	AR286953	AR286953 Sequence	612	12	36.4	20	6	AR2562	AR2562 Sequence 36
C 540	12.2	37.0	38	6	AR331791	AR331791 Sequence	613	12	36.4	20	6	AR101050	AR101050 Sequence
C 541	12.2	37.0	38	6	AR332630	AR332630 Sequence	614	12	36.4	20	6	E29054	E29054 Mutant S182
C 542	12.2	37.0	38	6	AR333408	AR333408 Sequence	615	12	36.4	20	6	E29056	E29056 Mutant S182
C 543	12.2	37.0	38	6	AR334450	AR334450 Sequence	616	12	36.4	20	6	E29064	E29064 Mutant S182
C 544	12.2	37.0	38	6	AR334597	AR334597 Sequence	617	12	36.4	21	6	I30540	I30540 Sequence 3
C 545	12.2	37.0	38	6	AR398943	AR398943 Sequence	618	12	36.4	21	6	I81272	I81272 Sequence 23
C 546	12.2	37.0	38	6	AX218533	AX218533 Sequence	619	12	36.4	22	6	AX250146	AX250146 Sequence
C 547	12.2	37.0	38	6	AX219417	AX219417 Sequence	620	12	36.4	23	6	AX015794	AX015794 Sequence
C 548	12.2	37.0	38	6	AX423947	AX423947 Sequence	621	12	36.4	23	6	AX167366	AX167366 Sequence
C 549	12.2	37.0	38	6	AX423968	AX423968 Sequence	622	12	36.4	24	6	AR074528	AR074528 Sequence
C 550	12.2	37.0	38	6	AX424461	AX424461 Sequence	623	12	36.4	24	6	AR369692	AR369692 Sequence
C 551	12.2	37.0	38	6	AX424514	AX424514 Sequence	624	12	36.4	24	6	AR289209	AR289209 Sequence
C 552	12.2	37.0	38	6	AX424609	AX424609 Sequence	625	12	36.4	25	6	AR238927	AR238927 Sequence
C 553	12.2	37.0	38	6	AX424800	AX424800 Sequence	626	12	36.4	25	6	AX278729	AX278729 Sequence
C 554	12.2	37.0	38	6	AX425435	AX425435 Sequence	627	12	36.4	25	6	AX689225	AX689225 Sequence
C 555	12.2	37.0	38	6	AX580370	AX580370 Sequence	628	12	36.4	25	6	AX689226	AX689226 Sequence
C 556	12.2	37.0	38	6	AX581121	AX581121 Sequence	629	12	36.4	25	6	AX689227	AX689227 Sequence
C 557	12.2	37.0	38	6	AX665049	AX665049 Sequence	630	12	36.4	25	6	AX689228	AX689228 Sequence
C 558	12.2	37.0	38	6	AX961528	AX961528 Sequence	631	12	36.4	25	6	AX689229	AX689229 Sequence
C 559	12.2	37.0	39	6	AX384023	AX384023 Sequence	632	12	36.4	25	6	AX689230	AX689230 Sequence
C 560	12.2	37.0	40	6	AR053674	AR053674 Sequence	633	12	36.4	25	6	AX689231	AX689231 Sequence
C 561	12.2	37.0	40	6	AR059120	AR059120 Sequence	634	12	36.4	25	6	AX784856	AX784856 Sequence
C 562	12.2	37.0	40	6	AR168200	AR168200 Sequence	635	12	36.4	25	6	AX784862	AX784862 Sequence
C 563	12.2	37.0	40	6	AR258609	AR258609 Sequence	636	12	36.4	27	6	AR143859	AR143859 Sequence
C 564	12.2	37.0	40	6	AX456329	AX456329 Sequence	637	12	36.4	27	6	BD206536	BD206536 Enzymatic
C 565	12.2	37.0	40	6	AX528105	AX528105 Sequence	638	12	36.4	27	6	BD209483	BD209483 Enzymatic
C 566	12.2	37.0	41	6	AR148815	AR148815 Sequence	639	12	36.4	27	6	E17050	E17050 Primer. 7/1
C 567	12.2	37.0	41	6	AR200861	AR200861 Sequence	640	12	36.4	28	6	AR473410	AR473410 Sequence
C 568	12.2	37.0	41	6	AX513844	AX513844 Sequence	641	12	36.4	28	6	AX092224	AX092224 Sequence
C 569	12.2	37.0	41	6	AX513940	AX513940 Sequence	642	12	36.4	28	6	BD138046	BD138046 Expression
C 570	12.2	37.0	41	6	AX515722	AX515722 Sequence	643	12	36.4	29	6	AR87519	AR87519 Sequence 5
C 571	12.2	37.0	41	6	AX516011	AX516011 Sequence	644	12	36.4	29	6	BD199676	BD199676 Method an
C 572	12.2	37.0	41	6	AX517049	AX517049 Sequence	645	12	36.4	29	6	BD252451	BD252451 Regulatio
C 573	12.2	37.0	41	6	AX517721	AX517721 Sequence	646	12	36.4	29	6	BD253328	BD253328 Regulatio
C 574	12.2	37.0	41	6	AX518317	AX518317 Sequence	647	12	36.4	29	6	BD257246	BD257246 Regulatio
C 575	12.2	37.0	41	6	AX519579	AX519579 Sequence	648	12	36.4	29	6	BD257253	BD257253 Regulatio
C 576	12.2	37.0	41	6	AX519572	AX519572 Sequence	649	12	36.4	29	6	AR254072	AR254072 Sequence
C 577	12.2	37.0	41	6	AX786812	AX786812 Sequence	650	12	36.4	29	6	AX100907	AX100907 Sequence
C 578	12.2	37.0	44	6	AX642221	AX642221 Sequence	651	12	36.4	29	6	AX100909	AX100909 Sequence
C 579	12.2	37.0	45	6	AR041121	AR041121 Sequence	652	12	36.4	29	6	BD135102	BD135102 Polyzinc
C 580	12.2	37.0	45	6	AR066015	AR066015 Sequence	653	12	36.4	30	6	CQ816716	CQ816716 Sequence
C 581	12.2	37.0	45	6	AR072757	AR072757 Sequence	654	12	36.4	30	6	AX166327	AX166327 Sequence
C 582	12.2	37.0	46	6	AR082367	AR082367 Sequence	655	12	36.4	30	6	AX320318	AX320318 Sequence
C 583	12.2	37.0	46	6	AR120809	AR120809 Sequence	656	12	36.4	31	6	AR117112	AR117112 Sequence
C 584	12.2	37.0	46	6	I78313	I78313 Sequence 11	657	12	36.4	31	6	AR338155	AR338155 Sequence
C 585	12.2	37.0	46	6	AX665048	AX665048 Sequence	658	12	36.4	31	6	AX249589	AX249589 Sequence
C 586	12.2	37.0	46	6	AX961527	AX961527 Sequence	659	12	36.4	31	6	AX429230	AX429230 Sequence
C 587	12.2	37.0	47	6	E37138	E37138 Method for	660	12	36.4	33	6	BD246984	BD246984 Improved
C 588	12.2	37.0	47	6	I04682	I04682 Sequence 6	661	12	36.4	33	6	BD270569	BD270569 Family of
C 589	12.2	37.0	47	6	AR289765	AR289765 Sequence	662	12	36.4	33	6	AR208966	AR208966 Sequence
C 590	12.2	37.0	47	6	AR290290	AR290290 Sequence	663	12	36.4	33	6	AR228359	AR228359 Sequence
C 591	12.2	37.0	47	6	AR290514	AR290514 Sequence	664	12	36.4	33	6	AX046964	AX046964 Sequence
C 592	12.2	37.0	47	6	BD016412	BD016412 Method of	665	12	36.4	33	6	AX428366	AX428366 Sequence
C 593	12.2	37.0	48	6	CQ816302	CQ816302 Sequence	666	12	36.4	33	6	BD082729	BD082729 Family of
C 594	12.2	37.0	48	6	CQ818897	CQ818897 Sequence	667	12	36.4	34	6	BD235856	BD235856 Gene-modi
C 595	12.2	37.0	48	9	S82270	S82270 Homo sapien	668	12	36.4	34	6	I28719	I28719 Sequence 22
C 596	12.2	37.0	49	6	A06246	A06246 Synthetic H	669	12	36.4	34	6	I89373	I89373 Sequence 22
C 597	12.2	37.0	49	6	AX769772	AX769772 Sequence	670	12	36.4	36	6	I01740	I01740 Sequence 7
C 598	12.2	37.0	50	6	CQ003143	CQ003143 Sequence	671	12	36.4	36	6	I79582	I79582 Sequence 5
C 599	12.2	37.0	50	6	CQ008834	CQ008834 Sequence	672	12	36.4	36	6	AX092228	AX092228 Sequence
C 600	12.2	37.0	50	6	CQ008835	CQ008835 Sequence	673	12	36.4	37	6	A03922	A03922 Nucleotide
C 601	12.2	37.0	50	6	CQ008836	CQ008836 Sequence	674	12	36.4	37	6	A03931	A03931 Nucleotide
C 602	12.2	37.0	50	6	AR282139	AR282139 Sequence	675	12	36.4	37	6	CQ759376	CQ759376 Sequence
C 603	12.2	37.0	50	6	AX225280	AX225280 Sequence	676	12	36.4	37	6	AR473388	AR473388 Sequence

677	12	36.4	37	6	BD138024	BD138024 Expressio	750	12	36.4	49	6	CQ812187	CQ812187 Sequence
678	12	36.4	38	6	AR045482	Sequence	751	12	36.4	49	6	CQ816633	Sequence
679	12	36.4	38	6	AR045482	Sequence	752	12	36.4	49	6	AX451996	Sequence
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681	12	36.4	38	6	AR047527	Sequence	754	12	36.4	49	6	AX538088	Sequence
682	12	36.4	38	6	I37792	Sequence 80	755	12	36.4	49	6	AX538775	Sequence
683	12	36.4	38	6	I52534	Sequence 27	756	12	36.4	49	6	AX538786	Sequence
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685	12	36.4	38	6	I54579	Sequence 23	758	12	36.4	50	6	AR032866	Sequence
686	12	36.4	38	6	I94642	Sequence 80	759	12	36.4	50	6	CQ008995	Sequence
687	12	36.4	38	6	AR182142	Sequence	760	12	36.4	50	6	CQ818808	Sequence
688	12	36.4	38	6	AR286888	Sequence	761	12	36.4	50	6	I29606	Sequence 47
689	12	36.4	38	6	AR287080	Sequence	762	12	36.4	50	6	I91280	Sequence 47
690	12	36.4	38	6	AR330026	Sequence	763	12	36.4	50	6	AR209530	Sequence
691	12	36.4	38	6	AR330279	Sequence	764	12	36.4	50	6	AR486916	Sequence
692	12	36.4	38	6	AR330833	Sequence	765	12	36.4	50	6	AR486928	Sequence
693	12	36.4	38	6	AR331579	Sequence	766	12	36.4	50	6	AX418536	Sequence
694	12	36.4	38	6	AR332280	Sequence	767	12	36.4	50	6	AX418548	Sequence
695	12	36.4	38	6	AR332374	Sequence	768	12	36.4	50	6	AX538790	Sequence
696	12	36.4	38	6	AR332774	Sequence	769	12	36.4	50	6	AX952275	Sequence
697	12	36.4	38	6	AR333379	Sequence	770	12	36.4	50	6	AX952287	Sequence
698	12	36.4	38	6	AR333552	Sequence	771	11.8	35.8	17	6	AX960361	Sequence
699	12	36.4	38	6	AR334446	Sequence	772	11.8	35.8	17	6	AX457016	Sequence
700	12	36.4	38	6	AR334634	Sequence	773	11.8	35.8	17	6	AX781782	Sequence
701	12	36.4	38	6	AR334881	Sequence	774	11.8	35.8	18	6	BD244767	Isolation
702	12	36.4	38	6	AR335180	Sequence	775	11.8	35.8	18	6	AR255273	Sequence 13
703	12	36.4	38	6	AR336234	Sequence	776	11.8	35.8	19	6	I33289	Sequence
704	12	36.4	38	6	AR339878	Sequence	777	11.8	35.8	19	6	AX286618	Sequence
705	12	36.4	38	6	AR399070	Sequence	778	11.8	35.8	20	6	AR009308	Sequence
706	12	36.4	38	6	AX166338	Sequence	779	11.8	35.8	20	6	AR009367	Sequence
707	12	36.4	38	6	AX219683	Sequence	780	11.8	35.8	20	6	AR220993	Sequence
708	12	36.4	38	6	AX219766	Sequence	781	11.8	35.8	20	6	AR475590	Sequence
709	12	36.4	38	6	AX219836	Sequence	782	11.8	35.8	20	6	AX119392	Sequence
710	12	36.4	38	6	AX222319	Sequence	783	11.8	35.8	20	6	AX293633	Sequence
711	12	36.4	38	6	AX222379	Sequence	784	11.8	35.8	20	6	AX293842	Sequence
712	12	36.4	38	6	AX227957	Sequence	785	11.8	35.8	20	6	AX488338	Sequence
713	12	36.4	38	6	AX273746	Sequence	786	11.8	35.8	21	6	AX1440	Sequence 3
714	12	36.4	38	6	AX273985	Sequence	787	11.8	35.8	21	6	AX1609	Sequence 3
715	12	36.4	38	6	AX424347	Sequence	788	11.8	35.8	21	6	AX096455	Sequence
716	12	36.4	38	6	AX424429	Sequence	789	11.8	35.8	21	6	AX282116	Sequence
717	12	36.4	38	6	AX424440	Sequence	790	11.8	35.8	21	6	BD005339	Enhanced
718	12	36.4	38	6	AX424902	Sequence	791	11.8	35.8	21	6	BD056582	Method to
719	12	36.4	38	6	AX425394	Sequence	792	11.8	35.8	21	6	AX020018	Sequence
720	12	36.4	38	6	AX580578	Sequence	793	11.8	35.8	23	6	E06028	Probe. 9/19
721	12	36.4	38	6	AX581308	Sequence	794	11.8	35.8	23	6	E06029	Probe. 9/19
722	12	36.4	38	6	AX581522	Sequence	795	11.8	35.8	24	6	AR037804	Sequence
723	12	36.4	40	6	A22795	NS1 HCV pro	796	11.8	35.8	24	6	E31851	Novel Cance
724	12	36.4	40	6	AR031222	Sequence	797	11.8	35.8	24	6	I32637	Sequence 22
725	12	36.4	40	6	AR059110	Sequence	798	11.8	35.8	24	6	AR438478	Sequence
726	12	36.4	40	6	AR145038	Sequence	799	11.8	35.8	24	6	AX289000	Sequence
727	12	36.4	40	6	BD184748	Transcrip	800	11.8	35.8	24	6	AX292797	Sequence
728	12	36.4	40	6	BD169790	Transcrip	801	11.8	35.8	24	6	AX443659	Sequence
729	12	36.4	41	6	BD173587	Method of	802	11.8	35.8	24	6	AX443869	Sequence
730	12	36.4	41	6	E27284	Method for	803	11.8	35.8	24	6	BD169465	Novel qua
731	12	36.4	41	6	AX411405	Sequence	804	11.8	35.8	25	6	AR038152	Sequence
732	12	36.4	41	6	AX516786	Sequence	805	11.8	35.8	25	6	AR094115	Sequence
733	12	36.4	42	9	AX516786	Sequence	806	11.8	35.8	25	6	CQ620107	Sequence
734	12	36.4	42	9	AX516786	Sequence	807	11.8	35.8	25	6	CQ620108	Sequence
735	12	36.4	42	9	AX516786	Sequence	808	11.8	35.8	25	6	AR461170	Sequence
736	12	36.4	43	6	BD264585	Beta-1,3-	809	11.8	35.8	25	6	AR461171	Sequence
737	12	36.4	43	6	BD264585	Beta-1,3-	810	11.8	35.8	25	6	AX447847	Sequence
738	12	36.4	43	6	E02955	Single repe	811	11.8	35.8	25	6	AX609295	Sequence
739	12	36.4	45	6	AR257380	Sequence	812	11.8	35.8	25	6	AX609296	Sequence
740	12	36.4	45	6	AX611800	Sequence	813	11.8	35.8	25	6	AX692126	Sequence
741	12	36.4	45	6	AX612206	Sequence	814	11.8	35.8	25	6	AX692127	Sequence
742	12	36.4	45	6	AX612207	Sequence	815	11.8	35.8	25	6	AX782525	Sequence
743	12	36.4	46	6	BD083665	Diulifide	816	11.8	35.8	25	6	AX782526	Sequence
744	12	36.4	46	6	AR032576	Sequence	817	11.8	35.8	25	6	BD106828	Methods o
745	12	36.4	46	6	I29316	Sequence 18	818	11.8	35.8	26	6	AX782522	Sequence 8
746	12	36.4	46	6	I90990	Sequence 18	819	11.8	35.8	26	6	AR003353	Sequence
747	12	36.4	46	6	AR209240	Sequence	820	11.8	35.8	26	6	AR064178	Sequence
748	12	36.4	47	9	HUMTCCVJ32	L39499 Homo sapien	821	11.8	35.8	26	6	BD235194	Voltage g
749	12	36.4	48	6	AX068199	Sequence	822	11.8	35.8	26	6	E55060	Hydrocephal
	12	36.4	49	6	A59581	Sequence 1							

823	11.8	35.8	26	6	I32225	I32225 Sequence 22	896	11.8	35.8	40	6	CQ800974	CQ800974 Sequence
824	11.8	35.8	26	6	AR453354	AR453354 Sequence	897	11.8	35.8	40	6	CQ827518	CQ827518 Sequence
825	11.8	35.8	26	6	BD012011	BD012011 Hydroceph	898	11.8	35.8	40	6	I44686	I44686 Sequence 11
826	11.8	35.8	26	6	BD078192	BD078192 Modulator	899	11.8	35.8	40	6	I92731	I92731 Sequence 11
827	11.8	35.8	27	6	BD206506	BD206506 Enzymatic	900	11.8	35.8	40	6	AX235178	AX235178 Sequence
828	11.8	35.8	27	6	BD207834	BD207834 Enzymatic	901	11.8	35.8	41	6	AX327079	AX327079 Sequence
829	11.8	35.8	27	6	E31594	E31594 Tight Junct	902	11.8	35.8	41	6	AX513961	AX513961 Sequence
830	11.8	35.8	27	6	AR403169	AR403169 Sequence	903	11.8	35.8	41	6	AX514053	AX514053 Sequence
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c 997 11.6 35.2 28 6 AX135117 Sequence
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ALIGNMENTS

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RESULT 1
BD181366 34 bp DNA linear PAT 15-MAY-2003
LOCUS A method for determination of a nucleic acid using a control.
DEFINITION
ACCESSION BD181366
VERSION BD181366.1 GI:30792284
KEYWORDS JP 2002335981-A/5.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 34)
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: JP 2002335981-A 5 26-NOV-2002;
F HOFFMANN LA ROCHE AG
COMMENT OS Artificial Sequence
PN JP 2002335981-A/5
PD 26-NOV-2002
PF 04-MAR-2002 JP 2002057515
PR 02-MAR-2001 EP 01105172.9
PI STEPHAN JAEGER
PC C12N15/09,C12Q1/68,G01N33/50,G01N33/566,G01N33/58,
PC C12N15/00
CC Description of Artificial Sequence: ST650pc probe sequence CC
(parallel-complementary to ST650)
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Matches 33; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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RESULT 2
AX523946 34 bp DNA linear PAT 21-NOV-2002
LOCUS Sequence 5 from Patent EP1236804.
DEFINITION
ACCESSION AX523946
VERSION AX523946.1 GI:25168877
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for determination of a nucleic acid using a control
JOURNAL Patent: EP 1236804-A 5 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
FEATURES
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RESULT 3
AX524844 34 bp DNA linear PAT 21-NOV-2002
LOCUS Sequence 5 from Patent EP1236805.
DEFINITION
ACCESSION AX524844
VERSION AX524844.1 GI:25169938
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Jaeger,S.
TITLE A method for the determination of a nucleic acid using a control
JOURNAL Patent: EP 1236805-A 5 04-SEP-2002;
Roche Diagnostics GmbH (DE) ; F. Hoffmann-La Roche AG (CH)
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LOCUS AX403706/c 43 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 61 from Patent WO0077037.
ACCESSION AX403706
VERSION AX403706.1 GI:21437151
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ashkenazi,A., Baker,K., Botstein,D., Desnoyers,I., Eaton,D.L.,
Ferrara,N., Fong,S., Gao,W.Q., Garber,H., Gerritsen,M.E.,
Goddard,A., Godowski,P., Gurney,A., Kljavin,I.J., Mather,J.,
Napier,M., Pan,J., Paoni,N., Roy,M., Tumas,D., Watanabe,C.,
Williams,P.M., Wood,W.I. and Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 61 21-DEC-2000;
Genentech Inc. (US)
FEATURES source
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DB 43 GCCACATGTTGGCAAGATGTGTGT 18

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LOCUS CQ753200 40 bp DNA linear PAT 01-MAR-2004
DEFINITION Sequence 27 from Patent WO2004001032.
ACCESSION CQ753200
VERSION CQ753200.1 GI:44844676
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Vogels,R., Havenga,M.J. and Zuidgeest,D.A.
TITLE Stable adenoviral vectors and methods for propagation thereof
JOURNAL Patent: WO 2004001032-A 27 31-DEC-2003;
Crucell Holland B.V. (NL)
FEATURES source
Location/Qualifiers
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/organism="synthetic construct"
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DEFINITION Sequence 7 from Patent WO03087371.
ACCESSION AX930614
VERSION AX930614.1 GI:40312362
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS de Haan,P.T.
TITLE Antiviral therapy on the basis of rna interference
JOURNAL Patent: WO 03087371-A 7 23-OCT-2003;
Viruvation B.V. (NL)
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DB 12 GCCGATGGTGGCAAGTGGTC 33

RESULT 7
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DEFINITION Humanized antibody specific to human 4-1BB and medicinal
compositions containing the same.
ACCESSION BD263504
VERSION BD263504.1 GI:33073272
KEYWORDS JP 2002531383-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Hong,H.J., Park,S.S., Kang,Y.J., Kang,C.Y. and Yo,S.K.
TITLE Humanized antibody specific to human 4-1BB and medicinal
compositions containing the same
JOURNAL Patent: JP 2002531383-A 4 24-SEP-2002;
LG CHEMICAL LTD
COMMENT OS Artificial Sequence
PN JP 2002531383-A/4
PD 24-SEP-2002
PF 17-NOV-1999 JP 2000582430
PR 17-NOV-1998 KR 1998/49177,11-MAY-1999 KR 1999/16750 PI
HYO JEONG HONG, SUNG SUP PARK, YOUNG JUN KANG, CHANG YUL KANG, PI
SUNG KWAN YOON
PC A61K39/395, A61K38/00, A61P19/02, A61P29/00, A61P37/06, C07K16/28,
C07K16/46,
PC
C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/09, G01N33/15, G01N33/PC
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Db 2 GACTGCCAGGTTTGTGTTGATACC 26

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DEFINITION Sequence 8 from patent US 6458934.
ACCESSION AR235054
VERSION AR235054.1 GI:27278149
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hong,H.J., Park,S.S., Kang,Y.J., Kang,C.-Y. and Yoon,S.K.
TITLE Humanized antibody specific for human 4-1BB
JOURNAL Patent: US 6458934-A 8 01-OCT-2002;
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Db 2 GACTGCCAGGTTTGTGTTGATACC 26

RESULT 9
LOCUS AR124548/c 33 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 28 from patent US 6171861.
ACCESSION AR124548
VERSION AR124548.1 GI:14109909
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6171861-A 28 09-JAN-2001;
FEATURES
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Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 10
LOCUS AR163199/c 33 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 28 from patent US 6270969.
ACCESSION AR163199
VERSION AR163199.1 GI:16233719
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6270969-A 28 07-AUG-2001;
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DEFINITION Sequence 28 from patent US 6720140.
ACCESSION AR493800
VERSION AR493800.1 GI:47266236
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: US 6720140-A 28 13-APR-2004;
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Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 12
LOCUS AX491667/c 33 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 28 from Patent EP1227147.
ACCESSION AX491667
VERSION AX491667.1 GI:23224175
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1227147-A 28 31-JUL-2002;
INVENTOR INVITROGEN CORPORATION (US)
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FEATURES             Location/Qualifiers
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Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
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Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 13
LOCUS AX498638 33 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 28 from Patent EP1229113.
ACCESSION AX498638
VERSION AX498638.1 GI:23343435
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Hartley,J.L. and Brasch,M.A.
TITLE Recombinational cloning using engineered recombination sites
JOURNAL Patent: EP 1229113-A 28 07-AUG-2002;
INVITROGEN CORPORATION (US)
FEATURES             Location/Qualifiers
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Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 14
LOCUS BD131354/c 33 bp DNA linear PAT 18-SEP-2002
DEFINITION Recombinational cloning using nucleic acids having recombination
ACCESSION BD131354
VERSION BD131354.1 GI:23226299
KEYWORDS JP 2002500861-A/28.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
TITLE Recombinational cloning using nucleic acids having recombination
JOURNAL Patent: JP 2002500861-A 28 15-JAN-2002;
LIFE TECHNOLOGIES INC
COMMENT OS Artificial Sequence
PN JP 2002500861-A/28
PD 15-JAN-2002
PP 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..33

FEATURES             Location/Qualifiers
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                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"
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Query Match          46.7%; Score 15.4; DB 6; Length 33;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGCGGGCGGTAATA 8

RESULT 15
LOCUS AR048018 34 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 22 from patent US 5820871.
ACCESSION AR048018
VERSION AR048018.1 GI:5970361
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA virus expression systems and
vaccines
JOURNAL Patent: US 5820871-A 22 13-OCT-1998;
VACCINES
FEATURES             Location/Qualifiers
  source              1..34
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                    /mol_type="unassigned DNA"
ORIGIN
Query Match          46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 7 ATGAGTGGCAGGCGCGGGCGGTAATA 31

RESULT 16
LOCUS AR048020 34 bp DNA linear PAT 29-SEP-1999.
DEFINITION Sequence 24 from patent US 5820871.
ACCESSION AR048020
VERSION AR048020.1 GI:5970363
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA virus expression systems and
vaccines
JOURNAL Patent: US 5820871-A 24 13-OCT-1998;
VACCINES
FEATURES             Location/Qualifiers
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                    /mol_type="unassigned DNA"
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Query Match          46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
|||||
Db 7 ATGAGTGGCAGGCGCGGGCGGTAATA 31

Query Match          46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
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Db 7 ATGAGTGGCAGGCGCGGGCGGTAATA 31
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Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGGCGCGTAATA 31

RESULT 22
AR094256 AR094256 34 bp DNA linear PAT 08-SEP-2000
LOCUS Sequence 24 from patent US 6001634.
DEFINITION AR094256
ACCESSION AR094256
VERSION AR094256.1 GI:10021011
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 34)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA viruses
JOURNAL Patent: US 6001634-A 24 14-DEC-1999;
FEATURES
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        /mol_type="unassigned DNA"
ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 34;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 7 ATGAGTGGCAGGCGGGCGCGTAATA 31

RESULT 23
AR048019/c AR048019 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 23 from patent US 5820871.
DEFINITION AR048019
ACCESSION AR048019
VERSION AR048019.1 GI:5970362
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 38)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA virus expression systems and
JOURNAL Patent: US 5820871-A 23 13-OCT-1998;
FEATURES
  Location/Qualifiers
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        /organism="unknown"
        /mol_type="unassigned DNA"
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Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGCGTAATA 8

RESULT 24
AR048021/c AR048021 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 25 from patent US 5820871.
DEFINITION AR048021
ACCESSION AR048021
VERSION AR048021.1 GI:5970364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA virus expression systems and
JOURNAL Patent: US 5820871-A 25 13-OCT-1998;
FEATURES
  Location/Qualifiers
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ORIGIN
Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGCGTAATA 8

RESULT 25
AR059773/c AR059773 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 23 from patent US 5840520.
DEFINITION AR059773
ACCESSION AR059773
VERSION AR059773.1 GI:5986223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 38)
AUTHORS Clarke,D,Kirkwood. and Palese,P.M.
TITLE Recombinant negative strand RNA virus expression systems
JOURNAL Patent: US 5840520-A 23 24-NOV-1998;
FEATURES
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Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 ATGAGTGGCAAGGCGTCTGGTGATA 30
Db 32 ATGAGTGGCAGGCGGGCGCGTAATA 8

RESULT 26
AR068647/c AR068647 38 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 23 from patent US 5854037.
DEFINITION AR068647
ACCESSION AR068647
VERSION AR068647.1 GI:6000854
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 38)
AUTHORS Palese,P. and Garcia-Sastre,A.
TITLE Recombinant negative strand RNA virus expression systems and
JOURNAL Patent: US 5854037-A 23 29-DEC-1998;
FEATURES
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Query Match 46.7%; Score 15.4; DB 6; Length 38;
Best Local Similarity 76.0%; Pred. No. 5.6e+04;
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Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 27									
AR068649/c	AR068649	Sequence 25 from patent US 5854037.	38 bp	DNA	linear	PAT 29-SEP-1999			
LOCUS	AR068649	Sequence 25 from patent US 5854037.							
DEFINITION	AR068649	Sequence 25 from patent US 5854037.							
ACCESSION	AR068649	Sequence 25 from patent US 5854037.							
VERSION	AR068649.1	GI:6000856							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA virus expression systems and vaccines								
JOURNAL	Patent: US 5854037-A 25 29-DEC-1998;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 28									
AR094255/c	AR094255	Sequence 23 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094255	Sequence 23 from patent US 6001634.							
DEFINITION	AR094255	Sequence 23 from patent US 6001634.							
ACCESSION	AR094255	Sequence 23 from patent US 6001634.							
VERSION	AR094255.1	GI:10021010							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 29									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 30									
AR225168/c	AR225168	Sequence 1 from patent US 6441158.	40 bp	RNA	linear	PAT 26-SEP-2002			
LOCUS	AR225168	Sequence 1 from patent US 6441158.							
DEFINITION	AR225168	Sequence 1 from patent US 6441158.							
ACCESSION	AR225168	Sequence 1 from patent US 6441158.							
VERSION	AR225168.1	GI:23334332							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 40)								
AUTHORS	Dynan, W.S. and Yoo, S.								
TITLE	Oligomers that bind to ku protein								
JOURNAL	Patent: US 6441158-A 1 27-AUG-2002;								
FEATURES	Location/Qualifiers								
source	1..40								
ORIGIN	1..40								
Query Match 46.7%; Score 15.4; DB 6; Length 40;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	2	CCACATGAGTGGCAAGCGCTCTGGT 26							
Db	37	CAAGACCATGGGAGGCGTATGGT 13							
RESULT 31									
AX665041/c	AX665041	Sequence 87 from Patent EP1275728.	38 bp	DNA	linear	PAT 26-MAR-2003			
LOCUS	AX665041	Sequence 87 from Patent EP1275728.							
DEFINITION	AX665041	Sequence 87 from Patent EP1275728.							
ACCESSION	AX665041	Sequence 87 from Patent EP1275728.							
VERSION	AX665041.1	GI:29290196							
KEYWORDS	synthetic construct								
SOURCE	synthetic construct								
ORGANISM	artificial sequences.								
REFERENCE	1								
AUTHORS	Nomoto, T., Yano, T., Kozaki, S. and Honma, T.								
TITLE	Polyhydroxyalkanoate-containing structure and manufacturing method thereof								
JOURNAL	Patent: EP 1275728-A 87 15-JAN-2003;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 32									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 33									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
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ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 34									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 35									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 36									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							
ACCESSION	AR094257	Sequence 25 from patent US 6001634.							
VERSION	AR094257.1	GI:10021013							
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	1 (bases 1 to 38)								
AUTHORS	Palese, P. and Garcia-Sastre, A.								
TITLE	Recombinant negative strand RNA viruses								
JOURNAL	Patent: US 6001634-A 23 14-DEC-1999;								
FEATURES	Location/Qualifiers								
source	1..38								
ORIGIN	1..38								
Query Match 46.7%; Score 15.4; DB 6; Length 38;									
Best Local Similarity 76.0%; Pred. No. 5.6e+04;									
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	6	ATGAGTGGCAAGCGCTCTGGTGATA 30							
Db	32	ATGAGTGGCAGGCGGGCGGTAATA 8							
RESULT 37									
AR094257/c	AR094257	Sequence 25 from patent US 6001634.	38 bp	DNA	linear	PAT 08-SEP-2000			
LOCUS	AR094257	Sequence 25 from patent US 6001634.							
DEFINITION	AR094257	Sequence 25 from patent US 6001634.							


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ORIGIN
Query Match      45.5%; Score 15; DB 6; Length 38;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32
Db 38 CAACGTGACCGACCGCGTTTATTGATACC 8

RESULT 32
AX961520/c      38 bp      DNA      linear      PAT 14-JAN-2004
LOCUS
DEFINITION      Sequence 66 from Patent EPI371983.
ACCESSION      AX961520
VERSION        AX961520.1 GI:40880979
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1
AUTHORS        Honma,T., Yano,T., Nomoto,T. and Kozaki,S.
TITLE          Immunoassay, reagent for immunoassay, and production method of the
                same
JOURNAL        Patent: EP 1371983-A 66 17-DEC-2003;
                Canon Kabushiki Kaisha (JP)
FEATURES       source
                1..38
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="complementary to 65"

ORIGIN
Query Match      45.5%; Score 15; DB 6; Length 38;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32
Db 38 CAACGTGACCGACCGCGTTTATTGATACC 8

RESULT 33
AX665040
LOCUS
DEFINITION      Sequence 86 from Patent EPI275728.
ACCESSION      AX665040
VERSION        AX665040.1 GI:29290195
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1
AUTHORS        Nomoto,T., Yano,T., Kozaki,S. and Honma,T.
TITLE          Polyhydroxyalkanoate-containing structure and manufacturing method
                thereof
JOURNAL        Patent: EP 1275728-A 86 15-JAN-2003;
                CANON KABUSHIKI KAISHA (JP)
FEATURES       source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Primer for PCR multiplication"

ORIGIN
Query Match      45.5%; Score 15; DB 6; Length 46;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32
Db 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32

RESULT 34
AX961519
LOCUS
DEFINITION      Sequence 65 from Patent EPI371983.
ACCESSION      AX961519
VERSION        AX961519.1 GI:40880978
KEYWORDS       .
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1
AUTHORS        Honma,T., Yano,T., Nomoto,T. and Kozaki,S.
TITLE          Immunoassay, reagent for immunoassay, and production method of the
                same
JOURNAL        Patent: EP 1371983-A 65 17-DEC-2003;
                Canon Kabushiki Kaisha (JP)
FEATURES       source
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="binding peptide"

ORIGIN
Query Match      45.5%; Score 15; DB 6; Length 46;
Best Local Similarity 67.7%; Pred. No. 8.6e+04;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32
Db 5 CAACGTGACCGACCGCGTTTATTGATACC 35

RESULT 35
CQ006075/c      50 bp      DNA      linear      PAT 16-JAN-2004
LOCUS
DEFINITION      Sequence 4715 from Patent WO0147944.
ACCESSION      CQ006075
VERSION        CQ006075.1 GI:41012707
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS        Shimkets,R.A. and Leach,M.
TITLE          Nucleic acids containing single nucleotide polymorphisms and
                methods of use thereof
JOURNAL        Patent: WO 0147944-A 4715 05-JUL-2001;
                Curagen Corporation (US)
FEATURES       source
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Qy 2 CCACATGAGTGCACAGCGCTCTGGTGATACC 32
Db 49 CCAGCTAAGGGGCGCTGGCCACTGGTGCCACC 19
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LOCUS AX539350 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 137 from Patent WO02059142.
ACCESSION AX539350
VERSION AX539350.1 GI:25272666
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 137 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
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RESULT 37
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LOCUS AX539351 21 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 138 from Patent WO02059142.
ACCESSION AX539351
VERSION AX539351.1 GI:25272668
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Brinkmann,U., Hoffmeyer,S. and Mornhinweg,E.
TITLE Polymorphisms in the human gene for the multidrug
resistance-associated protein 1 (mrp-1) and their use in diagnostic
and therapeutic applications
JOURNAL Patent: WO 02059142-A 138 01-AUG-2002;
Epidaurus Biotechnologie AG (DE)
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Best Local Similarity 88.9%; Pred. No. 1.1e+05;
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Db 4 GCCACAGAGTGGAAAGG 21

RESULT 38
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LOCUS BD091354 30 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for detection of specific nucleotide
sequences.
ACCESSION BD091354
VERSION BD091354.1 GI:22636965

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KEYWORDS JP 2001522588-A/8.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 30)
AUTHORS Ramberg,E.R.
TITLE Methods and compositions for detection of specific nucleotide
JOURNAL Patent: JP 2001522588-A 8 20-NOV-2001;
CYGENE INC
COMMENT OS Artificial Sequence
PN JP 2001522588-A/8
PD 20-NOV-2001
PF 12-NOV-1998 JP 2000519613
PR 12-NOV-1997 US 60/065378,24-FEB-1998 US 60/075812 PR
05-MAR-1998 US 60/076872
PI ELLIOT R RAMBERG
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: primary probe FH Key
Location/Qualifiers
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Db 30 CCTGAGTAGCAAGCTATCTAGTGGTACTG 2

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DEFINITION Sequence 8 from Patent WO9909055.
ACCESSION A99000
VERSION A99000.1 GI:6781957
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Sablon,E. and Buysee,M.
TITLE INTERFERON-GAMMA-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
JOURNAL Patent: WO 9909055-A 8 25-FEB-1999;
INNOGENETICS NV (BE); SABLON ERWIN (BE)
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RESULT 40
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DEFINITION Sequence 8 from patent US 6350860.

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ACCESSION      AR195317
VERSION        AR195317.1  GI:20244754
KEYWORDS
SOURCE
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               Unknown.
REFERENCE      1 (bases 1 to 40)
               Unclassified.
AUTHORS        Buyse,M.-A. and Sablon,E.
TITLE          Interferon-gamma-binding molecules for treating septic shock,
               cachexia, immune diseases and skin disorders
JOURNAL        Patent: US 6350860-A 8 26-FEB-2002;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 23, 2004, 16:49:29 ; Search time 177.112 Seconds
(without alignments)
978.085 Million cell updates/sec

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Perfect score: 33
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Searched: 4134886 seqs, 2624710521 residues
Total number of hits satisfying chosen parameters: 3992700
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	16.4	49.7	43	8	ACA04963				ACA04963 Human sec
C 6	16.4	49.7	43	8	ACA04483				ACA04483 Human sec
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C 9	16.4	49.7	43	9	ACD30240				ACD30240 Human sec
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C 12	16.4	49.7	43	12	ADE41156				ADE41156 Human sec
C 13	16.4	49.7	43	12	ADG63591				ADG63591 Human sec
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C 26	15.4	46.7	33	9	ACD28602				ACD28602 CAT 5' ur
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C 29	15.4	46.7	33	12	ADL93443				Adl93443 Chloramph
C 30	15.4	46.7	34	3	AAZ56255				Aaz56255 pIVCAT1 c
C 31	15.4	46.7	34	3	AAZ56253				Aaz56253 CAT gene
C 32	15.4	46.7	38	3	AAZ56254				Aaz56254 CAT gene
C 33	15.4	46.7	38	3	AAZ56256				Aaz56256 pIVCAT1 c
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C 35	15.2	46.1	41	12	ADJ14522				Adj14522 Debrisoqu
C 36	15.2	46.1	41	12	ADO60821				Ado60821 Human deb
C 37	15.2	46.1	41	12	ADO60624				Ado60624 Human deb
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C 41	15	45.5	38	12	ADC01853				Adc01853 Copper ph
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C 65	14.6	44.2	40	2	AAAT85544				Aat85544 gp160 PCR
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118	14	42.4	41	12	ADH06128	ADH06128 Gene poly	c 191	13.6	41.2	44	3	AAV71887	AAV71887 Plasmid p
119	14	42.4	45	8	ABZ22715	ABZ22715 Oligonucle	c 192	13.6	41.2	44	4	AAZ09819	AAZ09819 Oligo #1
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134	13.8	41.8	23	4	AAZ06352	AAZ06352 Murine cy	c 207	13.4	40.6	22	12	ADQ80760	ADQ80760 Porcine 3
135	13.8	41.8	23	4	AAZ08723	AAZ08723 Murine cy	c 208	13.4	40.6	24	6	ABZ58569	ABZ58569 Capture o
136	13.8	41.8	25	9	ACI57908	ACI57908 Human mic	209	13.4	40.6	24	6	ABZ58568	ABZ58568 Capture o
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144	13.8	41.8	36	6	ABX02714	ABX02714 HCV hamme	217	13.4	40.6	33	2	AAQ67027	AAQ67027 3' end of
145	13.8	41.8	38	4	ABX05335	ABX05335 Human NOG	c 218	13.4	40.6	33	6	ABZ25712	ABZ25712 Human NAD
146	13.8	41.8	38	6	ACN17610	ACN17610 WNV Inozy	c 219	13.4	40.6	33	8	ABZ57491	ABZ57491 Pogo tran
147	13.8	41.8	38	6	ACN28284	ACN28284 WNV minus	c 220	13.4	40.6	33	12	ADH39833	ADH39833 Subtilisi
148	13.8	41.8	39	8	ABZ99487	ABZ99487 FGF-8 rel	c 221	13.4	40.6	34	8	ABZ24404	ABZ24404 HIV envel
149	13.8	41.8	39	8	ABZ99488	ABZ99488 FGF-8 rel	c 222	13.4	40.6	34	10	ACF79710	ACF79710 HIV-1 env
150	13.8	41.8	39	10	ADE36524	ADE36524 Anti-FGF-	223	13.4	40.6	35	6	ABR85547	ABR85547 35S promo
151	13.8	41.8	39	10	ABZ36525	ABZ36525 Anti-FGF-	c 224	13.4	40.6	37	6	ACN31006	ACN31006 WNV minus
152	13.8	41.8	41	6	ABZ45699	ABZ45699 Human ATP	c 225	13.4	40.6	37	6	ACN18972	ACN18972 WNV Zinzy
153	13.8	41.8	41	6	ABZ47899	ABZ47899 Human ATP	c 226	13.4	40.6	38	2	AAQ88041	AAQ88041 Oligo U6A
154	13.8	41.8	41	6	ABZ48034	ABZ48034 Human ATP	c 227	13.4	40.6	38	2	AAZ36439	AAZ36439 U6 specif
155	13.8	41.8	41	10	ABZ57521	ABZ57521 IGF bindi	c 228	13.4	40.6	38	8	ABZ24403	ABZ24403 HIV envel
156	13.8	41.8	41	10	ABZ57522	ABZ57522 IGF bindi	c 229	13.4	40.6	38	10	ACF79709	ACF79709 HIV-1 env
157	13.8	41.8	43	8	AAZ55658	AAZ55658 5' forwar	c 230	13.4	40.6	41	6	ABA93677	ABA93677 Human kin
158	13.8	41.8	44	10	ADB38873	ADB38873 PCR prime	c 231	13.4	40.6	41	6	ABA93677	ABA93677 Human kin
159	13.8	41.8	47	4	AAI76615	AAI76615 Human sil	232	13.4	40.6	41	6	ABZ50260	ABZ50260 Human tra
160	13.8	41.8	48	2	AAZ99204	AAZ99204 M. avium	233	13.4	40.6	41	6	ABZ43433	ABZ43433 Human tra
161	13.8	41.8	50	4	AAZ03080	AAZ03080 1466-92 P	c 234	13.4	40.6	41	6	ABZ44615	ABZ44615 Human ATP
162	13.8	41.8	50	6	ABZ05885	ABZ05885 Human leu	c 235	13.4	40.6	41	6	ABZ47083	ABZ47083 Human ATP
163	13.8	41.8	50	12	ADP93338	ADP93338 Microorga	c 236	13.4	40.6	41	11	ADP75529	ADP75529 Human ADA
164	13.6	41.2	20	2	AAZ27015	AAZ27015 Kappa fat	c 237	13.4	40.6	42	2	AAQ54958	AAQ54958 cyd-lacZ
165	13.6	41.2	20	2	AAZ95010	AAZ95010 Castor ka	c 238	13.4	40.6	49	10	ADC03175	ADC03175 Colon spe
166	13.6	41.2	20	9	ACD06830	ACD06830 Forward R	c 239	13.4	40.6	50	2	AAV81433	AAV81433 Antisense
167	13.6	41.2	20	10	ADC98371	ADC98371 ITGA08 po	240	13.4	40.6	50	2	AAZ26185	AAZ26185 Antisens

C 241	13.4	40.6	50	4	AAI76317	Aai76317 Human sil	314	13.2	40.0	40	12	ADP53987	Adp53987 Positive
242	13.4	40.6	50	6	ABZ05256	Abz05256 Human leu	315	13.2	40.0	40	12	ADP53965	Adp53965 Candida a
243	13.2	40.0	19	12	AQ62427	Aq62427 Anti-HIST	316	13.2	40.0	41	6	ABS58364	Abs58364 Hmonorphi
C 244	13.2	40.0	20	4	AAH47274	Aah47274 Nucleotid	C 317	13.2	40.0	41	6	ABZ50275	Abz50275 Human cyt
245	13.2	40.0	20	10	ADF72267	Adf72267 Human CD4	C 318	13.2	40.0	41	6	ABZ44450	Abz44450 Human cyt
246	13.2	40.0	20	10	ABZ92207	Abz92207 Human oli	C 319	13.2	40.0	41	8	ABZ57493	Abz57493 Pogo trian
C 247	13.2	40.0	20	11	ABD28437	Abd28437 R78585-de	320	13.2	40.0	42	2	AAAT93080	Aaat93080 PCR prime
C 248	13.2	40.0	21	2	AXA226635	Axa226635 PCR prime	321	13.2	40.0	42	9	ADB39065	Adb39065 Human tra
C 249	13.2	40.0	21	4	AAF96247	Aaf96245 Human gen	C 322	13.2	40.0	43	6	AAAL46486	Aaal46486 M catarrh
C 250	13.2	40.0	21	6	ABS66806	Abs66806 Human MRP	C 323	13.2	40.0	44	2	AAV74273	Aav74273 HTLV-III
251	13.2	40.0	21	6	ABS66807	Abs66807 Human MRP	C 324	13.2	40.0	44	6	ABO78093	Abq78093 HuVKF tel
252	13.2	40.0	21	8	ACF62441	Acf62441 Cancer ba	C 325	13.2	40.0	44	6	ABQ78087	Abq78087 Humanised
C 253	13.2	40.0	21	8	ACF62440	Acf62440 Cancer ba	C 326	13.2	40.0	44	6	ABK15776	Abk15776 Mutation
254	13.2	40.0	21	8	ADB21112	Adb21112 MRP1 base	C 327	13.2	40.0	44	8	ABX10686	Abx10686 Humanised
C 255	13.2	40.0	21	8	ADB21111	Adb21111 MRP1 base	C 328	13.2	40.0	44	8	ACA71602	Act71602 Humanised
C 256	13.2	40.0	21	10	ADB88200	Adb88200 Human UGT	329	13.2	40.0	44	9	ACD27913	Act27913 E' bacter
257	13.2	40.0	21	10	ADB88201	Adb88201 Human UGT	C 330	13.2	40.0	44	10	ACD13576	Actd13576 Humanised
C 258	13.2	40.0	21	10	ADB97183	Adb97183 Human MRP	C 331	13.2	40.0	44	12	ADH29128	Adh29128 Humanised
C 259	13.2	40.0	21	10	ADB97184	Adb97184 Human MRP	332	13.2	40.0	44	12	ADO26438	Ado26438 HTLV-III
260	13.2	40.0	21	10	ADB92375	Adb92375 Human MRP	333	13.2	40.0	45	2	AAQ95042	Aaq95042 Human hip
C 261	13.2	40.0	21	10	ADB92374	Adb92374 Human MRP	334	13.2	40.0	45	2	AAQ95042	Aat35990 39-1.106
262	13.2	40.0	21	12	ADO16379	Ado16379 4 synthet	335	13.2	40.0	45	3	AAA40154	Aaa40154 H. pylori
263	13.2	40.0	22	2	AAT08691	Aat08691 CRH relat	336	13.2	40.0	45	6	ABK88133	Abk88133 DNA encod
264	13.2	40.0	25	9	ACI41258	Act41258 Human mic	337	13.2	40.0	45	9	AAAL60622	Aal60622 Mouse ant
265	13.2	40.0	25	9	ACI91817	Act91817 Human mic	338	13.2	40.0	45	12	ADJ87929	Adj87929 Mouse Hef
266	13.2	40.0	25	10	ADF62961	Adf62961 Human PCC	339	13.2	40.0	47	3	AAZ68644	Aaz68644 Human map
267	13.2	40.0	25	10	ADF62958	Adf62958 Human PCC	340	13.2	40.0	47	3	AAZ68644	Aaz68644 Human map
268	13.2	40.0	25	10	ADF62959	Adf62959 Human PCC	341	13	39.4	16	2	AAZ57818	Aaz57818 PCR prime
269	13.2	40.0	25	10	ADF62960	Adf62960 Human PCC	C 342	13	39.4	17	2	AAZ57838	Aaz57838 PCR prime
270	13.2	40.0	25	10	ADF62957	Adf62957 Human PCC	C 343	13	39.4	17	10	ADH79342	Adh79342 Human pro
271	13.2	40.0	25	10	ADF62955	Adf62955 Human PCC	344	13	39.4	20	2	AAZ79780	Aaz79780 PCR prime
272	13.2	40.0	25	10	ADF62962	Adf62962 Human PCC	345	13	39.4	20	2	ADF32512	Adf32512 Chlamydia
273	13.2	40.0	25	10	ADF62956	Adf62956 Human PCC	C 346	13	39.4	21	12	ADQ78336	Adq78336 Bovine po
274	13.2	40.0	25	12	ADP16940	Adp16940 Renal cel	C 347	13	39.4	22	2	AAQ68521	Aaq68521 Bacillus
C 275	13.2	40.0	28	10	ADD01566	Ado01566 Human Fc	C 348	13	39.4	22	6	AAAT09116	Aat09116 crytB gen
C 276	13.2	40.0	29	12	ADE52184	Ade52184 Rhesus mo	349	13	39.4	24	6	ABX97283	Abx97283 Human NOV
C 277	13.2	40.0	30	3	AAA64835	Aaa64835 PCR prime	350	13	39.4	24	12	ADN62185	Adn62185 Human NOV
C 278	13.2	40.0	30	3	AAA64836	Aaa64836 PCR prime	C 351	13	39.4	25	3	AAA68806	Aaa68806 Bacteriop
C 279	13.2	40.0	30	5	AAAD16849	Aad16849 Mutagenic	C 352	13	39.4	25	9	ACH64741	Ach64741 DNA targe
280	13.2	40.0	30	5	ADJ16848	Adj16848 Mutagenic	353	13	39.4	25	10	ADF65284	Adf65284 Human PCC
C 281	13.2	40.0	32	12	ADJ93354	Adj93354 Bptase 3	354	13	39.4	25	10	ADF65287	Adf65287 Human PCC
C 282	13.2	40.0	33	2	AT42740	Aat42740 Human FGF	355	13	39.4	25	10	ADF65285	Adf65285 Human PCC
283	13.2	40.0	33	2	AAV23987	Aav23987 PCR prime	356	13	39.4	25	10	ADF65286	Adf65286 Human PCC
284	13.2	40.0	33	3	AAA75025	Aaa75025 PCR prime	357	13	39.4	25	10	ADF65288	Adf65288 Human PCC
285	13.2	40.0	33	3	AAA75029	Aaa75029 PCR prime	C 358	13	39.4	26	6	ABS78782	Abs78782 Human NOV
286	13.2	40.0	33	3	AAA75027	Aaa75027 PCR prime	C 359	13	39.4	26	10	ADD28531	Add28531 Escherich
287	13.2	40.0	33	5	AAAC91273	Aac91273 Human FGF	C 360	13	39.4	26	10	ADD28530	Add28530 Escherich
288	13.2	40.0	33	5	AAAC91271	Aac91271 Human FGF	361	13	39.4	27	3	AAZ62085	Aaz62085 Hammerhea
289	13.2	40.0	33	5	AAAC91269	Aac91269 Human FGF	362	13	39.4	27	3	AAZ62334	Aaz62334 Hammerhea
290	13.2	40.0	35	2	AAAT32397	Aat32397 PCR prime	363	13	39.4	29	2	AAZ23442	Aaz23442 Human p75
C 291	13.2	40.0	35	8	ABZ24402	Abz24402 HIV envel	364	13	39.4	30	2	AAZ24471	Aaz24471 Bovine my
C 292	13.2	40.0	35	10	ACF79708	Acf79708 HIV-1 env	365	13	39.4	33	3	AAA05658	Aaa05658 Oligonuc
C 293	13.2	40.0	38	4	AHH96412	Ahh96412 Human Chk	C 366	13	39.4	33	3	AAAS7745	Aas7745 PCR prime
294	13.2	40.0	38	4	ABK05936	Abk05936 Human NOG	C 367	13	39.4	35	3	AAAC70083	Aac70083 TGF-beta
295	13.2	40.0	38	4	ABL47859	AbL47859 Human GRI	C 368	13	39.4	35	10	ADH71103	Adh71103 Infectiou
C 296	13.2	40.0	38	6	ABK20266	Abk20266 Human ERG	C 369	13	39.4	35	10	ADH62859	Adh62859 Infectiou
297	13.2	40.0	38	6	ABK20299	Abk20299 Human ERG	370	13	39.4	37	6	ACN19632	Acn19632 WNV Zinz
C 298	13.2	40.0	38	6	ACN15983	Actn15983 WNV Hamme	371	13	39.4	38	3	AAZ39308	Aaz39308 Human sta
C 299	13.2	40.0	38	6	ACN29981	Actn29981 WNV minus	372	13	39.4	38	6	ABS52995	Abs52995 Human sta
C 300	13.2	40.0	38	6	ACN15467	Actn15467 WNV Hamme	373	13	39.4	38	10	ADI30572	Adi30572 Human sta
C 301	13.2	40.0	38	6	ACN30138	Actn30138 WNV minus	374	13	39.4	38	10	AAAS1856	Aas1856 bYF-Cyr-L
302	13.2	40.0	38	6	ACN26240	Actn26240 WNV minus	C 375	13	39.4	39	2	AAV72036	Aav72036 Human CPG
C 303	13.2	40.0	38	6	ACD50802	Actd50802 HBV hamme	C 376	13	39.4	41	2	AAV47778	Aav47778 Maize pol
304	13.2	40.0	38	10	ADB67710	Adb67710 HIV-1 nef	C 377	13	39.4	41	2	AAV47777	Aav47777 Maize pol
C 305	13.2	40.0	38	11	ADL55798	Adl55798 Human PKR	C 378	13	39.4	41	4	AAI71685	Aai71685 Human ATP
C 306	13.2	40.0	38	11	ADL55915	Adl55915 Human PKR	C 379	13	39.4	41	4	AAI71684	Aai71684 Human ATP
307	13.2	40.0	38	11	ADM55144	Adm55144 Zinzyme t	C 380	13	39.4	41	6	ABZ46650	Abz46650 Human ATP
308	13.2	40.0	38	12	ADQ38174	Adq38174 HIV envel	381	13	39.4	41	6	ABZ49877	Abz49877 Human HNK
309	13.2	40.0	38	12	ADO38206	Ado38206 HIV envel	382	13	39.4	41	6	ABZ43693	Abz43693 Human HNK
310	13.2	40.0	38	12	ADO38095	Ado38095 HIV envel	383	13	39.4	41	9	ADA01593	Ada01593 Mouse car
311	13.2	40.0	38	12	ADO38063	Ado38063 HIV envel	384	13	39.4	41	10	ADB71332	Adb71332 Mouse car
312	13.2	40.0	39	2	AAT85562	Aat85562 HIV-1 LAI	C 385	13	39.4	42	2	AAT13811	Aat13811 Murine VR
C 313	13.2	40.0	40	8	ABV77144	Abv77144 Reverse p	386	13	39.4	42	2	AAT86880	Aat86880 Plasmid p

533	12.6	38.2	36	6	ABX02368	Abx02368 HCV hamme	606	12.6	38.2	50	2	AA17494	Aax17494 Test sequ
534	12.6	38.2	36	6	ABX02002	Abx02002 HCV hamme	607	12.6	38.2	50	4	AA130844	Aa130844 Human SNP
535	12.6	38.2	36	6	AAD35819	Aad35819 Human MIS	608	12.6	38.2	50	4	AA128905	Aa128905 Human SNP
C 536	12.6	38.2	37	10	ADC59339	Adc59339 Cell deat	C 609	12.6	38.2	50	6	AA2020297	Aa2020297 Human Ig
C 537	12.6	38.2	37	8	AA151603	Aa151603 Human jun	C 610	12.6	38.2	50	6	AA2020320	Aa2020320 Human svn
538	12.6	38.2	38	2	AA641192	Aa641192 Rabbit et	611	12.6	38.2	50	6	ABK82985	Abk82985 DNA bindi
539	12.6	38.2	38	4	AAX66852	Aax66852 Human Chk	C 612	12.6	38.2	50	6	AB208063	Ab208063 Human leu
540	12.6	38.2	38	4	ABK04957	Abk04957 Human NOG	C 613	12.6	38.2	50	6	AB202278	Ab202278 Human leu
541	12.6	38.2	38	6	ABK19581	Abk19581 Human ERG	C 614	12.6	38.2	50	6	AB204108	Ab204108 Human leu
542	12.6	38.2	38	6	ABK20506	Abk20506 Human ERG	C 615	12.6	38.2	50	6	AB204909	Ab204909 Human leu
543	12.6	38.2	38	6	ACN17241	Acn17241 WNV Inozy	616	12.6	38.2	50	6	AB203177	Ab203177 Human leu
544	12.6	38.2	38	6	ACN18571	Acn18571 WNV Inozy	C 617	12.6	38.2	50	8	ACCT1883	Acc71883 Synthetic
545	12.6	38.2	38	6	ACN29921	Acn29921 WNV minus	618	12.6	38.2	50	8	ACCT1888	Acc71888 Synthetic
546	12.6	38.2	38	6	ACN26039	Acn26039 WNV minus	619	12.6	38.2	50	12	ADE80524	Ade80524 Duplex oi
547	12.6	38.2	38	6	ACN26195	Acn26195 WNV minus	620	12.4	37.6	18	2	AA336717	Aax336717 PCR prime
548	12.6	38.2	38	6	ACN18465	Acn18465 WNV Inozy	621	12.4	37.6	18	4	AAC66690	Aac66690 Human PDE
549	12.6	38.2	38	6	ACN17114	Acn17114 WNV Inozy	622	12.4	37.6	18	10	AAD59995	Aad59995 Human PDE
550	12.6	38.2	38	8	ACA07006	ACA07006 Necrosis	623	12.4	37.6	18	10	ADM34026	Adm34026 Human PDE
551	12.6	38.2	38	8	ACA07495	ACA07495 Necrosis	C 624	12.4	37.6	18	12	ADP75385	Adp75385 Human NRG
552	12.6	38.2	38	8	ACD50819	ACD50819 HBV hamme	625	12.4	37.6	20	11	ADP75385	Adp75385 Human NRG
553	12.6	38.2	38	8	ACD52232	ACD52232 HBV inozy	C 626	12.4	37.6	21	3	AAA73211	Aaa73211 Cyclooxvg
554	12.6	38.2	38	11	ADL75361	Adl75361 Human PTG	C 627	12.4	37.6	22	5	AA433612	Aa433612 Corneodes
555	12.6	38.2	38	11	ADL75364	Adl75364 Human PTG	C 628	12.4	37.6	22	6	ABQ74976	Abq74976 Chloromph
556	12.6	38.2	38	11	ADL5581	Adl5581 Human PKR	C 629	12.4	37.6	23	2	AAQ42227	Aaq42227 PCR prime
557	12.6	38.2	38	12	ADM61336	Adm61336 Hepatitis	630	12.4	37.6	23	2	ADG78004	Adg78004 Canine di
558	12.6	38.2	38	12	ADM60642	Adm60642 Hepatitis	631	12.4	37.6	23	6	AAS97807	Aas97807 Murine SA
559	12.6	38.2	39	2	AAQ99901	Aaq99901 Humanized	C 632	12.4	37.6	23	12	ADM16147	Adm16147 Murine SA
560	12.6	38.2	39	2	AAT74767	Aat74767 Alpha-4 i	633	12.4	37.6	24	4	AAZ98411	Aaz98411 Rat GAPDH
561	12.6	38.2	39	2	AAV85722	Aav85722 LRP5 exon	C 634	12.4	37.6	24	6	ABK40750	Abk40750 Rat GAPDH
C 562	12.6	38.2	39	3	AA61063	AA61063 SEN virus	C 635	12.4	37.6	24	6	ABK40750	Abk40750 Rat GAPDH
563	12.6	38.2	39	4	AAF86605	Aaf86605 PCR prime	C 636	12.4	37.6	25	2	AAT39525	Aat39525 Flea calr
564	12.6	38.2	40	2	AA764085	Aa764085 Human BMP	C 637	12.4	37.6	25	6	ABK40746	Abk40746 Rat GAPDH
565	12.6	38.2	40	3	AA295749	Aa295749 Human bon	C 638	12.4	37.6	25	9	ACK13358	Ack13358 Human mic
C 566	12.6	38.2	40	10	AAZ60412	Aaz60412 R-3D' rev	C 639	12.4	37.6	25	9	ACI54111	Act54111 Human mic
C 567	12.6	38.2	40	12	ADI34581	Adi34581 Human ESM	640	12.4	37.6	25	9	ACI20712	Act20712 Human mic
C 568	12.6	38.2	41	4	AA168175	AA168175 Human mol	641	12.4	37.6	25	9	ACI48136	Act48136 Human mic
C 569	12.6	38.2	41	6	AAK47591	AAK47591 Human tro	642	12.4	37.6	25	9	ACI88530	Act88530 Human mic
C 570	12.6	38.2	41	6	AB04790	Ab04790 Ribosomal	643	12.4	37.6	25	9	ACI20713	Act20713 Human mic
C 571	12.6	38.2	41	6	AB248987	Ab248987 Human AID	C 644	12.4	37.6	25	9	ACI22507	Act22507 Human mic
C 572	12.6	38.2	41	6	AB245136	Ab245136 Human ATP	C 645	12.4	37.6	25	9	ACI46878	Act46878 Human mic
C 573	12.6	38.2	41	6	AB246463	Ab246463 Human AID	C 646	12.4	37.6	25	9	ACI50692	Act50692 Human mic
C 574	12.6	38.2	41	6	AB247731	Ab247731 Human ATP	647	12.4	37.6	25	9	ACK01458	Act01458 Human mic
C 575	12.6	38.2	41	11	ADP75599	Adp75599 Human ADA	C 648	12.4	37.6	25	9	ACH60776	Act60776 DNA targe
C 576	12.6	38.2	41	12	ADK17891	Adk17891 Cytochrom	C 649	12.4	37.6	25	9	ACH51077	Act51077 DNA targe
C 577	12.6	38.2	42	2	ABX17658	Abx17658 Modified	C 650	12.4	37.6	25	10	ADJ58462	Adj58462 Primer #2
C 578	12.6	38.2	42	2	ABX17658	Abx17658 Modified	651	12.4	37.6	25	12	ADJ58462	Adj58462 Primer #2
C 579	12.6	38.2	42	12	ADQ76049	Adq76049 TBEI in f	652	12.4	37.6	26	2	AAQ56221	Aaq56221 pX amplif
C 580	12.6	38.2	44	2	AAT86307	Aat86307 Primer ol	653	12.4	37.6	26	2	AAT08932	Aat08932 Forward p
C 581	12.6	38.2	45	2	AQ04944	Aq04944 Oligonuci	654	12.4	37.6	26	2	AAV66288	Aav66288 5' PCR pr
C 582	12.6	38.2	45	2	AAV27926	Aav27926 rGALR3 pr	655	12.4	37.6	26	2	AAV56251	Aav56251 HCV forwa
C 583	12.6	38.2	45	6	AAZ35869	Aaz35869 Rat galan	656	12.4	37.6	26	2	AAV16479	Aav16479 PCR prime
C 584	12.6	38.2	45	9	ACD28979	Act28979 Human gal	657	12.4	37.6	26	2	AAZ02526	Aaz02526 US5856134
C 585	12.6	38.2	45	10	AAZ61145	Aaz61145 Rat galan	658	12.4	37.6	26	2	AAZ82222	Aaz82222 Spodopter
C 586	12.6	38.2	47	2	AAZ52568	Aaz52568 Human gen	659	12.4	37.6	26	2	ABK65977	Abk65977 Human gen
C 587	12.6	38.2	47	3	AAZ67153	Aaz67153 Human map	C 660	12.4	37.6	26	12	ADP11332	Adp11332 Taqman pr
C 588	12.6	38.2	47	4	AAZ67153	Aaz67153 Coxsackie	C 661	12.4	37.6	27	12	ADG31438	Adg31438 PCR prime
C 589	12.6	38.2	47	4	AAZ25535	Aaz25535 Multiplex	C 662	12.4	37.6	27	12	ADK1849	Adk1849 Human MN
C 590	12.6	38.2	47	4	AAZ25535	Aaz25535 Multiplex	663	12.4	37.6	29	2	AAV00585	Aav00585 PCR prime
C 591	12.6	38.2	48	2	AAQ22423	Aaq22423 Human v k	664	12.4	37.6	29	2	AAT84969	Aat84969 PCR prime
C 592	12.6	38.2	48	2	AAQ50327	Aaq50327 Human kap	665	12.4	37.6	29	2	AAV17632	Aav17632 Homo sapi
C 593	12.6	38.2	48	2	AAQ44193	Aaq44193 Probe oli	666	12.4	37.6	29	2	AAV17632	Aav17632 Homo sapi
C 594	12.6	38.2	48	2	AAT37184	Aat37184 Human var	667	12.4	37.6	29	2	AAV17632	Aav17632 Homo sapi
C 595	12.6	38.2	48	2	AAT37281	Aat37281 Human ant	668	12.4	37.6	29	2	AAV17632	Aav17632 Homo sapi
C 596	12.6	38.2	48	2	AAV12576	Aav12576 Probe oli	669	12.4	37.6	29	2	AAV92303	Aav92303 Human A-R
C 597	12.6	38.2	48	2	AAV73479	Aav73479 Human kap	670	12.4	37.6	29	2	AAV92303	Aav92303 Human A-R
C 598	12.6	38.2	48	2	AAV70526	Aav70526 Human imm	671	12.4	37.6	29	3	AAA03891	Aaa03891 Polymorph
C 599	12.6	38.2	48	2	AAV38172	Aav38172 Probe oli	672	12.4	37.6	29	3	AAA08068	Aaa08068 Human arg
C 600	12.6	38.2	48	2	AAZ06048	Aaz06048 Human kap	673	12.4	37.6	29	3	AAAF01215	Aaf01215 Hammerhea
C 601	12.6	38.2	48	2	AAZ21964	Aaz21964 Probe spe	C 674	12.4	37.6	29	6	ABA00439	Aba00439 Human arg
C 602	12.6	38.2	48	2	AAZ21973	Aaz21973 Probe spe	675	12.4	37.6	29	6	ABA00439	Aba00439 Human arg
C 603	12.6	38.2	50	2	AAQ69744	Aaq69744 Herpes si	676	12.4	37.6	29	6	AAI72345	Aai72345 Human arg
C 604	12.6	38.2	50	2	AAZ64206	Aaz64206 Herpes si	C 677	12.4	37.6	29	6	ADA47346	Ada47346 Mutagenic
C 605	12.6	38.2	50	2	AAZ31138	Aaz31138 RNA ligan	C 678	12.4	37.6	29	9	ACA62507	Aca62507 Human SMN

679	12.4	37.6	29	12	ADN35130	Adn35130 Primer of	752	12.4	37.6	50	5	ABL01018	Ab101018 Human SNP
680	12.4	37.6	29	12	ADP88461	Adp88461 Antibody	c 753	12.4	37.6	50	6	ABZ02384	Abz02384 Human leu
681	12.4	37.6	30	6	ABS55396	Abs55396 Arabidops	754	12.4	37.6	50	6	ABZ01228	Abz01228 Human leu
682	12.4	37.6	30	10	AAD36857	Aad36857 Chloramph	755	12.2	37.0	17	8	ACD55737	AcD55737 HBV amber
683	12.4	37.6	30	12	ADO04218	Ado04218 Primer P1	756	12.2	37.0	17	10	ADP62211	Adp62211 Human PCC
684	12.4	37.6	31	8	ABX08328	Abx08328 Forward R	757	12.2	37.0	17	10	ADF62212	Adf62212 Human PCC
685	12.4	37.6	31	11	ADM79775	Adm79775 Thermus t	758	12.2	37.0	17	12	ADM60271	Adm60271 Hepatitis
686	12.4	37.6	32	2	AAV54297	Aav54297 Primer JW	759	12.2	37.0	18	2	AAX36724	Aax36724 PCR prime
687	12.4	37.6	32	2	AAX55379	Aax55379 Soluble s	760	12.2	37.0	18	2	AAX36724	Aax36724 PCR prime
688	12.4	37.6	32	9	ADA73934	Ada73934 Carcinoma	761	12.2	37.0	18	4	AAA92634	Aaa92634 Antisense
689	12.4	37.6	32	9	ADA02408	Ada02408 Mouse car	762	12.2	37.0	18	4	AAC66697	Aac66697 Human PDE
690	12.4	37.6	32	10	ADB72147	Adb72147 Mouse car	763	12.2	37.0	18	10	AAAD60002	AAa60002 Human PB6
691	12.4	37.6	32	10	ADK12384	Adk12384 Cytochrom	764	12.2	37.0	19	12	ADM34033	Adm34033 Human pho
692	12.4	37.6	33	2	AAA33976	Aaa33976 Probe for	765	12.2	37.0	20	3	AAA72094	AAA72094 Anti-cort
693	12.4	37.6	33	3	AAAG60543	AAa60543 Human TIE	766	12.2	37.0	20	2	AAT05687	Aat05687 HB15 3' I
694	12.4	37.6	33	4	AAAS02926	AAa02926 PCR prime	767	12.2	37.0	20	3	AAZ46684	Aaz46684 Blast dis
695	12.4	37.6	33	4	AAI68121	AAi68121 Human gro	768	12.2	37.0	20	3	AAZ46684	Aaz46684 Blast dis
696	12.4	37.6	33	4	AAC97393	Aac97393 Human PRO	769	12.2	37.0	20	6	ABK90234	Abk90234 Dog multi
697	12.4	37.6	33	4	AAC90584	Aac90584 Human PRO	770	12.2	37.0	20	6	AAI38136	AAi38136 HIV-1 RNA
698	12.4	37.6	33	6	ABL58581	Ab158581 Oligonuc1	771	12.2	37.0	20	9	ACD06833	AcD06833 Forward R
699	12.4	37.6	33	6	ABQ79779	Abq79779 Human TIE	772	12.2	37.0	20	10	ABZ91513	Abz91513 Human oli
700	12.4	37.6	33	6	ADQ32089	Adq32089 Human TIE	773	12.2	37.0	20	10	ABZ91513	Abz91513 Human oli
701	12.4	37.6	33	9	ACA62660	ACA62660 TIE ligan	774	12.2	37.0	20	11	ABD27743	Abd27743 AA102454-
702	12.4	37.6	33	10	ADI33461	Adi33461 DNA oligo	775	12.2	37.0	20	11	ABD27743	Abd27743 AA102454-
703	12.4	37.6	33	10	ABX13830	Abx13830 Human TIE	776	12.2	37.0	20	11	ABD31942	Abd31942 Human PDE
704	12.4	37.6	33	10	ABZ83477	Abz83477 Toxicolog	777	12.2	37.0	20	12	ADH44489	Adh44489 Extracell
705	12.4	37.6	33	12	ADP84074	Adp84074 Small nuc	778	12.2	37.0	20	12	ADJ32665	Adj32665 Human ERK
706	12.4	37.6	34	2	AAAT00568	AAa00568 Hemagglut	779	12.2	37.0	20	12	ADJ32632	Adj32632 Human ERK
707	12.4	37.6	34	12	ADP67064	Adp67064 TGR5 CDNA	780	12.2	37.0	20	12	ADJ32632	Adj32632 Human ERK
708	12.4	37.6	36	3	AAAS35700	AAa35700 Permutatein	781	12.2	37.0	20	12	ADO46283	Ado46283 Human oli
709	12.4	37.6	36	6	ABK85548	Abk85548 35S promo	782	12.2	37.0	20	12	ADO53280	Ado53280 Farnesoid
710	12.4	37.6	36	12	ADQ25971	Adq25971 Method of	783	12.2	37.0	20	12	ADO54162	Ado54162 Farnesoid
711	12.4	37.6	36	12	ADQ25971	Adq25971 Method of	784	12.2	37.0	20	12	ADO53113	Ado53113 Farnesoid
712	12.4	37.6	36	12	ADQ25966	Adq25966 Method of	785	12.2	37.0	20	12	ADO54244	Ado54244 Farnesoid
713	12.4	37.6	36	12	ADQ25983	Adq25983 Method of	786	12.2	37.0	20	12	ADN31407	Adn31407 Human for
714	12.4	37.6	37	3	AAAC66121	Aac66121 PCR prime	787	12.2	37.0	20	12	ADP85767	Adp85767 Mitochond
715	12.4	37.6	37	4	AAH91231	Aah91231 Human inf	788	12.2	37.0	20	12	ADP85843	Adp85843 Mitochond
716	12.4	37.6	37	6	ACN31163	Acn31163 WNV minus	789	12.2	37.0	21	4	AAF96868	Aaf96868 Human gen
717	12.4	37.6	37	6	ACN19340	Acn19340 WNV Zinzv	790	12.2	37.0	22	2	AAV72810	Aav72810 Trypoptoha
718	12.4	37.6	37	6	ACN19683	Acn19683 WNV Zinzv	791	12.2	37.0	22	3	AAC65353	Aac65353 Human TPO
719	12.4	37.6	38	6	AAAL45275	AAa45275 Human pap	792	12.2	37.0	22	6	ABL31906	Ab131906 Human CYP
720	12.4	37.6	38	10	ADH79198	Adh79198 Mallard d	793	12.2	37.0	22	10	ABZ99041	Abz99041 Human PDE
721	12.4	37.6	39	2	AAQ22111	Aaq22111 S2 chimr	794	12.2	37.0	22	11	ABD32072	Abd32072 Human PDE
722	12.4	37.6	39	4	AAAS00942	Aas00942 Beetle lu	795	12.2	37.0	22	12	ADK95817	Adk95817 Primer of
723	12.4	37.6	39	5	AAAF28341	Aaf28341 eryAI gen	796	12.2	37.0	22	12	ADJ61300	Adj61300 Oligonuc1
724	12.4	37.6	39	10	ADG79066	Adg79066 Schizophr	797	12.2	37.0	22	12	ADJ60924	Adj60924 Oligonuc1
725	12.4	37.6	39	12	ADL60999	Adl60999 Human org	798	12.2	37.0	22	12	ADO46413	Ado46413 Human oli
726	12.4	37.6	40	3	AAAS38886	Aaa38886 PCR prime	799	12.2	37.0	22	12	ADO46690	Ado46690 Human oli
727	12.4	37.6	40	3	ADE31881	Ade31881 Surfactin	800	12.2	37.0	23	2	AAQ32567	Aaq32567 HCV NS4-N
728	12.4	37.6	40	3	AAAC66119	Aac66119 PCR prime	801	12.2	37.0	23	2	AAQ32567	Aaq32567 HCV NS4-N
729	12.4	37.6	41	3	AAAC66119	Aac66119 PCR prime	802	12.2	37.0	23	2	AAQ32567	Aaq32567 HCV NS4-N
730	12.4	37.6	41	6	ABA95874	AbA95874 Human dih	803	12.2	37.0	23	10	ADB67778	Adb67778 HIV-1 nef
731	12.4	37.6	41	10	ACC71672	Acc71672 Human mac	804	12.2	37.0	23	12	ADO38170	Ado38170 HIV envel
732	12.4	37.6	41	12	ADK17689	Adk17689 Cytochrom	805	12.2	37.0	24	6	ABQ02757	Abq02757 Oligonuc1
733	12.4	37.6	41	12	ADK17790	Adk17790 Cytochrom	806	12.2	37.0	24	6	ABQ09453	Abq09453 Oligonuc1
734	12.4	37.6	42	3	AAAC66117	Aac66117 PCR prime	807	12.2	37.0	24	6	ABQ09412	Abq09412 Oligonuc1
735	12.4	37.6	42	4	AAAF31523	Aaf31523 Oligonuc1	808	12.2	37.0	24	6	ABT03812	Abt03812 Human TRA
736	12.4	37.6	43	6	ABQ74991	Abq74991 Chloramph	809	12.2	37.0	25	2	AAAX77708	Aax77708 Murine Zc
737	12.4	37.6	43	6	ABZ27922	Abz27922 Candida e	810	12.2	37.0	25	6	ABNO4854	Abn04854 Human GDM
738	12.4	37.6	43	12	ADJ933004	Adj933004 Chrelin-b	811	12.2	37.0	25	6	ABN15122	Abn15122 Human GDM
739	12.4	37.6	44	8	ABZ09612	Abz09612 Human oli	812	12.2	37.0	25	6	ABN15122	Abn15122 Human GDM
740	12.4	37.6	44	10	ABZ79065	Abz79065 Tumour su	813	12.2	37.0	25	8	ADB03871	Adb03871 Human MD2
741	12.4	37.6	45	2	AAQ94195	Aaq94195 Transmemb	814	12.2	37.0	25	8	ADB03870	Adb03870 Human MD2
742	12.4	37.6	45	3	AAAS2168	Aaa52168 Hemophill	815	12.2	37.0	25	9	ACK19992	Ack19992 Human mic
743	12.4	37.6	46	8	ACFI19116	Acfi19116 Tumour ce	816	12.2	37.0	25	9	ACI29518	Act29518 Human mic
744	12.4	37.6	46	8	ABV76178	Abv76178 Chloramph	817	12.2	37.0	25	9	ACI12010	Act12010 Human mic
745	12.4	37.6	46	10	ADC84939	Adc84939 MCP-7 bre	818	12.2	37.0	25	9	ACI97718	Act97718 Human mic
746	12.4	37.6	49	12	ADJ93018	Adj93018 Chrelin-b	819	12.2	37.0	25	9	ACI35963	Act35963 Human mic
747	12.4	37.6	50	2	AAAT40902	Aat40902 HIV neutr	820	12.2	37.0	25	9	ACK00981	Ack00981 Human mic
748	12.4	37.6	50	4	AAAL34256	AAa34256 Human SNP	821	12.2	37.0	25	9	ACI31493	Act31493 Human mic
749	12.4	37.6	50	4	AAAL33572	AAa33572 Human SNP	822	12.2	37.0	25	9	ACK08351	Ack08351 Human mic
750	12.4	37.6	50	4	AAAD06099	AAa06099 Drosophill	823	12.2	37.0	25	9	ACI49017	Act49017 Human mic
751	12.4	37.6	50	4	AAH25964	Aah25964 Rice geno	824	12.2	37.0	25	9	ACI99434	Act99434 Human mic

825	12.2	37.0	25	9	ACI24975	Ac124975 Human mic	c 898	12.2	37.0	37	2	AAQ49810	AaQ49810 bGH gene
c 826	12.2	37.0	25	9	ACI35733	Ac135733 Human mic	c 899	12.2	37.0	37	2	AAV16745	AaV16745 Human Wnt
c 827	12.2	37.0	25	9	ACI23708	Ac123708 Human mic	c 900	12.2	37.0	38	2	AAV16745	AaV16745 Human Wnt
828	12.2	37.0	25	9	ACF05177	AcF05177 Murine in	c 901	12.2	37.0	38	2	AAV64134	AaV64134 Rabbit st
829	12.2	37.0	25	10	ADP61837	AdP61837 RACE PCR	c 902	12.2	37.0	38	2	AAV36630	AaV36630 Nucleotid
830	12.2	37.0	25	10	ADP62954	AdP62954 Human PCC	c 903	12.2	37.0	38	4	ABK04859	AbK04859 Human NOG
831	12.2	37.0	25	10	ADG62963	AdG62963 Human PCC	c 904	12.2	37.0	38	4	ABK03975	AbK03975 Human NOG
832	12.2	37.0	25	10	ADG64708	AdG64708 Mouse Zcy	c 905	12.2	37.0	38	6	ABK20298	AbK20298 Human ERG
c 833	12.2	37.0	26	2	AAQ06941	AaQ06941 MMY9bis n	c 906	12.2	37.0	38	6	ABK20489	AbK20489 Human ERG
c 834	12.2	37.0	26	2	AAQ06941	AaQ06941 Human or	c 907	12.2	37.0	38	6	ABK19636	AbK19636 Human ERG
c 835	12.2	37.0	26	3	AAQ70025	AaQ70025 VEGF-bind	c 908	12.2	37.0	38	6	ABK20203	AbK20203 Human ERG
c 836	12.2	37.0	26	6	ABK66442	AbK66442 Human gen	c 909	12.2	37.0	38	6	ABK19657	AbK19657 Human ERG
c 837	12.2	37.0	26	10	ADL52278	AdL52278 Intestina	c 910	12.2	37.0	38	6	ABK20150	AbK20150 Human ERG
838	12.2	37.0	27	2	AAQ01814	AaQ01814 H. medici	c 911	12.2	37.0	38	6	ABK21124	AbK21124 Human ERG
839	12.2	37.0	27	2	AAQ32395	AaQ32395 Ab2 varia	c 912	12.2	37.0	38	6	ABK57837	AbK57837 Human CIC
840	12.2	37.0	27	4	AAV55661	AaV55661 Probe for	c 913	12.2	37.0	38	6	ABK58588	AbK58588 Human CIC
841	12.2	37.0	27	4	AAQ04128	AaQ04128 Oligomer	c 914	12.2	37.0	38	6	ACN15570	AcN15570 WNV Hamme
842	12.2	37.0	27	9	ACC84821	AcC84821 Nucleotid	c 915	12.2	37.0	38	6	ACN18239	AcN18239 WNV Inozy
843	12.2	37.0	27	12	ADO39677	AdO39677 Human SE5	c 916	12.2	37.0	38	6	ACN17385	AcN17385 WNV Inozy
844	12.2	37.0	28	3	AAQ97203	AaQ97203 NIM1 homo	c 917	12.2	37.0	38	6	ACN18693	AcN18693 WNV Inozy
845	12.2	37.0	29	2	AAAL8206	AaA18206 Human TIE	c 918	12.2	37.0	38	6	ACN16329	AcN16329 WNV Hamme
c 846	12.2	37.0	29	2	AAAL7830	AaA17830 Human TIE	c 919	12.2	37.0	38	6	ACN17911	AcN17911 WNV Inozy
847	12.2	37.0	29	2	AAV92256	AaV92256 Human A-R	c 920	12.2	37.0	38	6	ACN18270	AcN18270 WNV Inozy
848	12.2	37.0	29	2	AAV91650	AaV91650 Human C-r	c 921	12.2	37.0	38	6	ACN18454	AcN18454 WNV Hamme
c 849	12.2	37.0	29	2	AAV91722	AaV91722 Human C-r	c 922	12.2	37.0	38	6	ACN16256	AcN16256 WNV Hamme
c 850	12.2	37.0	29	3	AAA23863	AaA23863 Oestrogen	c 923	12.2	37.0	38	6	ACN26716	AcN26716 WNV Inozy
851	12.2	37.0	29	3	AAA24661	AaA24661 Oestrogen	c 924	12.2	37.0	38	6	ACN27005	AcN27005 WNV minus
852	12.2	37.0	29	3	AAA24252	AaA24252 Oestrogen	c 925	12.2	37.0	38	8	ACD50898	AcD50898 HBV hamme
c 853	12.2	37.0	29	3	AAA23595	AaA23595 Oestrogen	c 926	12.2	37.0	38	8	ACD51221	AcD51221 HBV hamme
c 854	12.2	37.0	29	3	AAFO1077	AaF01077 Hammerhea	c 927	12.2	37.0	38	8	ACD51221	AcD51221 HBV hamme
c 855	12.2	37.0	29	3	AAFO4988	AaF04988 Hammerhea	c 928	12.2	37.0	38	10	ADC64096	AdC64096 Polyhydro
c 856	12.2	37.0	29	3	AAFO3432	AaF03432 Hammerhea	c 929	12.2	37.0	38	10	ADL13543	AdL13543 PPARD, Ba
c 857	12.2	37.0	29	3	AAFO1007	AaF01007 Hammerhea	c 930	12.2	37.0	38	11	ADL75339	AdL75339 Human PKR
c 858	12.2	37.0	29	3	AAFO3880	AaF03880 Hammerhea	c 931	12.2	37.0	38	11	ADL56462	AdL56462 Human PKR
c 859	12.2	37.0	29	5	AAFO8055	AaF08055 5' and 3'	c 932	12.2	37.0	38	11	ADL52061	AdL52061 Human NOG
c 860	12.2	37.0	29	6	ABL58395	AbL58395 RSV F env	c 933	12.2	37.0	38	12	ADG01861	AdG01861 Carbon bl
c 861	12.2	37.0	30	2	AAAT42490	AaT42490 Primer fo	c 934	12.2	37.0	38	12	ADM60670	AdM60670 Hepatitis
c 862	12.2	37.0	30	2	AAV02339	AaV02339 Intimin e	c 935	12.2	37.0	39	12	ADM60840	AdM60840 Hepatitis
c 863	12.2	37.0	30	2	AAV09922	AaV09922 Primer MW	c 936	12.2	37.0	39	12	AAK98903	AaK98903 PCR prime
864	12.2	37.0	30	2	AAV71964	AaV71964 Thymidyla	c 937	12.2	37.0	40	2	AAAT92662	AaT92662 BNLFI gen
865	12.2	37.0	30	4	AAI66592	AaI66592 Human ske	c 938	12.2	37.0	40	2	AAK88920	AaK88920 Circular
866	12.2	37.0	30	4	AAI66592	AaI66592 Human ske	c 939	12.2	37.0	40	2	AAK88920	AaK88920 Circular
867	12.2	37.0	30	10	ADN36656	AdN36656 Nef probe	c 940	12.2	37.0	40	3	AAAC68838	AaA68838 Antibiota
c 868	12.2	37.0	30	12	ADN11093	AdN11093 HIV-1 nef	c 941	12.2	37.0	40	6	ABA98196	AbA98196 Oligonuc1
c 869	12.2	37.0	31	2	AAV14367	AaV14367 Primer M2	c 942	12.2	37.0	40	6	ABN86041	AbN86041 Oligonuc1
c 870	12.2	37.0	31	4	AAI30357	AaI30357 Human sin	c 943	12.2	37.0	40	6	ABL99219	AbL99219 Green/red
871	12.2	37.0	31	4	AAI31211	AaI31211 Human sin	c 944	12.2	37.0	40	12	ADJ74038	AdJ74038 Human 5'
c 872	12.2	37.0	31	4	AAO09871	AaO09871 Human CYP	c 945	12.2	37.0	40	12	ADJ74037	AdJ74037 Human 5'
873	12.2	37.0	32	2	AAAT85188	AaT85188 Equine rh	c 946	12.2	37.0	40	12	ADK90623	AdK90623 Template
874	12.2	37.0	32	10	ADJ76943	AdJ76943 Anti-IGF-	c 947	12.2	37.0	41	2	AAZ226997	AaZ226997 Human chr
875	12.2	37.0	33	2	AAK06696	AaK06696 Murine BR	c 948	12.2	37.0	41	4	AAH46480	AaH46480 Ribosome
876	12.2	37.0	33	2	AAZ31900	AaZ31900 PCR prime	c 949	12.2	37.0	41	4	AAH78919	AaH78919 Human spe
877	12.2	37.0	33	3	AAZ58951	AaZ58951 Murine MA	c 950	12.2	37.0	41	4	AAH78920	AaH78920 Human spe
878	12.2	37.0	33	3	AAZ58951	AaZ58951 Murine MA	c 951	12.2	37.0	41	6	ABL54068	AbL54068 Human ute
879	12.2	37.0	33	4	AAAF80436	AaA80436 5-enolpyr	c 952	12.2	37.0	41	12	ADL92607	AdL92607 Expressio
c 880	12.2	37.0	33	6	ABN86204	AbN86204 UGT1A1*6	c 953	12.2	37.0	41	12	ADL64117	AdL64117 Human sin
c 881	12.2	37.0	33	6	ABN86204	AbN86204 UGT1A1*6	c 954	12.2	37.0	43	2	AAAT70884	AaT70884 Primer WD
c 882	12.2	37.0	33	9	ADA00621	AdA00621 Murine rib	c 955	12.2	37.0	44	6	ABQ73661	AbQ73661 Murine IS
883	12.2	37.0	33	12	ADL67269	AdL67269 Murine mo	c 956	12.2	37.0	45	2	AAZ10954	AaZ10954 15D3 VL c
c 884	12.2	37.0	33	12	ADL56778	AdL56778 Chimeric	c 957	12.2	37.0	45	2	AAZ87597	AaZ87597 ClYTA ant
c 885	12.2	37.0	34	10	ABX17503	AbX17503 Human Igb	c 958	12.2	37.0	45	12	ADH17972	AdH17972 Human mod
c 886	12.2	37.0	35	2	AAK32845	AaK32845 Tumour su	c 959	12.2	37.0	45	12	ADH17939	AdH17939 Human 15H
c 887	12.2	37.0	35	6	ABK40179	AbK40179 Rabbit Ck	c 960	12.2	37.0	45	12	ADH17980	AdH17980 Human mod
c 888	12.2	37.0	36	2	AAAT56016	AaA56016 Human TNF	c 961	12.2	37.0	45	12	ADQ92394	AdQ92394 Human hul
c 889	12.2	37.0	36	2	AAAT55444	AaA55444 Human rel	c 962	12.2	37.0	45	12	ADQ80583	AdQ80583 Human lig
c 890	12.2	37.0	36	2	AAK65959	AaK65959 Human B7-	c 963	12.2	37.0	46	2	AAQ83061	AaQ83061 HIV hamme
c 891	12.2	37.0	36	2	AAK66397	AaK66397 Mouse B7-	c 964	12.2	37.0	46	6	ABK85738	AbK85738 Mouse Btk
c 892	12.2	37.0	36	2	AAK66398	AaK66398 Mouse B7-	c 965	12.2	37.0	46	10	ADC64095	AdC64095 Polyhydro
c 893	12.2	37.0	36	2	AAK66399	AaK66399 Mouse B7-	c 966	12.2	37.0	46	12	ADG01860	AdG01860 Carbon bl
c 894	12.2	37.0	36	2	AAAT70166	AaT70166 Scal meth	c 967	12.2	37.0	47	3	AAZ67362	AaZ67362 Human map
c 895	12.2	37.0	36	6	ABX02083	AbX02083 HCV hamme	c 968	12.2	37.0	47	3	AAZ67362	AaZ67362 Human map
c 896	12.2	37.0	36	6	ABX02115	AbX02115 HCV hamme	c 969	12.2	37.0	47	3	AAA72095	AaA72095 SCET ant1
c 897	12.2	37.0	36	12	ADL59425	AdL59425 Inozyme s	c 970	12.2	37.0	47	4	AAAC92423	AaC92423 T7pBR4287

971	12.2	37.0	47	12	ADN11538	Adn11538
C 972	12.2	37.0	48	12	ADH17790	Adh17790
C 973	12.2	37.0	48	12	ADO32116	Ado32116
C 974	12.2	37.0	48	12	ADO32121	Ado32121
975	12.2	37.0	48	12	ADO38186	Ado38186
976	12.2	37.0	48	12	ADO38075	Ado38075
977	12.2	37.0	49	2	Aaz22836	Aaz22836
978	12.2	37.0	49	10	ADCG0966	Adcg0966
979	12.2	37.0	50	2	AAx52110	Aax52110
980	12.2	37.0	50	4	AAx134267	Aax134267
981	12.2	37.0	50	4	AAx134266	Aax134266
982	12.2	37.0	50	4	AAx134268	Aax134268
983	12.2	37.0	50	4	AAx128575	Aax128575
C 984	12.2	37.0	50	4	ABD17298	Abd17298
C 985	12.2	37.0	50	6	ABZ02969	Abz02969
C 986	12.2	37.0	50	6	ABZ04364	Abz04364
987	12.2	37.0	50	12	ADQ303995	Adq303995
988	12.2	37.0	50	12	ADQ303997	Adq303997
989	12	36.4	17	8	ADA99466	Ada99466
990	12	36.4	17	8	ADA99467	Ada99467
991	12	36.4	17	8	ADA99464	Ada99464
992	12	36.4	17	8	ADA99468	Ada99468
993	12	36.4	17	8	ADA99465	Ada99465
994	12	36.4	17	8	ADA99469	Ada99469
995	12	36.4	20	2	AAT73404	Aat73404
996	12	36.4	20	2	AAT93655	Aat93655
997	12	36.4	20	2	AAV00284	Aav00284
998	12	36.4	20	2	AAV83883	Aav83883
999	12	36.4	20	3	Aaz49936	Aaz49936
1000	12	36.4	20	3	Aaz40602	Aaz40602

ALIGNMENTS

RESULT 1	
ADF52991	
ID	ADF52991 standard; RNA; 23 BP.
XX	
XX	
AC	ADF52991;
XX	
XX	
DT	12-FEB-2004 (first entry)
XX	
XX	
DE	Hepatitis C virus modified siNA sense strand SeqID1582.
XX	
XX	short interfering nucleic acid; siNA; virus replication inhibition;
KW	hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
KW	hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
KW	hepatocellular cancer; cirrhosis; ss.

DR	WPI; 2003-689778/65.
XX	
PT	New double-stranded short interfering nucleic acid comprises sugar-
PT	modified pyrimidine bases useful for treating infection with hepatitis C
PT	virus.
XX	
PS	Example 3; SEQ ID NO 1582; 183pp; English.
XX	
CC	This invention relates to novel double-stranded short interfering nucleic
CC	acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
CC	one strand is an antisense strand (ASS) that is complementary to (part
CC	of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC	ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC	modification. The invention may allow development of compounds with
CC	virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC	modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC	interference. The siNA's of the invention may be used to inhibit
CC	replication of HCV, in cells, tissue explants or organisms, for treating
CC	HCV infection and its consequences (liver failure; hepatocellular cancer
CC	and cirrhosis), and also for drug screening, diagnosis, target
CC	identification and validation, genetic engineering, pharmacogenomics,
CC	studying gene function and gene mapping (for example of single-nucleotide
CC	polymorphisms). The chemical modification improves stability, activity,
CC	cellular uptake and/or binding affinity. The siNA can be directed to
CC	conserved regions of HCV genes, so are active against many different
CC	strains. NOTE: This sequence may contain one or more of several
CC	modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC	(T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC	base 5-nitroindole (X); universal base 3-nitropyrole (Z). These
CC	modifications are specified in table 3 of the specification (pages 150-
CC	158).
XX	
SQ	Sequence 23 BP; 3 A; 4 C; 8 G; 2 T; 4 U; 2 Other;
	Query Match 49.7%; Score 16.4; DB 10; Length 23;
	Best Local Similarity 77.8%; Pred. No. 2.3e+03;
	Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0
Oy	12 GCACAGGCGCTCTGTGGAT 29
	:
Db	4 GCCAAGGCCGCUCUGUGAT 21

```

PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Macejak D, Morrissey D;
XX
XX WPI; 2003-689778/65.
XX
XX New double-stranded short interfering nucleic acid comprises sugar-
PT modified pyrimidine bases useful for treating infection with hepatitis C
PT virus.
XX
XX Example 3; SEQ ID NO 1525; 183pp; English.
XX
XX This invention relates to novel double-stranded short interfering nucleic
CC acids (siRNA) that inhibits replication of hepatitis C virus (HCV), where
CC one strand is an antisense strand (ASS) that is complementary to (part
CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
CC modification. The invention may allow development of compounds with
CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
CC interference. The siRNA's of the invention may be used to inhibit
CC replication of HCV, in cells, tissue explants or organisms, for treating
CC HCV infection and its consequences (liver failure; hepatocellular cancer
CC and cirrhosis), and also for drug screening, diagnosis, target
CC identification and validation, genetic engineering, pharmacogenomics,
CC studying gene function and gene mapping (for example of single-nucleotide
CC polymorphisms). The chemical modification improves stability, activity,
CC cellular uptake and/or binding affinity. The siRNA can be directed to
CC conserved regions of HCV genes, so are active against many different
CC strains. NOTE: This sequence may contain one or more of several
CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
CC modifications are specified in table 3 of the specification (pages 150-
CC 158).
XX
XX SQ Sequence 23 BP; 3 A; 4 C; 8 G; 2 T; 4 U; 2 Other;

Query Match 49.7%; Score 16.4; DB 10; Length 23;
Best Local Similarity 77.8%; Pred. No. 2.3e+03;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCCAAGGCGTCTGGTGAT 29
DB 4 GCCAAGGCGCUGUGAT 21

RESULT 3
AAC87004/c
ID AAC87004 standard; DNA; 43 BP.
AC
AC AAC87004;
XX
XX 20-APR-2001 (first entry)
XX
XX Probe used to isolate cDNA encoding human polypeptide PRO4999.
XX
XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW PRO246; PRO265; PRO941; PRO1096; PRO6003; PRO6004; PRO350; PRO2630;
KW PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW probe; ss.
XX
XX Homo sapiens.
OS
XX WO200077037-A2.
PN
XX

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PD 21-DEC-2000.
XX 22-MAY-2000; 2000WO-US014042.
XX
PR 15-JUN-1999; 99US-0139695P.
PR 26-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Klijavin IG, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
XX WPI; 2001-050091/06.
XX
XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides.
XX
XX Example 17; Page 112; 244pp; English.
XX
XX The present probe was used to isolate cDNA encoding a human secreted and
XX transmembrane polypeptide. The specification describes human
XX polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215,
XX PRO217, PRO242, PRO288, PRO365, PRO1361, PRO1308, PRO1183, PRO1272,
XX PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940,
XX PRO533, PRO301, PRO187, PRO337, PRO411, PRO4356, PRO246, PRO265, PRO941,
XX PRO1096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6309. The biological
XX activity of cells can be modulated with agents that bind to these
XX polypeptides, resulting in the death of the cells. The polynucleotides
XX encoding these polypeptides are useful in the recombinant production of
XX the polypeptides, as a hybridisation probe to screen libraries to isolate
XX homologous sequences, or to map the gene. They may also be used for
XX analysing genetic disorders, and to produce transgenic animals which are
XX useful for the development and screening of therapeutically useful
XX reagents. The polynucleotides can also be used in gene therapy e.g. to
XX replace a defective gene
XX
XX SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 4; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGTCGACAGCGTCTGCT 26
DB 43 GCCACAGTTGTGCGAAGATGTGTGT 18

RESULT 4
ACA04963/c

```

ID ACA04963 standard; DNA; 43 BP.
 AC ACA04963;
 DT 28-MAY-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein related probe #9.
 XX
 KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
 KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
 KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
 KW fibroblast growth factor receptor; cell death; chromosome mapping;
 KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
 KW obesity; diabetes; insulinemia; vascular permeability;
 KW cardiac insufficiency disorder; immune response; hearing loss;
 KW auditory hair cell regeneration; bone disorder; cartilage disorder;
 KW sports injury; arthritis; probe; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2003032063-A1.
 PN
 XX 13-FEB-2003.
 PD
 XX
 PF 01-FEB-2002; 2002US-00066494.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095998P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US0214855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 03-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.

PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DJ; for
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas' D, Watanabe CK, Williams PN;
 PI Wood WI, Zhang Z;
 XX
 XX WPI; 2003-341964/32.

XX Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
 PT polypeptides, useful for modulating biological activity of cell
 PT expressing the polypeptide, and in chromosome and gene mapping.

Example 17; Page 60; 255pp; English.

CC The invention describes an isolated, secreted and transmembrane
 CC polypeptide (I), termed PRO polypeptide. (I) is useful for detecting
 CC PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307,
 CC PRO6003, PRO6004, PRO4356, PRO265, PRO941, fibroblast growth
 CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
 CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
 CC cell expressing the polypeptides. The bioactive molecule causes cell
 CC death. (II) Is useful as hybridisation probes, in chromosome and gene
 CC mapping, in generation of antisense RNA and DNA, in the preparation of
 CC PRO polypeptide, for generating transgenic animals or knockout animals
 CC which in turn are useful in the development and screening of
 CC therapeutically useful reagents, and for the genetic analysis of
 CC individuals with genetic disorders, in gene therapy, and for chromosome
 CC identification. (I) Or Ab is useful for the preparation of medicament for
 CC treating conditions which are responsive to the PRO polypeptide or anti-
 CC PRO antibody e.g. a tumour. (I) is useful for treating obesity, diabetes
 CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
 CC inhibiting tumour growth, enhances vascular permeability and immune
 CC response, for inducing regeneration of auditory hair cells and for
 CC treating hearing loss in mammals, and for treating bone and/or cartilage
 CC disorders such as sports injuries and arthritis. This sequence represents
 CC a probe used to detect DNA encoding a novel human secreted and
 CC transmembrane polypeptide

Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;
 Best Local Similarity 76.9%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCAAGGGCTGTGT 26
 ||||| ||||| |||||
 Db 43 GCCACAGTTGTGGCAAGATGTGTGT 18

RESULT 5

ACAA60493/c

ID ACAA60493 standard; DNA; 43 BP.

XX AC ACAA60493;

XX DT 11-JUN-2003 (first entry)

XX DE Human secreted and transmembrane protein related probe #9.

XX KW Human; secreted and transmembrane polypeptide; PRO;

XX KW fibroblast growth factor receptor; PRO533; PRO301; PRO187; PRO337;

XX KW PRO1411; PRO10096; PRO246; PRO6307; PRO6003; FGFR-3; FGFR-4; FGFR-1;

XX KW FGFR-2; PRO6004; PRO4350; PRO2630; PRO265; PRO951; bioactive molecule;

XX KW toxin; radiolabel; antibody; cell death; chromosome mapping;

XX KW gene mapping; transgenic animal; knockout animal; gene therapy;

XX KW tissue typing; PCR; primer; ss.

XX OS Homo sapiens.

XX XX US2002177165-A1.

XX PN 28-NOV-2002.

XX PD 01-FEB-2002; 2002US-00066500.

XX PF 26-AUG-1997; 97US-0056974P.

XX PR 17-SEP-1997; 97US-0059115P.

XX PR 18-SEP-1997; 97US-0059263P.

XX PR 19-SEP-1997; 97US-0059588P.

XX PR 17-OCT-1997; 97US-0062285P.

XX PR 24-OCT-1997; 97US-0062816P.

XX PR 24-OCT-1997; 97US-0063082P.

XX PR 27-OCT-1997; 97US-0063329P.

XX PR 29-OCT-1997; 97US-0063733P.

XX PR 21-NOV-1997; 97US-0066364P.

XX PR 25-NOV-1997; 97US-0066840P.

XX PR 16-DEC-1997; 97US-0069694P.

XX PR 09-FEB-1998; 98US-0074086P.

XX PR 09-FEB-1998; 98US-0074092P.

XX PR 25-MAR-1998; 98US-0079294P.

XX PR 08-APR-1998; 98US-0081049P.

XX PR 14-JUL-1998; 98WO-US014552.

XX PR 10-AUG-1998; 98US-0095998P.

XX PR 18-AUG-1998; 98US-0097000P.

XX PR 10-SEP-1998; 98US-009801P.

XX PR 10-SEP-1998; 98US-009811P.

XX PR 10-SEP-1998; 98US-009812P.

XX PR 10-SEP-1998; 98WO-US018824.

XX PR 14-SEP-1998; 98WO-US019093.

XX PR 16-SEP-1998; 98WO-US019330.

XX PR 17-SEP-1998; 98US-0100858P.

XX PR 17-SEP-1998; 98WO-US019437.

XX PR 24-SEP-1998; 98US-0101922P.

XX PR 28-OCT-1998; 98US-0106032P.

XX PR 20-NOV-1998; 98US-0109304P.

XX PR 20-NOV-1998; 98WO-US024855.

XX PR 25-NOV-1998; 98WO-US025190.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 08-NAR-1999; 99WO-US005028.

XX PR 23-MAR-1999; 99US-0125778P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 15-JUN-1999; 99US-0139695P.

XX PR 20-JUL-1999; 99US-0145070P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 17-AUG-1999; 99US-0149396P.

XX PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

PI Fedowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;

PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;

XX Wood WI, Zhang Z;

DR WPI; 2003-328482/31.

Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, for identifying agonists or antagonists of polypeptide, and as molecular weight markers.

Example 17; Page 60; 254pp; English.

The invention describes an isolated, secreted and transmembrane polypeptide (PP), termed PRO PP or fibroblast growth factor receptor PP (I). (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307, PRO6003, fibroblast growth factor receptor (FGFR)-3, FGFR-4, FGFR-1, FGFR-2, PRO6004, PRO4356, PRO2630, PRO265 or PRO951 polypeptide, and for linking a bioactive molecule to a cell expressing the above polypeptides. The bioactive molecule, a toxin, radiolabel or an antibody, causes cell death. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. The polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes the PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification and as a chromosome marker. (I) and (II) are useful for tissue typing. This sequence represents a novel human secreted and transmembrane PRO polypeptide associated primer

Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;

Best Local Similarity 76.9%; Pred. No. 2.5e+03;


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Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCACATGATGCGCAGGCGTCTGGT 26
DB 43 GCCACATGTTGGCAAGATGTGTGGT 18

RESULT 6
ACA04483/C
ID ACA04483 standard; DNA; 43 BP.
XX
AC ACA04483;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human secreted and transmembrane protein related probe #9.
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW PRO187; PRO337; PRO1411; PRO10096; PRO246; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGFR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
OS Homo sapiens.
XX
XX US2003032062-A1.
XX
XX 13-FEB-2003.
XX
XX 01-FEB-2002; 2002US-00066273.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019130.
PR 17-SEP-1998; 98US-0100058P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-01339695P.
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PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US02678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
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(GETH) GENENTECH INC.

Ashtenazi AJ, Baker KP, Rotstein DA, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
Wood WI, Zhang Z;
WPI; 2003-341963/32.

New secreted and transmembrane polypeptide for modulating biological activity of a cell expressing the polypeptide, identifying agonists or antagonists of the polypeptide, and as molecular weight markers.

Example 17; Page 60; 254pp; English.

The invention describes an isolated, secreted and transmembrane polypeptide (I), termed PRO polypeptide. (I) is useful for detecting PRO533, PRO301, PRO187, PRO337, PRO1411, PRO10096, PRO246, PRO6307, PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a cell expressing the polypeptides. The bioactive molecule causes cell death. (ii) Is useful as hybridisation probes, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, and for the genetic analysis of individuals with genetic disorders, in gene therapy, and for chromosome identification. (i) Or Ab is useful for the preparation of medicament for treating conditions which are responsive to the PRO polypeptide or anti-PRO antibody e.g. a tumour. (i) is useful for treating obesity, diabetes or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for inhibiting tumour growth, enhances vascular permeability and immune response, for inducing regeneration of auditory hair cells and for

CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This sequence encodes a
CC novel human secreted and transmembrane polypeptide

XX Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 8; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCACATGAGTGGCAAGGCTGTGCT 26
||||| ||||| ||||| |||||
Db 43 GCCACAGTGTGGCAAGATGTGTGT 18

RESULT 7
ACA65624/c
ID ACA65624 standard; DNA; 43 BP.

XX ACA65624;

XX 19-JUN-2003 (first entry)

XX Human secreted/transmembrane protein PRO4999 probe.

XX Human; ss; probe; secreted protein; transmembrane protein; PRO;
KW genetic disorder; gene therapy.

XX Homo sapiens.

XX US2003032057-A1.

XX 13-FEB-2003.

XX 15-NOV-2001; 2001US-00002796.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-00591115P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059588P.

XX 17-OCT-1997; 97US-0062285P.

XX 24-OCT-1997; 97US-0062815P.

XX 24-OCT-1997; 97US-0063082P.

XX 27-OCT-1997; 97US-0063329P.

XX 29-OCT-1997; 97US-0063733P.

XX 21-NOV-1997; 97US-0066364P.

XX 25-NOV-1997; 97US-0066840P.

XX 16-DEC-1997; 97US-0069694P.

XX 09-FEB-1998; 98US-0074086P.

XX 09-FEB-1998; 98US-0074092P.

XX 25-MAR-1998; 98US-0079294P.

XX 08-APR-1998; 98US-0081049P.

XX 14-JUL-1998; 98WO-US014552.

XX 10-AUG-1998; 98US-0095998P.

XX 18-AUG-1998; 98US-0097000P.

XX 09-SEP-1998; 98US-0099601P.

XX 10-SEP-1998; 98US-0099803P.

XX 10-SEP-1998; 98US-0099811P.

XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98US-0100858P.
XX 17-SEP-1998; 98WO-US019437.
XX 24-SEP-1998; 98US-0101922P.
XX 28-OCT-1998; 98US-0106032P.
XX 20-NOV-1998; 98US-0109304P.
XX 20-NOV-1998; 98WO-US024855.
XX 25-NOV-1998; 98WO-US025190.
XX 01-DEC-1998; 98WO-US025108.
XX 08-MAR-1999; 98WO-US005028.
XX 23-MAR-1999; 99US-0125778P.
XX 02-JUN-1999; 99WO-US012252.

PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030399.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 09-MAR-2000; 2000WO-US006471.
PR 30-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein DA, Deanovers L, Eaton DL;
Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Kljavin IG, Mather JP, Napier MA, Pan J;
Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
Wood WI, Zhang Z;
WPI; 2003-341960/32.

Novel secreted and transmembrane polypeptide for modulating biological
activity of cell expressing the polypeptide, identifying agonists or
antagonists of polypeptide, and as molecular weight markers.

Example 17; Page 60; 255pp; English.

The invention relates to an isolated, secreted/transmembrane polypeptide,
termed PRO polypeptide, having at least 80% sequence identity to a
sequence selected from any one of the 37 sequences appearing as ABU79779
-ABU79815 or to a sequence encoded by a nucleic acid molecule deposited
under any one of the ATCC numbers given in the specification. Also
included are an isolated nucleic acid molecule having at least 80%
sequence identity to a sequence selected from any one of the 37 cDNA
sequences defined in the specification (or encoding the mature PRO
protein or a PRO protein extracellular domain), a PRO expression vector,
a host cell comprising the vector, PRO fusion proteins, anti-PRO
antibodies and a method for linking a bioactive molecule to a cell
expressing the above PRO polypeptides, the bioactive molecule is a toxin,
radiolabel or an antibody and causes the death of the cell. PRO or the
antibody is useful for modulating at least one biological activity of
cell expressing the above polypeptides. PRO is useful for identifying
agonists or antagonists of PRO, for preparing a variant of PRO, as
molecular weight markers for protein electrophoresis purpose and PRO
nucleic acid is useful for recombinantly expressing those markers. PRO is
also useful as therapeutic agent. PRO is useful in assays to identify

CC other proteins or molecules involved in binding interaction. PRO nucleic
CC acid is useful as hybridisation probes, in chromosome and gene mapping,
CC in generation of antisense RNA and DNA, in the preparation of PRO
CC polypeptide, in gene therapy, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes the PRO and for the genetic
CC analysis of individuals with genetic disorders, for chromosome
CC identification, as a chromosome marker, and for generating probes for
CC polymerase chain reaction (PCR), Northern analysis, Southern analysis and
CC Western analysis. The antibody is useful in diagnostic assays for PRO,
CC e.g. detecting its expression in specific cells, tissues or serum, for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. PRO or Ab is useful for the preparation of medicament for
CC treating conditions which is responsive to the PRO polypeptide or anti-
CC PRO antibody. PRO and PRO nucleic acid are useful for tissue typing. The
CC present sequence is a probe used to isolate cDNA encoding a PRO
CC polypeptide
XX
SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCCACATGAGTGCACAGGCGTCTGGT 26
Db 43 GCCACATGTTGTGCAAGATGTGGT 18

RESULT 8
ADA47233/c
ID ADA47233 standard; DNA; 43 BP.
XX AC ADA47233;
XX DT 20-NOV-2003 (first entry)
XX DE Human secreted/transmembrane polypeptide PRO4999 probe.
XX KW human; ss; probe; secreted protein; transmembrane protein; PRO;
KW VEGF inhibitor; vascular endothelial growth factor;
KW endothelial cell proliferation; T-lymphocyte proliferation;
KW endothelial cell apoptosis; c-fos stimulation;
KW pancreatic beta cell differentiation; chondrocyte proliferation;
KW Glucose uptake; free fatty acid; FFA uptake; tissue typing.
XX OS Homo sapiens.
XX PN US2003044844-A1.
XX PD 06-MAR-2003.
XX PF 01-FEB-2002; 2002US-00066211.
XX PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069694P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014552.
PR 10-AUG-1998; 98US-0095998P.

PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 14-SEP-1998; 98WO-US018824.
PR 16-SEP-1998; 98WO-US019093.
PR 17-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 25-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004342.
PR 01-MAR-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005601.
PR 09-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US006471.
PR 30-MAR-2000; 2000WO-US007377.
PR 15-MAY-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013358.
PR 22-MAY-2000; 2000WO-US013705.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;
XX Wood WI, Zhang Z;
XX WPI; 2003-615775/58.
XX Novel isolated PRO polypeptides e.g. PRO365 and PRO187, useful for
XX inducing redifferentiation and/or proliferation of chondrocytes, and for
XX modulating glucose or free fatty acid uptake by skeletal muscle cells.
XX Example 17; Page 60; 254pp; English.

XX The invention relates to an isolated secreted/transmembrane PRO
 CC polypeptide. The polypeptide and its nucleic acid is useful as an
 CC inhibitor of vascular endothelial growth factor stimulated proliferation
 CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
 CC pancreatic beta cell precursors into mature cell, for induction of
 CC redifferentiation and/or proliferation of chondrocytes and for modulating
 CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
 CC polypeptide and its nucleic acid is useful for generating transgenic or
 CC knock-out animals, for tissue typing and for chromosome identification.
 CC The polypeptide is useful in a number of functional biological assays, as
 CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation PRO polypeptides. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a human
 CC secreted/transmembrane PRO polypeptide probe.

SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
 Best Local Similarity 76.9%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGAGTGGCAAGCGGTGGT 26

Db 43 GCCACATGTTGGCAAGATGTGGT 18

RESULT 9

ACD30240/c

ID ACD30240 standard; DNA; 43 BP.

XX ACD30240;

DT 29-AUG-2003 (first entry)

XX Human secreted/transmembrane protein PRO4999 probe.

XX Human; ss; PCR; PRO; secreted and transmembrane protein; gene therapy;
 KW enterocolitis; gastrointestinal ulceration; skin disease; asthma; primer;
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
 KW squamous cell carcinoma; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; inflammatory disease; organ failure;
 KW rheumatoid arthritis; multiple sclerosis; atherosclerosis; infertility;
 KW cardiac injury; birth defect; premature aging; AIDS; cancer;
 KW diabetic complication; wound repair.

XX Homo sapiens.

XX US2003044902-A1.

XX 06-MAR-2003.

XX 01-FEB-2002; 2002US-00066193.

XX 26-AUG-1997; 97US-0056974P.

XX 17-SEP-1997; 97US-0059115P.

XX 18-SEP-1997; 97US-0059263P.

XX 19-SEP-1997; 97US-0059588P.

XX 17-OCT-1997; 97US-0062288P.

XX 24-OCT-1997; 97US-0062816P.

XX 24-OCT-1997; 97US-0063082P.

XX 27-OCT-1997; 97US-0063329P.

XX 27-OCT-1997; 97US-0063733P.

XX 21-NOV-1997; 97US-0066364P.

XX 25-NOV-1997; 97US-0066840P.

XX 16-DEC-1997; 97US-0069694P.

PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 10-AUG-1998; 98US-0095988P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 PI Gadowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Padoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WT, Zhang Z;
 XX WPI; 2003-492261/46.

XX New PRO polypeptides and nucleic acid molecules, useful in diagnosing or

PT treating inflammatory diseases, organ failure, atherosclerosis, cardiac
 PT injury, infertility, cancer, AIDS, Alzheimer's disease or Parkinson's
 XX disease.

PS Example 17; Page 60; 154pp; English.

XX The invention relates to an isolated native sequence PRO polypeptide
 CC (secreted and transmembrane protein) having 80% sequence similarity to
 CC one of 37 proteins sequences (or PRO lacking its signal peptide, a PRO
 CC extracellular domain (with or without a signal peptide) encoded by a
 CC nucleic acids, 80% identical to one of 37 cDNA sequences, shown in the
 CC specification. Also included are vectors comprising the PRO nucleic
 CC acids, host cells comprising the vectors (used to produce the PRO
 CC proteins), a chimeric molecule comprising the PRO polypeptide fused to a
 CC heterologous amino acid sequence, an anti-PRO antibody, linking a
 CC bioactive molecule to a cell expressing the PRO polypeptides and
 CC modulating at least one biological activity of a cell expressing the
 CC polypeptides. The PRO polypeptides and nucleic acids are useful in
 CC diagnosing or treating enterocolitis, gastrointestinal ulceration, skin
 CC diseases associated with abnormal keratinocyte differentiation, e.g.
 CC psoriasis or epithelial cancers such as squamous cell carcinoma.
 CC Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis,
 CC inflammatory diseases, e.g. rheumatoid arthritis, asthma or multiple
 CC sclerosis, organ failure, atherosclerosis, cardiac injury, infertility,
 CC birth defects, premature aging, AIDS, cancer, diabetic complications, or
 CC mutations in general. The polypeptides are also useful for wound repair
 CC and associated therapies concerned with re-growth of tissue. The
 CC nucleotide sequences may be used as hybridisation probes in chromosome
 CC and gene mapping, or in generating antisense RNA and DNA. PRO nucleic
 CC acids are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in binding reaction, to
 CC generate transgenic animals or knockout animals, which in turn are useful
 CC in the development and screening of therapeutically useful reagents, for
 CC chromosome identification, and tissue typing. The PRO polypeptides and
 CC nucleic acid molecules are also useful in gene therapy, and as molecular
 CC weight markers for protein electrophoresis purposes. The anti-PRO
 CC antibodies may be used in diagnostic assays for PRO, or for the affinity
 CC purification of PRO from recombinant cell culture or natural sources. The
 CC present sequence is a PCR primer used to isolate a cDNA encoding a PRO
 CC protein of the invention

XX SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 9; Length 43;
 Best Local Similarity 76.9%; Pred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGTCACAGCGCTCTGGT 26
 ||||| ||||| ||||| |||||
 Db 43 GCCACAGTTGTGCAAGATGTGTGGT 18

RESULT 10

ADG63742/c

ID ADG63742 standard; DNA; 43 BP.

XX AC ADG63742;

XX DT 11-MAR-2004 (first entry)

DE Human secreted/transmembrane polypeptide PRO4999 probe.

XX human; ss; probe; secreted protein; transmembrane protein; PRO;
 KW VEGF inhibitor; vascular endothelial growth factor;
 KW endothelial cell proliferation; T-lymphocyte proliferation;
 KW endothelial cell apoptosis; c-fos stimulation;
 KW pancreatic beta cell differentiation; chondrocyte proliferation;
 KW Glucose uptake; free fatty acid; FFA uptake; tissue typing.

XX OS Homo sapiens.

XX PN US2003170721-A1.

XX

PD 11-SEP-2003.
 XX
 PF 01-FEB-2002; 2002US-00066198.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063082P.
 PR 29-OCT-1997; 97US-0063329P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066164P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-0069694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 05-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-0095988P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0098601P.
 PR 10-SEP-1998; 98US-0098803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101222P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 25-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 22-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.

PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX (GETH) GENENTECH INC.
 PA
 XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gao W, Gerber H, Gerratzen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX WPI; 2003-787545/74.
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 PT as a hybridization probe, and in gene therapy.
 XX Example 17; SEQ ID NO 61; 161pp; English.
 CC The invention relates to an isolated secreted/transmembrane PRO
 CC polypeptide. The polypeptide and its nucleic acid is useful as an
 CC inhibitor of vascular endothelial growth factor stimulated proliferation
 CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
 CC pancreatic beta cell precursors into mature cell, for induction of
 CC redifferentiation and/or proliferation of chondrocytes and for modulating
 CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
 CC polypeptide and its nucleic acid is useful for generating transgenic or
 CC knock-out animals, for tissue typing and for chromosome identification.
 CC The polypeptide is useful in a number of functional biological assays, as
 CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation PRO polypeptides. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a human
 CC secreted/transmembrane PRO polypeptide probe.
 XX
 SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 49.7%; Score 16.4; DB 10; Length 43;
 Best Local Similarity 76.9%; Fred. No. 2.5e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 GCCACATGAGTGGCAAGGCGTCTGGT 26
 Db 43 GCCACAGTTGTGGCAAGATGTGTGT 18
 RESULT 11
 ACD42354/c
 ID ACD42354 standard; DNA; 43 BP.
 XX ACD42354;
 XX
 XX 05-SEP-2003 (first entry)
 DT
 XX Novel human secreted and transmembrane protein related probe #8.
 DE
 XX Human; secreted and transmembrane protein; PRO; antidiabetic;
 KW ophthalmological; cytostatic; immunostimulant; gene therapy;
 KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
 KW protein secretion disorder; pancreas disorder; diabetes;
 KW vascular permeability; retinal neuron cell survival; retinal disorder;
 KW immune response; inflammation; mononuclear cell infiltration;
 KW eosinophil infiltration; apoptosis; neoplastic growth; probe; ss.

XX Homo sapiens.
 OS
 XX US2003040014-A1.
 PN
 XX 27-FEB-2003.
 PD
 XX
 PF 01-FEB-2002; 2002US-00066269.
 XX
 PR 26-AUG-1997; 97US-0056974P.
 PR 17-SEP-1997; 97US-0059115P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 19-SEP-1997; 97US-0059588P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 27-OCT-1997; 97US-0063082P.
 PR 29-OCT-1997; 97US-0063733P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 25-NOV-1997; 97US-0066840P.
 PR 16-DEC-1997; 97US-006694P.
 PR 09-FEB-1998; 98US-0074086P.
 PR 09-FEB-1998; 98US-0074092P.
 PR 25-MAR-1998; 98US-0079294P.
 PR 08-APR-1998; 98US-0081049P.
 PR 14-JUL-1998; 98WO-US014552.
 PR 10-AUG-1998; 98US-009598P.
 PR 18-AUG-1998; 98US-0097000P.
 PR 09-SEP-1998; 98US-0099601P.
 PR 10-SEP-1998; 98US-0099803P.
 PR 10-SEP-1998; 98US-0099811P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 20-NOV-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 99WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99US-0169495P.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 30-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.

PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2003-503396/47.
DR
XX New secreted and transmembrane PRO polypeptides, useful for treating
PT diabetes, retinal disorders and stimulating an immune response.
PT
XX Example 17; Page 60; 254pp; English.
PS
XX The invention describes an isolated polypeptide (I) having at least 80 %
CC amino acid sequence identity to 30 secreted and transmembrane
CC polypeptides. PRO polypeptides are also useful for stimulating
CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
CC factor stimulated proliferation of endothelial cells, stimulating
CC proliferation of stimulated T-lymphocytes and for inducing proliferation
CC of PDB12 pancreatic ductal cells and are thus useful in the treatment of
CC disorders which involve protein secretion by the pancreas, including
CC diabetes. PRO polypeptides are useful for inducing vascular permeability
CC and in enhancing survival of retinal neurons cells and are thus useful
CC for the treatment of retinal disorders. PRO polypeptides are also useful
CC for stimulating an immune response and inducing inflammation by inducing
CC mononuclear cells and eosinophil infiltration at the site of infection of
CC an animal. The PRO polypeptides are further useful for inducing apoptosis
CC in endothelial cells for inhibiting neoplastic growth. This sequence
CC represents a probe used to detect DNA encoding a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;
Query Match 49.7%; Score 16.4; DB 10; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GCCACATGAGTGGCAAGCGCTGGT 26
Db 43 GCCACAGTTGGCAAGATGTGGT 18
RESULT 12
ADE41156/c
ID ADE41156 standard; DNA; 43 BP.
XX AC
XX ADE41156;
XX
XX 29-JAN-2004 (first entry)
DT
DE Human secreted/transmembrane polypeptide PRO4999 probe.
XX human, ss; probe; secreted protein; transmembrane protein; PRO;
KW VEGF inhibitor; vascular endothelial growth factor;
KW endothelial cell proliferation; T-lymphocyte proliferation;
KW endothelial cell apoptosis; c-fos stimulation;
KW pancreatic beta cell differentiation; chondrocyte proliferation;
KW glucose uptake; free fatty acid; FFA uptake; tissue typing.
XX

OS Homo sapiens.
XX
PN US2003104558-A1.
XX
PD 05-JUN-2003.
XX
PF 23-AUG-2002; 2002US-00226739.
XX
PR 15-JUN-1999; 99US-0139695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145698P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.
PR 05-JAN-2000; 2000WO-US000219.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX
PA (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
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PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2004-008995/01.
DR
XX New isolated, secreted and transmembrane PRO polypeptides and nucleic
PT acids, useful for diagnosing, preventing and/or treating diabetes
PT mellitus and tumors, such as renal, colon, breast, prostate and/or
PT ovarian tumors.
XX
XX Example 17; SEQ ID NO 61; 259pp; English.
XX
CC The invention relates to an isolated secreted/transmembrane PRO
CC polypeptide. The polypeptide and its nucleic acid is useful as an
CC inhibitor of vascular endothelial growth factor stimulated proliferation
CC of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
CC an inducer of endothelial cell apoptosis, c-fos and differentiation of
CC pancreatic beta cell precursors into mature cell, for induction of
CC redifferentiation and/or proliferation of chondrocytes and for modulating
CC glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The
CC polypeptide and its nucleic acid is useful for generating transgenic or
CC knock-out animals, for tissue typing and for chromosome identification.
CC The polypeptide is useful in a number of functional biological assays, as

CC molecular weight marker for protein electrophoresis, and as therapeutic
 CC agents. The nucleic acid is useful as a hybridisation probe, in
 CC chromosome and gene mapping, in the generation of antisense RNA and DNA,
 CC and for the preparation of PRO polypeptides. The nucleic acid is also useful
 CC as hybridisation probe for a cDNA library to isolate the full length PRO
 CC cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also
 CC useful in the construction of hybridisation probes for mapping the gene
 CC encoding PRO, and for the genetic analysis of individuals with the
 CC genetic disorders. The present sequence represents a human
 CC secreted/transmembrane PRO polypeptide probe.

SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 12; Length 43;

-Best Local Similarity 76.9%; Pred. No. 2.5e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GCCACATGATGGCAGGCGTCTGGT 26

Db 43 GCCACATGATGGCAGGCGTCTGGT 18

RESULT 13

ID ADG63591/C
 ADG63591 standard; DNA; 43 BP.

XX AC ADG63591;

XX DT 11-MAR-2004 (first entry)

XX DE Human secreted/transmembrane polypeptide PRO4999 probe.

XX KW human; ss; probe; secreted protein; transmembrane protein; PRO;
 KW VEGF inhibitor; vascular endothelial growth factor;
 KW endothelial cell proliferation; T-lymphocyte proliferation;
 KW endothelial cell apoptosis; c-fos stimulation;
 KW pancreatic beta cell differentiation; chondrocyte proliferation;
 KW glucose uptake; free fatty acid; FFA uptake; tissue typing.

XX OS Homo sapiens.

XX PN US2003180796-A1.

XX PD 25-SEP-2003.

XX PF 01-FEB-2002; 2002US-00066203.

XX PR 26-AUG-1997; 97US-0056974P.

PR 17-SEP-1997; 97US-00591113P.

PR 18-SEP-1997; 97US-0059263P.

PR 19-SEP-1997; 97US-0059588P.

PR 17-OCT-1997; 97US-0062285P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063082P.

PR 27-OCT-1997; 97US-0063329P.

PR 29-OCT-1997; 97US-0063733P.

PR 21-NOV-1997; 97US-0066364P.

PR 25-NOV-1997; 97US-0066840P.

PR 09-FEB-1998; 97US-0069694P.

PR 09-FEB-1998; 98US-0074086P.

PR 09-FEB-1998; 98US-0074092P.

PR 25-MAR-1998; 98US-0079294P.

PR 08-APR-1998; 98US-0081049P.

PR 14-JUL-1998; 98WO-US014552.

PR 10-AUG-1998; 98US-0095998P.

PR 18-AUG-1998; 98US-0097000P.

PR 09-SEP-1998; 98US-0098601P.

PR 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98US-0099811P.

PR 10-SEP-1998; 98US-0099812P.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98US-0100858P.
 PR 17-SEP-1998; 98WO-US019437.
 PR 24-SEP-1998; 98US-0101922P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0109304P.
 PR 20-NOV-1998; 98WO-US024855.
 PR 25-NOV-1998; 98WO-US025190.
 PR 01-DEC-1998; 98WO-US025108.
 PR 08-MAR-1999; 98WO-US005028.
 PR 23-MAR-1999; 99US-0125778P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 15-JUN-1999; 99US-0139695P.
 PR 20-JUL-1999; 99US-0145070P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028565.
 PR 07-DEC-1999; 99US-0169495P.
 PR 20-DEC-1999; 99WO-US030399.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US032878.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.

(GETH) GENENTECH INC.

Askenazi AJ, Baker KP, Botstein DA, Deanovers L, Eaton DL;
 Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
 Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 Wood WI, Zhang Z;

WPI; 2004-031858/03.

Seventy four nucleic acids encoding PRO polypeptides, useful for treating
 pericyte-associated tumors,.

Example 17; SEQ ID NO 61; 261pp; English.

The invention relates to an isolated secreted/transmembrane PRO
 polypeptide. The polypeptide and its nucleic acid is useful as an
 inhibitor of vascular endothelial growth factor stimulated proliferation
 of endothelial cells, as a stimulator of T-lymphocyte proliferation, as
 an inducer of endothelial cell apoptosis, c-fos and differentiation of
 pancreatic beta cell precursors into mature cell, for induction of
 redifferentiation and/or proliferation of chondrocytes and for modulating
 glucose or free fatty acid (FFA) uptake by skeletal muscle cells. The

polypeptide and its nucleic acid is useful for generating transgenic or knock-out animals, for tissue typing and for chromosome identification. The polypeptide is useful in a number of functional biological assays, as molecular weight marker for protein electrophoresis, and as therapeutic agents. The nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation of cDNA libraries. The nucleic acid is also useful as hybridisation probe for a cDNA library to isolate the full length cDNA, to isolate other cDNA and in gene therapy. The nucleic acid is also useful in the construction of hybridisation probes for mapping the gene encoding PRO, and for the genetic analysis of individuals with the genetic disorders. The present sequence represents a human secreted/transmembrane PRO polypeptide probe.

XX
SQ Sequence 43 BP; 9 A; 14 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 49.7%; Score 16.4; DB 12; Length 43;
Best Local Similarity 76.9%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 GCCACATGATGGCAAGCGTCTGGT 26
Db 43 GCCACATGTTGTGGCAAGATGTGGT 18

RESULT 14
AC165292/c
ID AC165292 standard; DNA; 25 BP.
XX
AC AC165292;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human microarray DNA oligonucleotide SEQ ID NO 65283.
XX
KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW genetic variation; biallelic marker; polymorphism; human;
KW cross-species comparison.
XX
OS Homo sapiens.
XX
PN US2003104410-A1.
XX
PD 05-JUN-2003.
XX
PF 15-MAR-2002; 2002US-00098263.
XX
PR 16-MAR-2001; 2001US-0276759P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Mittmann MP;
XX
DR WPI; 2003-567953/53.
XX
PT New array of nucleic acid probes, useful for in situ hybridization, in
PT Southern, Northern or dot-blot hybridization to identify or detect the
PT sequence or specific mutations of any gene.
XX
PS Claim 1; SEQ ID NO 65283; 9pp; English.
XX

The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acids to at least two or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms,

or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid probes is useful in in situ hybridisation, in Southern, Northern or dot-blot hybridisation to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html

XX
SQ Sequence 25 BP; 2 A; 9 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 47.3%; Score 15.6; DB 9; Length 25;
Best Local Similarity 81.8%; Pred. No. 5.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCCACATGATGGCAAGCGTCT 22
Db 22 GCCACATGATGAGCGCGGAC 1

RESULT 15
ADI61875
ID ADI61875 standard; DNA; 40 BP.
XX
AC ADI61875;
XX
DT 22-APR-2004 (first entry)
XX
DE Adenovirus 35 pIX gene promoter deletion PCR primer pIXcosF-2.
XX
KW Adenovirus; viral vector; ss; PCR; primer; cytostatic; virucide; pIX;
KW E1B 55k; cancer; viral infection; gene therapy; vector stability;
KW vector packaging capacity.
XX
OS Human adenovirus type 35.
XX
PN WO2004001032-A2.
XX
PD 31-DEC-2003.
XX
PF 24-APR-2003; 2003WO-EP050126.
XX
PR 25-APR-2002; 2002WO-NL000281.
PR 15-OCT-2002; 2002WO-NL000656.
PR 25-NOV-2002; 2002EP-00102631.
XX
PA (CRUC-) CRUCELL HOLLAND BV.
XX
PI Vogels R, Havenga MJE, Zuidgeest DAT;
XX
DR WPI; 2004-082501/08.
XX
PT New recombinant adenovirus comprising a functional pIX coding sequence,
PT useful for preparing a medicament for the treatment and prevention of
PT diseases or disorders (e.g. cancer or viral infection) in humans or
PT animal subjects.
XX
PS Example 7; SEQ ID NO 27; 181pp; English.
XX

The invention relates to a recombinant adenovirus comprising a functional pIX coding sequence under the control of an expression sequence comprising part of an E1B 55k sequence capable of increasing expression of the pIX coding sequence in a given packaging cell, relative to the expression of the pIX coding sequence behind its endogenous proximal pIX upstream sequence without the part of the E1B 55k sequence, with the proviso that the part of an E1B 55k sequence does not code for a functional E1B 55k gene product. Also included are an isolated nucleic acid that upon introduction into a suitable packaging cell constitutes the genome of the above recombinant adenovirus, a method for increasing the stability and/or the packaging capacity of a recombinant adenovirus

CC having at least a deletion in the El-region (comprising expressing the
 CC elements necessary for production and assembly of the recombinant
 CC adenovirus into virus particles in a packaging cell in the presence of an
 CC elevated level of PIX gene product in the packaging cell, relative to the
 CC level of PIX gene product obtained when the PIX coding sequence is behind
 CC its endogenous proximal upstream sequence without E1B 55K sequences), a
 CC vaccine comprising the recombinant adenovirus (and, optionally, a
 CC suitable carrier or an adjuvant) and a recombinant adenovirus packaging
 CC cell comprising the above recombinant adenovirus. The composition and
 CC methods are useful for preventing or treating diseases or disorders (e.g.
 CC cancer or viral infection) in humans or animal subjects via gene therapy.
 CC The methods may also be used in increasing the stability and/or the
 CC packaging capacity of the recombinant adenovirus. The present sequence is
 CC a PCR primer used in the construction of the recombinant adenovirus
 CC vectors of the invention.

XX Sequence 40 BP; 7 A; 11 C; 14 G; 8 T; 0 U; 0 Other;

Query Match 47.3%; Score 15.6; DB 12; Length 40;

Best Local Similarity 81.8%; Pred. No. 5.4e+03;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GCCACATGATGCGCAAGGGTC 22

Db 19 GCGACATGATGGAATGCTTC 40

RESULT 16

ADF52946/c
 ID ADF52946 standard; RNA; 21 BP.

XX ADF52946;

XX ADF52946;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus modified siNA antisense strand SeqID1537.

XX short interfering nucleic acid; siNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

PN 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX WPI; 2003-689778/65.

XX New double-stranded short interfering nucleic acid comprises sugar-

PT modified pyrimidine bases useful for treating infection with hepatitis C

PT virus.

XX Example 3; SEQ ID NO 1537; 183pp; English.

XX

CC This invention relates to novel double-stranded short interfering nucleic
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 CC 158).

XX Sequence 21 BP; 4 A; 8 C; 4 G; 2 T; 3 U; 0 Other;

Query Match 46.7%; Score 15.4; DB 10; Length 21;

Best Local Similarity 94.1%; Pred. No. 6e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 GCGAAGGCGTCTGGTGA 28

Db 17 GCGAAGGCGTCTGGTGA 1

RESULT 17

ADF53003/c

ID ADF53003 standard; RNA; 21 BP.

XX ADF53003;

XX ADF53003;

DT 12-FEB-2004 (first entry)

DE Hepatitis C virus modified siNA antisense strand SeqID1594.

XX short interfering nucleic acid; siNA; virus replication inhibition;
 KW hepatitis C virus; HCV; sugar modification; virucide; antiinflammatory;
 KW hepatotropic; cytostatic; RNA interference; HCV infection; liver failure;
 KW hepatocellular cancer; cirrhosis; ss.

XX Synthetic.

OS Hepatitis C virus.

XX WO2003070750-A2.

PN 28-AUG-2003.

XX 20-FEB-2003; 2003WO-US005043.

XX 20-FEB-2002; 2002US-0358580P.

PR 11-MAR-2002; 2002US-0363124P.

PR 26-MAR-2002; 2002WO-US009187.

PR 06-JUN-2002; 2002US-0386782P.

PR 05-AUG-2002; 2002US-0401104P.

PR 29-AUG-2002; 2002US-0406784P.

PR 05-SEP-2002; 2002US-0408378P.

PR 09-SEP-2002; 2002US-0409293P.

PR 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Macejak D, Morrissey D;

XX

DR WPI; 2003-689778/65.
 XX New double-stranded short interfering nucleic acid comprises sugar-
 PT modified pyrimidine bases useful for treating infection with hepatitis C
 PT virus.
 XX
 PS Example 3; SEQ ID NO 1594; 183pp; English.
 XX
 CC This invention relates to novel double-stranded short interfering nucleic
 CC acids (siNA) that inhibits replication of hepatitis C virus (HCV), where
 CC one strand is an antisense strand (ASS) that is complementary to (part
 CC of) an HCV RNA (portion) and a sense strand (SS) that is complementary to
 CC ASS, and where most of the pyrimidine nucleotides comprise a sugar
 CC modification. The invention may allow development of compounds with
 CC virucide, antiinflammatory, hepatotropic or cytostatic activities by
 CC modulation (inhibition) of expression or activity of HCV RNA, by RNA
 CC interference. The siNA's of the invention may be used to inhibit
 CC replication of HCV, in cells, tissue explants or organisms, for treating
 CC HCV infection and its consequences (liver failure; hepatocellular cancer
 CC and cirrhosis), and also for drug screening, diagnosis, target
 CC identification and validation, genetic engineering, pharmacogenomics,
 CC studying gene function and gene mapping (for example of single-nucleotide
 CC polymorphisms). The chemical modification improves stability, activity,
 CC cellular uptake and/or binding affinity. The siNA can be directed to
 CC conserved regions of HCV genes, so are active against many different
 CC strains. NOTE: This sequence may contain one or more of several
 CC modifications, including 2'-deoxy-2'-fluoro U or C (u or c); thymidine
 CC (T); inverted deoxy abasic (B); phosphorothioate linkage (s); universal
 CC base 5-nitroindole (X); universal base 3-nitropyrrole (Z). These
 CC modifications are specified in table 3 of the specification (pages 150-
 XX 158).
 XX
 SQ Sequence 21 BP; 4 A; 8 C; 4 G; 2 T; 3 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 10; Length 21;
 Best Local Similarity 94.1%; Pred. No. 6e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 GGCAAGGCGTCTGGTGA 28
 DB 17 GCCAAGGCGTCTGGTGA 1
 RESULT 18
 ACI57909
 ID ACI57909 standard; DNA; 25 BP.
 XX
 AC ACI57909;
 XX
 DT 13-OCT-2003 (first entry)
 XX
 DE Human microarray DNA oligonucleotide SEQ ID NO 57900.
 XX
 KW EST; ss; probe; expressed sequence tag; microarray; gene expression;
 KW genetic variation; biallelic marker; polymorphism; human;
 KW cross-species comparison.
 XX
 OS Homo sapiens.
 XX
 PN US2003104410-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 15-MAR-2002; 2002US-00098263.
 XX
 PR 16-MAR-2001; 2001US-0276759P.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA Mittmann MP;
 XX
 PI WPI; 2003-567953/53.
 DR
 XX
 PT New array of nucleic acid probes, useful for in situ hybridization, in
 PT Southern, Northern or dot-blot hybridization to identify or detect the
 XX sequence or specific mutations of any gene.
 PS Claim 1; SEQ ID NO 57900; 9pp; English.
 XX
 CC The invention discloses a microarray comprising a plurality of nucleic
 CC acid probes including one of 2,018,500 fully defined sequences, or its
 CC perfect match, antisense match, antisense match or antisense mismatch.
 CC Also disclosed is a method of gene expression analysis. The array is used
 CC in monitoring gene expression levels by hybridisation to a DNA library,
 CC in analysis of genetic variation or in hybridisation of tag-labelled
 CC compounds. The nucleic acid probes are specifically designed for analysis
 CC of at least one tag sequence. The method of analysis comprises
 CC hybridising at least one or more nucleic acids to at least two or more
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid
 CC probes are attached to a solid support. The analysis comprises monitoring
 CC gene expression levels, identifying biallelic markers or polymorphisms,
 CC or family members of a gene and a cross-species comparison. Each of the
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid
 CC probes is useful in situ hybridisation, in Southern, Northern or dot-
 CC blot hybridisation to identify or detect the sequence or specific
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
 CC primer extensions or in screening cDNA or genomic libraries or subclones
 CC for additional subclones containing segments of DNA that have been
 CC isolated and previously sequenced. The sequence presented is one of the
 CC nucleic acid probes incorporated in the microarray. Note: The sequence
 CC data for this patent can also be obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 9; Length 25;
 Best Local Similarity 76.0%; Pred. No. 6.2e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 3 CACATGAGTGGCAAGCGCTCTGGTG 27
 DB 1 CACATGAGGCTCAAGTCGTCGCGAG 25
 RESULT 19
 AAD00911
 ID AAD00911 standard; DNA; 30 BP.
 XX
 AC AAD00911;
 XX
 DT 04-OCT-2000 (first entry)
 XX
 DE PCR Primer KXD to construct humanised antibody H24B4k-1 VL region.
 XX
 KW Humanised antibody; H24B4k-1; human 4-1BB receptor protein; mouse;
 KW light chain variable region; VL; heavy chain variable region; VH; Mab;
 KW monoclonal antibody 4B4-1-1; complementarity determining region; CDR; FR;
 KW framework region; treat; transplant rejection; rheumatoid arthritis;
 KW autoimmune disease; immunosuppressant; antirheumatic; antiarthritic;
 KW PCR primer; ss.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO200029445-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 17-NOV-1999; 99WO-KR000689.
 XX
 PR 17-NOV-1998; 98KR-00049177.
 PR 11-MAY-1999; 99KR-00016750.
 XX
 PA (GLDS) LG CHEM LTD.
 XX
 PI Hong HJ, Park SS, Kang YJ, Kang CY, Yoon SK;

XX WPI; 2000-387750/33.
 XX Humanized antibody specific for human 4-1BB, the composition comprising
 PT the antibody useful for treating autoimmune diseases e.g. rheumatoid
 PT arthritis or as an immuno suppressant to prevent graft rejection.
 XX Example 2; Page 63; 83pp; English.
 XX The present sequence is the PCR primer KXD, used to construct the gene
 CC encoding the humanised antibody H24B4k-1 kappa light chain variable
 CC region (VL). The humanised antibody is specific to human 4-1BB receptor
 CC protein and comprises of the complementarity determining region (CDR) of
 CC mouse monoclonal antibody (MAB) 4B4-1-1, grafted on to a human antibody.
 CC In order to increase the antigen binding affinity of this humanised
 CC antibody, about 10 critical amino acid substitutions are made in the
 CC framework region (FR) of humanised VL, to resemble the mouse antibody. It
 CC functions to block human 4-1BB protein receptor. The humanised antibody
 CC can be used to treat autoimmune diseases, especially rheumatoid arthritis
 CC and for immune suppression in transplant rejection. It acts as an
 CC effective immunosuppressant, by inhibiting T cell activation, without any
 CC adverse side effects
 XX Sequence 30 BP; 6 A; 5 C; 9 G; 10 T; 0 U; 0 Other;
 SQ
 Query Match 46.7%; Score 15.4; DB 3; Length 30;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 8 GAGTGGCAGGCGTCTGGTGATACC 32
 |||||
 DB 2 GACTGCCAGGTTTGTGTGATACC 26
 RESULT 20
 AAX789229/c
 ID AAX789229 standard; DNA; 33 BP.
 AC AAT48229;
 XX AAT48229;
 XX 20-OCT-1997 (first entry)
 XX Chloramphenicol acetyl transferase gene primer.
 DE att recombination site; core region; mutation; enhance; recombination;
 KW vector; subcloning; regulation; exchange; primer; PCR; toxic gene; ss.
 XX Synthetic.
 OS
 XX WO9640724-A1.
 PN 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US010082.
 PF
 XX 07-JUN-1995; 95US-00486139.
 PR
 XX (LIFE-) LIFE TECHNOLOGIES INC.
 PA
 XX Hartley JL, Brasch MA;
 PI
 XX WPI; 1997-065168/06.
 DR
 XX Nucleic acids, vectors and methods to obtain chimeric nucleic acid -
 PT using recombinant proteins and engineered recombination sites in vitro or
 PT in vivo.
 XX Example 6; Page 49; 106pp; English.
 PS
 XX AAT48228-29 are primers for amplification of the chloramphenicol acetyl
 CC transferase (CAT) gene. This reporter gene was cloned into a
 CC recombinational cloning gene donor plasmid (containing the uracil DNA
 CC glycosylase gene) using the method and vectors of the invention. The

CC vectors contain recombination sites having a core sequence having at
 CC least one engineered mutation that enhances recombination in vitro in the
 CC formation of a Co-integrate or Product DNA. The nucleic acids, vectors and
 CC methods of the invention are used to obtain chimeric nucleic acid using
 CC recombination proteins and engineered recombination sites in vitro or in
 CC vivo. The improved specificity, speed and yields of the invention for any
 CC facilitates DNA or RNA subcloning, regulation or exchange useful for any
 CC related purpose, e.g. in vitro recombination of DNA segments, and in
 CC vitro or in vivo insertion or modification of transcribed, replicated,
 CC isolated or genomic DNA or RNA
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ
 Query Match 46.7%; Score 15.4; DB 2; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 6 ATGAGTGGCAGGCGTCTGGTGATTA 30
 |||||
 DB 32 ATGAGTGGCAGGCGGCGGTAAATA 8
 RESULT 21
 AAX78962/c
 ID AAX78962 standard; DNA; 33 BP.
 AC AAX78962;
 XX 17-AUG-1999 (first entry)
 XX Oligonucleotide #28 for recombination and cloning method.
 DE Cloning; donor; recombination site; vector; chimeric; ss.
 KW Synthetic.
 OS
 XX WO9921977-A1.
 PN 06-MAY-1999.
 XX 26-OCT-1998; 98WO-US022589.
 PF
 XX 24-OCT-1997; 97US-0065930P.
 PR 23-OCT-1998; 98US-00177387.
 PA (LIFE-) LIFE TECHNOLOGIES INC.
 XX Hartley JL, Brasch MA, Temple GF, Fox DK;
 PI WPI; 1999-303011/25.
 DR New nucleic acid cloning methods.
 XX Disclosure; Page 166; 185pp; English.
 PS
 XX The invention relates to novel methods for cloning or subcloning one or
 CC more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or
 CC in vivo: (1) at least one insert donor molecules (IDMs) comprising one or
 CC more desired nucleic acid segments flanked by at least 2 recombination
 CC sites which do not recombine with each other; (2) one or more vector
 CC donor molecules (VDMs) comprising at least 2 recombination sites which do
 CC not recombine with each other; and (3) one or more site-specific
 CC recombination proteins; (b) incubating the combination to transfer one or
 CC more of the desired segments into one or more of the VDMs, thereby
 CC producing one or more desired product molecules (PMs). The methods can be
 CC used for the efficient and specific recombination of NAM segments. They
 CC can be used to generate chimeric DNA or RNA molecules that have the
 CC desired characteristics and/or nucleic acid segments. The methods can
 CC also be used for changing vectors. The oligonucleotides AAX78935-X78994
 CC are used in the method of the invention
 XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 SQ

Query Match 46.7%; Score 15.4; DB 2; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 22
AAC87893/C
ID AAC87893 standard; DNA; 33 BP.

XX AAC87893;
AC
XX
DT 02-MAR-2001 (first entry)
XX
DE Chloramphenicol acetyl transferase PCR primer SEQ ID NO:28.

XX Core region; recombination site; cloning; chimeric DNA; PCR primer;
KW characteristic; mutation; att site; lox site;
KW chloramphenicol acetyl transferase; CAT; ss.

XX Escherichia coli.

XX US6143557-A.

PN XX

PD 07-NOV-2000.

XX 20-JAN-1999; 99US-00233493.

XX 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

PR 12-JAN-1998; 98US-00005476.

XX (LIFE-) LIFE TECHNOLOGIES INC.

PA Brasch MA, Hartley JL;

PI WPI; 2001-049004/06.

DR Example 6; Col 30; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881), sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. The present sequence represents a PCR primer for chloramphenicol acetyl transferase (CAT), which is used in an example from the present invention

XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 23
AAF55762/C
ID AAF55762 standard; DNA; 33 BP.

XX AAF55762;
AC

XX 12-APR-2001 (first entry)

XX PCR primer CAT right.

XX Recombination site; cloning; CAT; chloramphenicol acetyl transferase;

KW PCR primer; ss.

XX Unidentified.

XX US6171861-B1.

XX 09-JAN-2001.

XX 12-JAN-1998; 98US-00005476.

PR 07-JUN-1995; 95US-00486139.

PR 07-JUN-1996; 96US-00663002.

XX (LIFE-) LIFE TECHNOLOGIES INC.

PA Hartley JL, Brasch MA;

PI WPI; 2001-136877/14.

XX In vitro cloning of nucleic acid involves mixing vectors comprising

PT recombination sites and/or nucleic acid, incubating mixture to produce

PT chimeric molecule, contacting hosts with mixture and selecting host.

XX Example 6; Col 29; 73pp; English.

XX The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a PCR primer for chloramphenicol acetyl transferase (CAT), which was used to exemplify the method of the present invention

XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
|||||
Db 32 ATGAGTGGCAGGCGGGCGGCGTAATA 8

RESULT 24
AAD14456/C
ID AAD14456 standard; DNA; 33 BP.

XX AAD14456;

XX 01-NOV-2001 (first entry)

XX

```
DE Chloramphenicol acetyl transferase gene amplifying CAT right PCR primer.
XX
XX Recombination site; copy number; replicon; recombinatorial cloning;
KW Chloramphenicol acetyl transferase; CAT; PCR primer; DNA-RNA hybrid; ss.
XX
XX Unidentified.
OS
XX
FH Key Location/Qualifiers
FT misc_RNA 1..11
FT /*tag= a
FT /label= RNA
XX
XX US6270969-B1.
PN
XX
XX 07-AUG-2001.
PD
XX
XX 20-JAN-1999; 99US-00233492.
PF
XX
XX 07-JUN-1995; 95US-00486139.
PR
XX 07-JUN-1996; 96US-00663002.
PR
XX (INVI-) INVITROGEN CORP.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2001-488248/53.
DR
XX
XX Methods for apposing nucleic acids comprising an expression signal and a
PT gene/partial gene, using recombinatorial cloning by incubating the
PT nucleic acids in the presence of a recombination protein under conditions
PT for recombination.
XX
XX Example 6; Col 29; 76pp; English.
PS
XX
XX The invention relates to a method for apposing an expression signal and a
CC gene or partial gene, using recombinatorial cloning. The method incubates
CC nucleic acids comprising the expression signal and the gene/partial gene
CC in the presence of a recombination protein under conditions sufficient to
CC cause recombination and therefore appose the expression signal and the
CC gene or partial gene. The methods are useful for apposing an expression
CC signal and a gene or partial gene using recombinatorial cloning. The
CC methods are also useful for changing vectors, constructing genes for
CC fusion proteins, changing copy number, changing replicons, cloning into
CC phages, and cloning e.g., PCR products (with an attB site at one end and
CC a loxP site at the other end), genomic DNAs, and cDNAs. The methods are
CC highly specific, rapid, and less labour intensive than prior art methods.
CC The present sequence is a PCR primer used for amplifying Chloramphenicol
CC acetyl transferase (CAT) gene used in the exemplification of the
CC invention
XX
XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
SQ
Query Match 46.7%; Score 15.4; DB 4; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
Db ||||| ||||| ||||| |||||
32 ATGAGTGGCAGGCGGCGGCGTAATA 8
RESULT 25
ACD28423/c
ID ACD28423 standard; DNA; 33 BP.
XX
XX ACD28423;
AC
XX
XX 02-OCT-2003 (first entry)
DT
XX
XX CAT 5' uracil extension primer CAT right.
DE
XX
XX CAT; 5' uracil extension; vector donor DNA; flanking recombination site;
KW ss; chloramphenicol acetyl transferase; PCR; primer.
XX
```

```
XX Synthetic.
OS
XX US2003064515-A1.
PN
XX
XX 03-APR-2003.
PD
XX
XX 30-JAN-2002; 2002US-00058291.
PF
XX
XX 07-JUN-1995; 95US-00486139.
PR
XX 07-JUN-1996; 96US-00663002.
PR
XX 20-JAN-1999; 99US-00233493.
PR
XX 02-NOV-1999; 99US-00432085.
PR
XX (HART/) HARTLEY J L.
XX (BRAS/) BRASCH M A.
XX
XX Hartley JL, Brasch MA;
XX
XX WPI; 2003-540791/51.
DR
XX
XX New Vector Donor DNA molecule for recombinational cloning using
PT engineered recombination sites, comprises first and second DNA segments
PT that do not recombine with each other and that contain a Selectable
PT marker.
XX
XX Example 6; Page 17; 71pp; English.
PS
XX
XX The invention relates to a vector donor DNA molecule comprising a first
CC DNA segment and a second DNA segment containing at least one selectable
CC marker. The first and second segments are separated either by, in a
CC circular vector donor, a first and a second recombination site, or in a
CC linear vector donor, at least a first recombination site, where each pair
CC of flanking recombination sites are engineered and do not recombine with
CC each other. The nucleic acid molecule, vectors and methods are useful for
CC moving or exchanging segments of DNA molecules using engineered
CC recombination sites and recombination proteins to provide chimeric DNA
CC molecules that have the desired characteristic(s) and/or DNA segment(s).
CC The present sequence represents the Chloramphenicol acetyl transferase,
CC CAT 5' uracil extension primer CAT right
XX
XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
SQ
Query Match 46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 6 ATGAGTGGCAGGCGCTCTGGTGATA 30
Db ||||| ||||| ||||| |||||
32 ATGAGTGGCAGGCGGCGGCGTAATA 8
RESULT 26
ACD28602/c
ID ACD28602 standard; DNA; 33 BP.
XX
XX ACD28602;
AC
XX
XX 09-OCT-2003 (first entry)
DT
XX
XX CAT 5' uracil extension primer CAT right.
DE
XX
XX CAT; 5' uracil extension; cointegrate DNA; flanking recombination site;
KW ss; chloramphenicol acetyl transferase; PCR; primer.
XX
XX Synthetic.
OS
XX
XX US2003068799-A1.
PN
XX
XX 10-APR-2003.
PD
XX
XX 06-JUN-2002; 2002US-00162879.
PF
XX
XX
```

```
PR 07-JUN-1995; 95US-00486139.
PR 07-JUN-1996; 96US-00663002.
PR 20-JAN-1999; 99US-00233493.
PR 02-NOV-1999; 99US-00432085.
XX
XX (INVI-) INVITROGEN CORP.
PA
XX
XX Hartley JL, Brasch MA;
XX WPI; 2003-540884/51.
XX
XX Making Cointegrate DNA molecule, by combining recombination sites
PT flanking the desired DNA segment in insert donor DNA, with the
PT recombination sites of vector donor DNA, using site specific
PT recombination protein.
XX
XX Example 6; Page 17; 71pp; English.
XX
XX The invention relates to a method of making a cointegrate DNA molecule.
CC The method is useful for making a cointegrate DNA molecule. The method is
CC useful for a variety of DNA exchanges, such as subcloning of DNA, in
CC vitro or in vivo. The method enables efficient and specific recombination
CC of DNA segments using recombination proteins. The method is highly
CC specific, rapid and less labour intensive. The improved specificity,
CC yield and speed of the method facilitates DNA or RNA subcloning,
CC regulation and exchange useful for other related purposes. Since single
CC molecules of the recombinations product can be introduced into a
CC biological host, propagation of the desired product DNA in the absence of
CC other DNA molecules is more readily realised. Reaction conditions can be
CC freely adjusted in vitro to optimise enzyme activities. The present
CC sequence represents the chloramphenicol acetyl transferase, CAT 5' uracil
CC extension primer CAT right
XX
XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
SQ
Query Match 46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
DB 32 ATGAGTGGCAGCGCGGGCGGTAATA 8
RESULT 27
ADA38189/c
ID ADA38189 standard; DNA; 33 BP.
XX
XX ADA38189;
XX
XX 20-NOV-2003 (first entry)
XX
XX PCR primer CAT right containing a 12-base 5' extension of uracil bases.
XX
XX engineered recombination site; cloning; recombinase; subcloning; attB;
XX attP; attL; attR; selectable marker; cointegrate; ss; primer; PCR;
XX DNA/RNA hybrid; CAT right; chloramphenicol acetyl transferase; pACYC184.
XX
XX Synthetic.
XX Unidentified.
XX
XX US2003054552-A1.
XX
XX 20-MAR-2003.
XX
XX 30-JAN-2002; 2002US-00058292.
XX
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 20-JAN-1999; 99US-00233493.
XX 02-NOV-1999; 99US-00432085.
XX (HART/) HARTLEY J L.
PA
(PBRAS/) BRASCH M A.
XX
XX Hartley JL, Brasch MA;
XX WPI; 2003-585168/55.
XX
XX New Vector Donor DNA molecule, useful for recombinational cloning
PT purposes, comprises a first and a second DNA segment that contains a
PT selectable marker and is separated by a pair of flanking, engineered
PT recombination sites.
XX
XX Example 6; Page 18; 72pp; English.
XX
XX This invention relates to novel DNA and vectors having engineered
CC recombination sites for use in a cloning method that enables efficient
CC and specific recombination of DNA segments using recombination proteins
CC including recombinases. As such, it provides a method for obtaining
CC chimeric nucleic acids with the desired characteristics, facilitating DNA
CC or RNA subcloning, regulation and/ or exchange. The recombination site is
CC derived from attB attP, attL or attR, where the att site is att1, att2 or
CC att3. Engineered mutations of the att sites (either one or multiple
CC mutations) can enhance specificity or efficiency of the recombination
CC reaction and the properties of the product DNA molecules. Accordingly,
CC the present invention describes a nucleic acid molecule comprising at
CC least one DNA segment having at least two engineered recombination sites
CC flanking a selectable marker and/ or a desired DNA segment. Furthermore,
CC at least one of the engineered sites must enhance recombination in vitro
CC to form a cointegrate or product DNA molecule. This oligonucleotide
CC sequence is the PCR primer CAT right used to amplify the chloramphenicol
CC acetyl transferase (CAT) gene from plasmid pACYC184, and containing a 12-
CC base 5' extension of uracil bases in an exemplification of the invention.
XX
XX Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
SQ
Query Match 46.7%; Score 15.4; DB 9; Length 33;
Best Local Similarity 76.0%; Pred. No. 6.4e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
DB 32 ATGAGTGGCAGCGCGGGCGGTAATA 8
RESULT 28
AAD60585/c
ID AAD60585 standard; DNA; 33 BP.
XX
XX AAD60585;
XX
XX 18-DEC-2003 (first entry)
XX
XX Chloramphenicol acetyl transferase gene amplifying primer, CAT right.
XX
XX Recombinational cloning; DNA exchange; core region; CAT; PCR; primer;
XX chloramphenicol acetyl transferase; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..11
XX FT /*tag= a
XX FT /label= RNA
XX
XX US2003100110-A1.
XX
XX 29-MAY-2003.
XX
XX 02-NOV-1999; 99US-00432085.
XX
XX 07-JUN-1995; 95US-00486139.
XX 07-JUN-1996; 96US-00663002.
XX 02-NOV-1999; 99US-00432085.
XX (HART/) HARTLEY J L.
```

PA (HART/) HARTLEY J L.
 PA (BRAS/) BRASCH M A.
 PI Hartley JL, Brasch MA;
 XX WPI; 2003-730143/69.
 DR
 XX
 PT New Vector Donor DNA molecule for recombinational cloning using
 PT engineered recombination sites, comprises first and second DNA segments
 PT that do not recombine with each other and that contain a Selectable
 PT marker.
 XX
 XX Example 6; Page 17; 71pp; English.
 XX
 XX The invention relates to a vector donor DNA molecule which comprises
 CC first and second DNA segments that do not recombine with each other and
 CC that contain a selectable marker. The invention also relates to a method
 CC for recombinational cloning using engineered recombination sites. The
 CC invention is useful for moving or exchanging segments of DNA molecules
 CC using engineered recombination sites and recombination proteins to
 CC provide chimeric DNA molecules that have the desired characteristic(s)
 CC and/or DNA segment(s). The present sequence is a PCR primer used for
 CC amplifying chloramphenicol acetyl transferase (CAT) gene. This sequence
 CC is used to illustrate the method of the invention
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 10; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 6 ATGAGTGGCAAGGCGTCTGTGTGATA 30
 Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 RESULT 29
 ID ADL93443/c
 XX ADL93443 standard; DNA; 33 BP.
 AC ADL93443;
 XX
 XX 01-JUL-2004 (first entry)
 XX Chloramphenicol acetyl transferase (CAT) primer seqid 28.
 DE
 XX recombination protein; recombination site; Insert Donor DNA;
 KW Vector Donor DNA; repression cassette; DNA cloning;
 KW recombination site core region; chloramphenicol acetyl transferase; CAT;
 KW PCR; primer; ss.
 XX
 XX Unidentified.
 OS
 XX US6720140-B1.
 FN 13-APR-2004.
 PD
 XX 04-FEB-2000; 2000US-00498074.
 XX
 XX 07-JUN-1995; 95US-00486139.
 PR 07-JUN-1996; 96US-00663002.
 PR 12-JAN-1998; 98US-00005476.
 XX
 XX (INVI-) INVITROGEN CORP.
 PA
 XX Hartley JL, Brasch MA;
 PI WPI; 2004-313648/29.
 DR
 XX New composition comprising recombination proteins and isolated nucleic
 PT acid molecule comprising recombination site, useful for moving or
 PT exchanging segments of DNA molecules to provide chimeric DNA molecules.
 XX

PS Example 6; SEQ ID NO 28; 80pp; English.
 XX
 XX The invention describes a composition comprising recombination proteins
 CC and an isolated nucleic acid molecule comprising a recombination site.
 CC The composition comprises one or more isolated recombination proteins and
 CC at least one Insert Donor DNA molecule comprises: at least a first
 CC recombination site, containing at least one mutation, where the mutation
 CC removes one or more stop codons from the recombination site and avoids
 CC hairpin formation; a first recombination site and a second recombination
 CC site where the first and second recombination sites do not recombine with
 CC each other, and at least one Vector Donor DNA molecule comprising a first
 CC recombination site and a second recombination site, where the first and
 CC second recombination sites do not recombine with each other. The Vector
 CC Donor DNA molecule comprises a repression cassette encoding a repressor
 CC and a Selectable marker that is repressed by the repressor where the
 CC Selectable marker and the repression cassette are on different DNA
 CC segments separated from each other by at least one recombination site; at
 CC least a first recombination site containing at least one nucleic acid
 CC sequence selected from a nucleic acid sequence comprising 25 bp (SEQ ID NO. 1-
 CC to one or more of a nucleic acid sequence comprising 25 bp (SEQ ID NO. 1-
 CC 16). Also described are: a kit for in vitro cloning of DNA segments
 CC comprising one or more isolated recombination proteins and at least one
 CC Insert Donor DNA molecule; a method for in vitro cloning; a method for
 CC making a reaction mixture; and a reaction mixture made by the method
 CC above. The compositions, methods and kits of the invention are useful for
 CC moving or exchanging segments of DNA molecules using engineered
 CC recombination sites and recombination proteins to provide chimeric DNA
 CC molecules that have the desired characteristics and/or DNA segments. This
 CC sequence represents a primer used to isolate DNA encoding chloramphenicol
 CC acetyl transferase (CAT) used in the creation of a vector for
 CC recombinational cloning.
 XX
 SQ Sequence 33 BP; 5 A; 17 C; 3 G; 3 T; 5 U; 0 Other;
 Query Match 46.7%; Score 15.4; DB 12; Length 33;
 Best Local Similarity 76.0%; Pred. No. 6.4e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 6 ATGAGTGGCAAGGCGTCTGTGTGATA 30
 Db 32 ATGAGTGGCAGGCGGGCGGTAATA 8
 RESULT 30
 ID AAZ56255
 XX AAZ56255 standard; DNA; 34 BP.
 AC AAZ56255;
 XX
 XX 15-MAR-2000 (first entry)
 DT
 XX pIVCAT1 construction oligonucleotide sequence SEQ ID NO:24.
 DE
 XX Recombinant negative strand viral RNA template; virus particle;
 KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
 KW packaging; ss.
 XX
 XX Influenza virus.
 OS
 XX Synthetic.
 XX
 XX US6001634-A.
 FN 14-DEC-1999.
 PD
 XX 29-JUN-1998; 98US-00106377.
 PF
 XX 28-AUG-1989; 89US-00399728.
 PR 21-NOV-1989; 89US-00440053.
 PR 22-MAY-1990; 90US-00527237.
 PR 04-AUG-1992; 92US-00925061.
 PR 01-FEB-1994; 94US-00190698.
 PR 01-JUN-1994; 94US-00252508.
 XX

```

PA (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
CC The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous
CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 34 BP; 8 A; 5 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.5e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
DB 7 ATGAGTGGCAGGGCGGGCGTAATA 31
RESULT 31
AAZ56253
ID AAZ56253 standard; DNA, 34 BP.
XX
AC AAZ56253;
XX
DT 15-MAR-2000 (first entry)
XX
DE CAT gene expression/packaging oligonucleotide SEQ ID NO:22.
XX
KW Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
PN US6001634-A.
XX
PD 14-DEC-1999.
XX
PF 29-JUN-1998; 98US-00106377.
XX
PR 28-AUG-1989; 89US-00399728.
PR 21-NOV-1989; 89US-00440053.
PR 22-MAY-1990; 90US-00527237.
PR 04-AUG-1992; 92US-00925061.
PR 01-FEB-1994; 94US-00190698.
PR 01-JUN-1994; 94US-00252508.
XX
XX (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
CC The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous
CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 34 BP; 8 A; 5 C; 15 G; 6 T; 0 U; 0 Other;
Query Match 46.7%; Score 15.4; DB 3; Length 34;
Best Local Similarity 76.0%; Pred. No. 6.5e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 6 ATGAGTGGCAAGCGCTCTGGTGATA 30
DB 7 ATGAGTGGCAGGGCGGGCGTAATA 31
RESULT 32
AAZ56254/c
ID AAZ56254 standard; DNA; 38 BP.
XX
AC AAZ56254;
XX
DT 15-MAR-2000 (first entry)
XX
DE CAT gene expression/packaging oligonucleotide SEQ ID NO:23.
XX
KW Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.
XX
OS Influenza virus.
OS Synthetic.
XX
PN US6001634-A.
XX
PD 14-DEC-1999.
XX
PF 29-JUN-1998; 98US-00106377.
XX
PR 28-AUG-1989; 89US-00399728.
PR 21-NOV-1989; 89US-00440053.
PR 22-MAY-1990; 90US-00527237.
PR 04-AUG-1992; 92US-00925061.
PR 01-FEB-1994; 94US-00190698.
PR 01-JUN-1994; 94US-00252508.
XX
XX (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.
XX
PI Palese P, Garcia-Sastre A;
XX
DR WPI; 2000-071660/06.
XX
XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.
XX
PS Example; Col 65; 67pp; English.
XX
CC The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of

```


CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous
CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 38 BP; 7 A; 16 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 46.7%; Score 15.4; DB 3; Length 38;

Best Local Similarity 76.0%; Pred. No. 6.6e+03;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAGGCGTCTGGTGATA 30

Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 33

AAZ56256/C
ID AAZ56256 standard; DNA; 38 BP.

AC AAZ56256;

XX 15-MAR-2000 (first entry)

DE pIVCAT1 construction oligonucleotide sequence SEQ ID NO:25.

XX Recombinant negative strand viral RNA template; virus particle;
KW RNA directed RNA polymerase complex; expression; chimeric virus; vaccine;
KW packaging; ss.

XX Influenza virus.

OS Synthetic.

XX US6001634-A.

PD 14-DEC-1999.

XX 29-JUN-1998; 98US-00106377.

XX 28-AUG-1989; 89US-00399728.

PR 21-NOV-1989; 89US-00440053.

PR 22-MAY-1990; 90US-00527237.

PR 04-AUG-1992; 92US-00925061.

PR 01-FEB-1994; 94US-00190698.

PR 01-JUN-1994; 94US-00252508.

XX (PALE/) PALESE P.

PA (GARC/) GARCIA-SASTRE A.

PI Palese P, Garcia-Sastre A;

XX WPI; 2000-071660/06.

XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems.

PS Example; Col 65; 67pp; English.

XX The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of influenza
CC virus, with each segment comprising the reverse complement of a mRNA
CC coding sequence operatively linked to a binding site specific for an RNA-
CC directed RNA polymerase of a negative strand RNA virus. The recombinant
CC negative strand virus RNA templates may be used to express heterologous
CC gene products in appropriate host cell systems and/or to construct
CC recombinant viruses that express, package and/or present the heterologous

CC gene product. The expression products and chimeric viruses may be used in
CC vaccine formulations. AAY57746 to AAY57748, and AAZ56234 to AAZ56290,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 38 BP; 7 A; 16 C; 6 G; 9 T; 0 U; 0 Other;

Query Match 46.7%; Score 15.4; DB 3; Length 38;

Best Local Similarity 76.0%; Pred. No. 6.6e+03;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 ATGAGTGGCAGGCGTCTGGTGATA 30

Db 32 ATGAGTGGCAGGCGGCGGCGTAATA 8

RESULT 34

ADJ14718/C

ID ADJ14718 standard; DNA; 41 BP.

AC ADJ14718;

XX 20-MAY-2004 (first entry)

DE Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 282.

XX SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.

XX Unidentified.

XX US2003235848-A1.

XX 25-DEC-2003.

XX 11-APR-2003; 2003US-00411954.

XX 11-APR-2002; 2002US-0371819P.

XX (NEVI/) NEVILLE M.

XX (INDI/) INDIG M D A.

XX Neville M, Indig MDA;

XX WPI; 2004-070577/07.

XX Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT with the primer set and detecting at least one of the footprint regions
PT with the assay probe.

XX Example 3; SEQ ID NO 282; 55pp; English.

XX The invention relates to a novel method for characterising a cytochrome
CC p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC comprises providing a sample with at least Y target sequences, a primer
CC set comprising a forward and a reverse primer sequence for each of the Y
CC target sequences and at least one assay probe configured to detect a
CC footprint region, amplifying the Y target sequences with the primer set
CC and detecting at least one of the footprint regions with the assay probe.
CC The method of the invention may be useful for characterising a cytochrome
CC p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC (cytochrome p450 2D6; CYP2D6)-related target oligonucleotide of the
CC invention.

XX Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 46.1%; Score 15.2; DB 12; Length 41;

Best Local Similarity 85.0%; Pred. No. 8.1e+03;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAGGCGTCTGGTGA 28

Db 37 AGTGGCAGGCGGCGCTGGTGA 18

```

RESULT 35
ADJ14522/c
ID ADJ14522 standard; DNA; 41 BP.
XX
AC ADJ14522;
XX
DT 20-MAY-2004 (first entry)
XX
DE Debrisoquine 4-hydroxylase (CYP2D6)-related target DNA - SEQ ID 85.
XX
XX SNP; single nucleotide polymorphism; cytochrome p450; CYP allele;
KW debrisoquine 4-hydroxylase; 2D6; CYP2D6; human; ss; target.
XX
OS Unidentified.
XX
XX US2003235848-A1.
XX
XX 25-DEC-2003.
XX
XX 11-APR-2003; 2003US-00411954.
XX
XX 11-APR-2002; 2002US-0371819P.
XX
XX (NEVI/) NEVILLE M.
XX (INDI/) INDIG M D A.
XX
XX Neville M, Indig MDA;
XX
XX WPI; 2004-070577/07.
XX
XX Characterizing a cytochrome p450 allele by amplifying Y target sequences
PT with the primer set and detecting at least one of the footprint regions
PT with the assay probe.
XX
XX Example 3; SEQ ID NO 85; 55pp; English.
XX
XX The invention relates to a novel method for characterising a cytochrome
CC p450 (CYP) allele (or single nucleotide polymorphism [SNP]) which
CC comprises providing a sample with at least Y target sequences, a primer
CC set comprising a forward and a reverse primer sequence for each of the Y
CC target sequences and at least one assay probe configured to detect a
CC footprint region, amplifying the Y target sequences with the primer set
CC and detecting at least one of the footprint regions with the assay probe.
CC The method of the invention may be useful for characterising a cytochrome
CC p450 allele. The current sequence is that of a debrisoquine 4-hydroxylase
CC [cytochrome p450 2D6; CYP2D6]-related target oligonucleotide of the
CC invention.
XX
XX Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 46.1%; Score 15.2; DB 12; Length 41;
Best Local Similarity 85.0%; Pred. No. 8.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGTCTGGTGA 28
Db ||||| ||| |||||
37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 36
ADJ14522/c
ID ADO60821 standard; DNA; 41 BP.
XX
XX ADO60821;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human debrisoquine 4-hydroxylase, CYP2D6 target #168.
XX
XX oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW cytochrome p450; human; ss.
XX
XX Homo sapiens.
XX
XX US2004096874-A1.
XX
XX 20-MAY-2004.
XX
XX 10-JUL-2003; 2003US-00617070.
XX
XX 11-APR-2002; 2002US-0371819P.
XX
XX 11-APR-2003; 2003US-00411954.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI

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OS Homo sapiens.
XX
XX US2004096874-A1.
XX
XX 20-MAY-2004.
XX
XX 10-JUL-2003; 2003US-00617070.
XX
XX 11-APR-2002; 2002US-0371819P.
XX
XX 11-APR-2003; 2003US-00411954.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
XX WPI; 2004-447680/42.
XX
XX New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
XX Example 1; SEQ ID NO 282; 172pp; English.
XX
XX The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles or for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
XX Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;
SQ
Query Match 46.1%; Score 15.2; DB 12; Length 41;
Best Local Similarity 85.0%; Pred. No. 8.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 AGTGGCAAGGCGTCTGGTGA 28
Db ||||| ||| |||||
37 AGTGGCAGGGGCGCTGGTGA 18

RESULT 37
ADJ14522/c
ID ADO60624 standard; DNA; 41 BP.
XX
XX ADO60624;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human debrisoquine 4-hydroxylase, CYP2D6 target #34.
XX
XX oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW cytochrome p450; human; ss.
XX
XX Homo sapiens.
XX
XX US2004096874-A1.
XX
XX 20-MAY-2004.
XX
XX 10-JUL-2003; 2003US-00617070.
XX
XX 11-APR-2002; 2002US-0371819P.
XX
XX 11-APR-2003; 2003US-00411954.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI

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PI Aizenstein BD, Davey K;
XX WPI; 2004-447680/42.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
XX Example 3; SEQ ID NO 85; 172bp; English.
PS
XX The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated
CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
SQ Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 46.1%; Score 15.2; DB 12; Length 41;
Best Local Similarity 85.0%; Pred. NO. 8.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 9 AGTGGCAGGGCGCTCGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGCGCTCGGTGA 18
||||| ||| |||||
RESULT 38
ADO60921/c
ID ADO60921 standard; DNA; 41 BP.
XX
AC ADO60921;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human debrisoquine 4-hydroxylase, CYP2D6 target #108.
XX
KW oligonucleotide detection assay; debrisoquine 4-hydroxylase; CYP2D6;
KW cytochrome p450; human; ss.
XX
OS Homo sapiens.
XX
PW US2004096874-A1.
XX
PD 20-MAY-2004.
XX
PF 10-JUL-2003; 2003US-00617070.
XX
PR 11-APR-2002; 2002US-0371819P.
PR 11-APR-2003; 2003US-00411954.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Neville M, Indig MDA, Cao F, Oldenburg MC, Koelbl JA;
PI Aizenstein BD, Davey K;
XX
DR WPI; 2004-447680/42.
XX
PT New kit comprising an oligonucleotide detection assay for detecting the
PT number of CYP2D6 gene copies in a sample and for identifying CYP2D6
PT associated polymorphisms.
XX
XX Example 4; SEQ ID NO 382; 172bp; English.
PS
XX The invention relates to a kit which comprises an oligonucleotide
CC detection assay configured for detecting the number of debrisoquine 4-
CC hydroxylase, CYP2D6, gene copies present in a sample and configured to
CC identify the presence or absence of at least two CYP2D6 associated

CC polymorphisms. The kit and methods are useful for characterising
CC cytochrome p450 genes and alleles for developing and optimising
CC nucleic acid detection assays for use in basic research, clinical
CC research and for the development of clinical detection assays. The
CC present sequence represents a human debrisoquine 4-hydroxylase, CYP2D6
CC target.
XX
SQ Sequence 41 BP; 5 A; 20 C; 10 G; 6 T; 0 U; 0 Other;
Query Match 46.1%; Score 15.2; DB 12; Length 41;
Best Local Similarity 85.0%; Pred. NO. 8.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 9 AGTGGCAGGGCGCTCGGTGA 28
||||| ||| |||||
Db 37 AGTGGCAGGGCGCTCGGTGA 18
||||| ||| |||||
RESULT 39
ABK88600
ID ABK88600 standard; DNA; 33 BP.
XX
AC ABK88600;
XX
DT 21-OCT-2002 (first entry)
XX
DE Nuclear factor kappa-B DNA binding subunit 10.23, PCR primer #1.
XX
KW Nuclear factor Kappa-B DNA binding subunit 10.23; malignant tumour;
KW inflammation; immunological disease; development disorder; haemopathy;
KW human immunodeficiency virus; HIV infection; PCR; primer; ss.
XX
OS Unidentified.
XX
PW CN1339458-A.
XX
PD 13-MAR-2002.
XX
PF 23-AUG-2000; 2000CN-00119736.
XX
PR 23-AUG-2000; 2000CN-00119736.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PW WPI; 2002-464049/50.
XX
PT New polypeptide-nuclear factor kappa-B DNA binding subunit 10.23 and
PT polynucleotide for encoding such polypeptide.
XX
PS Example 4; Page 18 (Disclosure); 33pp; Chinese.
XX
CC The invention describes a new kind of polypeptide, nuclear factor Kappa-B
CC DNA binding subunit 10.23, polynucleotides encoding the polypeptide and a
CC DNA recombination process to produce the polypeptide. Also disclosed is a
CC method of applying the polypeptide in treating various diseases, such as
CC malignant tumours, inflammations, immunological diseases, development
CC disorder, haemopathy and HIV infection. The present invention also
CC discloses the antagonist resisting the polypeptide and its treatment
CC effect. The present invention also discloses the application of the
CC polynucleotide for encoding nuclear factor Kappa-B DNA binding subunit
CC 10.23. This sequence represents a PCR primer used to amplify DNA encoding
CC the nuclear factor kappa-B DNA binding sub-unit 10.23
XX
SQ Sequence 33 BP; 9 A; 12 C; 7 G; 5 T; 0 U; 0 Other;
Query Match 45.5%; Score 15; DB 6; Length 33;
Best Local Similarity 67.7%; Pred. NO. 9.6e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 2 CCACATGATGGCAGGGCGCTCGGTGATACC 32
||||| ||||| ||||| |||||

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Db      3 CCATATGATGAGCAAGGAGACTGCCCATCCC 33

RESULT 40
ADC64088/c
ID      ADC64088 standard; DNA; 38 BP.
XX
AC      ADC64088;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Polyhydroxyalkanoate-related PCR primer #36.
XX
KW      polyhydroxyalkanoate-containing structure; PHA-containing structure;
KW      PHA synthase; polyhydroxyalkanoate synthase; 3-hydroxyacyl coenzyme A;
KW      pigment dispersant; electrophotography toner; laminated structure;
KW      OHP film; microcapsule pigment ink; electrophoresis particle;
KW      electrophoresis display; colour filter; enzyme; ss; primer; PCR.
XX
OS      Unidentified.
XX
PN      EP1275728-A1.
XX
PD      15-JAN-2003.
XX
PF      10-JUL-2002; 2002EP-00015374.
XX
PR      10-JUL-2001; 2001JP-00210052.
PR      13-JUN-2002; 2002JP-00172978.
XX
PA      (CANO ) CANON KK.
XX
PI      Nomoto T, Yano T, Kozaki S, Honma T;
XX      WPI; 2003-459566/44.
XX
PT      Manufacturing polyhydroxyalkanoate-containing structure useful as toner
PT      for electrophotography, by immobilizing polyhydroxyalkanoate synthase on
PT      base material and synthesizing polyhydroxyalkanoate on base material.
XX
PS      Example 16; SEQ ID NO 87; 277bp; English.
XX
CC      The invention comprises a method for producing a polyhydroxyalkanoate
CC      (PHA)-containing structure. The method involves immobilising a PHA
CC      synthase enzyme on a base material surface and then synthesising PHA
CC      using 3-hydroxyacyl coenzyme A as a substrate. The method of the
CC      invention is useful for manufacturing a PHA-containing structure. The PHA
CC      containing structure has a wide range of applications as a variety of
CC      functional structures, such as: a pigment dispersant of excellent
CC      dispersion stability; a toner for electrophotography of excellent
CC      electrostatic property; and the laminated structure as an OHP film. The
CC      structure is also useful for microcapsule pigment ink of excellent
CC      dispersion stability, an electrophoresis particle for electrophoresis
CC      display, and colouring composition for a colour filter. The present DNA
CC      sequence represents a PCR primer that was used in the exemplification of
CC      the invention.
XX
SQ      Sequence 38 BP; 8 A; 10 C; 12 G; 8 T; 0 U; 0 Other;

Query Match      45.5%; Score 15; DB 10; Length 38;
Best Local Similarity 67.7%; Pred. No. 9.8e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY      2 CCACATGAGTGGCAGGCGCTCTGGTGATACC 32
      |||||
Db      38 CACGTGACCAGCAGCCGCGTTATTGATACC 8
      |||||

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